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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 103 Seconds
(without alignments)
6217.605 Million cell updates/sec

Title: US-09-904-584-1

Perfect score: 1154

Sequence: 1 atgacgcacccgcacacagat.....ccagatgacacgctgtgga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1146	99.3	1182	4	US-09-016-434-1417
2	1143	99.0	1143	4	US-09-341-446B-1
3	1142	99.0	1142	3	US-08-765-743-1
4	1137.8	98.6	1284	4	US-09-341-446B-3
5	1001	86.7	1275	4	US-09-341-446B-5
6	996.2	86.3	1275	4	US-09-341-446B-7
7	910.8	78.9	1408	4	US-09-214-904-5
8	910.8	78.9	1410	4	US-08-147-592A-1
9	910.8	78.9	1410	4	US-08-292-694A-1
10	871.2	75.5	1000	4	US-08-147-592A-11
11	871.2	75.5	1000	4	US-08-292-694A-11
12	448	38.8	2135	3	US-08-430-286A-1
13	446.4	38.7	1618	3	US-08-889-108-1
14	446.4	38.7	1618	3	US-08-889-108-3
15	446.4	38.7	1618	3	US-08-120-601B-1
16	446.4	38.7	1618	3	US-08-120-601B-3
17	446.4	38.7	1618	5	PCT-US94-10358-1
18	446.4	38.7	1618	5	PCT-US94-10358-3
19	434.8	37.7	1610	5	US-08-889-108-7
20	434.8	37.7	1610	5	PCT-US94-10358-7
21	434.8	37.7	2160	4	US-08-188-275A-1
22	434.8	37.7	2162	4	US-09-351-198-1
23	434.8	37.7	2162	4	US-09-113-426-1
24	434.8	37.7	2162	4	US-09-016-434-1379
25	434.8	37.7	2162	4	US-09-355-709C-7
26	432.4	37.5	1334	4	US-09-761-962A-3
27	432.4	37.5	1365	4	US-09-761-962A-11

28	432.4	37.5	1423	4	US-09-761-962A-1	Sequence 1, Appl
29	432.4	37.5	1610	4	US-09-761-962A-16	Sequence 16, Appl
30	432.4	37.5	1729	4	US-09-761-962A-9	Sequence 9, Appl
31	432.4	37.5	2045	4	US-09-761-962A-10	Sequence 10, Appl
32	430.8	37.3	2229	4	US-09-214-904-1	Sequence 1, Appl
33	429.2	37.2	1542	4	US-09-761-962A-4	Sequence 4, Appl
34	429.2	37.2	1981	3	US-08-387-707-15	Sequence 15, Appl
35	429.2	37.2	1981	4	US-08-405-271A-15	Sequence 15, Appl
36	422.6	36.6	1829	2	US-08-411-859-1	Sequence 1, Appl
37	422.6	36.6	1829	3	US-08-387-707-7	Sequence 7, Appl
38	422.6	36.6	1829	3	US-08-405-271A-7	Sequence 7, Appl
39	422.6	36.6	2218	4	US-09-214-904-3	Sequence 3, Appl
40	422.6	36.6	2219	4	US-08-432-174A-1	Sequence 1, Appl
41	422.6	36.6	2272	3	US-08-147-592A-3	Sequence 3, Appl
42	422.6	36.6	2272	4	US-08-292-694A-3	Sequence 3, Appl
43	411	35.6	1346	4	US-09-761-962A-12	Sequence 12, Appl
44	408.6	35.4	1773	4	US-09-016-434-1405	Sequence 1405, Ap
45	399	34.6	998	4	US-08-432-174A-3	Sequence 3, Appl
46	393.4	34.1	1805	4	US-08-405-271A-18	Sequence 18, Appl
47	393.4	34.1	1973	4	US-09-016-434-1391	Sequence 1391, Ap
48	393.4	34.1	1973	4	US-09-023-655-1417	Sequence 1417, Ap
49	393.4	34.1	3205	4	US-09-976-594-171	Sequence 171, App
50	387.6	33.6	1238	4	US-09-761-962A-2	Sequence 2, Appl
51	387.6	33.6	1257	4	US-09-761-962A-5	Sequence 5, Appl
52	377.6	32.7	1567	3	US-08-889-108-16	Sequence 16, Appl
53	377.6	32.7	1567	5	PCT-US94-10358-16	Sequence 16, Appl
54	377.6	32.7	2706	2	US-08-454-549-1	Sequence 1, Appl
55	377.6	32.7	2706	3	US-08-454-552-1	Sequence 1, Appl
56	372.8	32.3	2706	3	US-08-676-351-1	Sequence 1, Appl
57	368	31.9	1452	1	US-08-149-093A-3	Sequence 3, Appl
58	368	31.9	1452	3	US-09-048-916B-3	Sequence 3, Appl
59	368	31.9	1452	1	US-08-911-245-3	Sequence 3, Appl
60	368	31.9	1452	2	US-08-553-058C-3	Sequence 3, Appl
61	368	31.9	1452	3	US-08-514-451A-3	Sequence 3, Appl
62	368	31.9	1452	3	US-09-170-331-3	Sequence 3, Appl
63	368	31.9	1452	4	US-09-048-916B-3	Sequence 3, Appl
64	367.8	31.9	1134	4	US-09-743-871B-14	Sequence 14, Appl
65	367.8	31.9	1330	3	US-08-147-592A-5	Sequence 5, Appl
66	367.8	31.9	1330	4	US-08-292-694A-5	Sequence 5, Appl
67	367.8	31.9	2600	4	US-08-986-209A-1	Sequence 1, Appl
68	357	30.9	1177	4	US-09-743-871B-13	Sequence 13, Appl
69	344.8	29.9	2600	1	US-08-147-949A-1	Sequence 1, Appl
70	336.2	29.1	1223	4	US-09-743-871B-11	Sequence 11, Appl
71	336.2	29.1	1283	4	US-09-743-871B-12	Sequence 12, Appl
72	327.4	28.4	2634	4	US-09-743-871B-8	Sequence 8, Appl
73	327	28.3	1256	4	US-09-743-871B-9	Sequence 9, Appl
74	319.6	27.7	830	3	US-08-387-707-13	Sequence 13, Appl
75	319.6	27.7	830	4	US-08-405-271A-13	Sequence 13, Appl
76	243	21.1	2447	3	US-08-387-707-12	Sequence 12, Appl
77	243	21.1	2447	4	US-09-016-434-1446	Sequence 1446, Ap
78	242.6	21.0	1317	4	US-08-417-103-5	Sequence 5, Appl
79	229.6	19.9	1205	1	US-08-417-103-13	Sequence 13, Appl
80	229.6	19.9	1634	1	US-07-816-283-1	Sequence 1, Appl
81	229.6	19.9	1634	1	US-08-417-103-1	Sequence 1, Appl
82	229.6	19.9	1634	4	US-09-016-434-1302	Sequence 1302, Ap
83	226.6	19.6	1265	1	US-07-816-283-3	Sequence 3, Appl
84	226.6	19.6	1265	1	US-08-417-103-3	Sequence 3, Appl
85	221.2	19.2	1244	1	US-07-816-283-7	Sequence 7, Appl
86	221.2	19.2	1244	1	US-08-417-103-7	Sequence 7, Appl
87	219.4	19.0	2518	4	US-09-743-871B-10	Sequence 10, Appl
88	214.8	18.6	1147	1	US-08-417-103-15	Sequence 15, Appl
89	214.8	18.6	1351	1	US-07-816-283-5	Sequence 5, Appl
90	214.8	18.6	1351	1	US-08-417-103-5	Sequence 5, Appl
91	214.8	18.6	1351	4	US-09-016-434-1303	Sequence 1303, Ap
92	210.4	18.2	1002	4	US-09-170-496D-15	Sequence 15, Appl
93	210.4	18.2	1518	1	US-08-148-215A-3	Sequence 3, Appl
94	210.4	18.2	1518	4	US-09-016-434-1480	Sequence 1480, Ap
95	207.2	18.0	1002	4	US-09-170-496D-171	Sequence 171, App
96	204.8	17.7	441	4	US-09-530-880-5	Sequence 5, Appl
97	175.6	15.2	987	4	US-09-170-496D-11	Sequence 11, Appl
98	175.6	15.2	1054	1	US-08-148-215A-1	Sequence 1, Appl
99	175.6	15.2	1596	4	US-09-016-434-1479	Sequence 1479, Ap
100	172.4	14.9	987	4	US-09-170-496D-169	Sequence 169, App

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102	162.2	14.1	1296	1	US-07-816-283-9	Sequence 9, Appli	175	92.6	8.0	1679	1	US-08-076-093A-5	Sequence 5, Appli
103	162.2	14.1	1296	1	US-08-417-103-9	Sequence 9, Appli	176	92.6	8.0	1679	1	US-08-701-265-5	Sequence 5, Appli
104	162.2	14.1	1413	4	US-09-016-434-1361	Sequence 1321, Ap	177	92.6	8.0	1679	2	US-08-284-586-5	Sequence 5, Appli
105	156.2	13.5	1796	1	US-07-816-283-11	Sequence 11, Appli	178	92.6	8.0	1679	2	US-08-805-478-5	Sequence 5, Appli
106	156.2	13.5	1796	1	US-08-417-103-11	Sequence 11, Appli	179	92.6	8.0	1679	2	US-08-802-627A-5	Sequence 5, Appli
107	123.4	10.7	1219	4	US-08-981-700A-3	Sequence 3, Appli	180	92.6	8.0	1679	2	US-08-801-238-5	Sequence 5, Appli
108	123.4	10.7	1365	4	US-08-899-1102A-27	Sequence 27, Appli	181	92.6	8.0	1679	2	US-08-801-228-5	Sequence 5, Appli
109	122.4	10.6	1164	3	US-08-993-088A-6	Sequence 6, Appli	182	92.6	8.0	1679	2	US-09-104-296-5	Sequence 5, Appli
110	122.4	10.6	1164	4	US-09-603-680-6	Sequence 6, Appli	183	92.6	8.0	1679	3	PCT-US94-06380-3	Sequence 3, Appli
111	122.4	10.6	1164	4	US-09-603-680-6	Sequence 6, Appli	184	92.6	8.0	2818	3	US-08-982-493-7	Sequence 7, Appli
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115	119	10.3	1495	4	US-09-023-655-1021	Sequence 1021, Ap	188	92	8.0	1088	4	US-09-077-674-6	Sequence 6, Appli
116	119	10.3	2156	1	US-08-012-988A-1	Sequence 1, Appli	189	92	8.0	1101	4	US-09-016-434-1148	Sequence 1148, Ap
117	119	10.3	2156	4	US-09-023-655-1247	Sequence 1247, Ap	190	92	8.0	1101	4	US-09-170-496D-87	Sequence 87, Appli
118	108	9.4	1116	3	US-08-993-088A-18	Sequence 18, Appli	191	92	8.0	1101	4	US-09-364-425B-44	Sequence 44, Appli
119	108	9.4	1116	3	US-08-993-088A-18	Sequence 18, Appli	192	92	8.0	2111	2	US-08-966-316-6	Sequence 6, Appli
120	108	9.4	1116	4	US-08-993-424B-18	Sequence 18, Appli	193	91.8	8.0	1083	4	US-09-131-827A-19	Sequence 19, Appli
121	108	9.4	1116	4	US-09-603-680-18	Sequence 18, Appli	194	91.6	7.9	1122	3	US-09-077-675A-9	Sequence 9, Appli
122	108	9.4	1116	4	US-09-603-680-19	Sequence 19, Appli	195	91.6	7.9	1122	3	US-09-077-674-9	Sequence 9, Appli
123	108	9.4	1116	2	US-08-626-685A-7	Sequence 7, Appli	196	90.8	7.9	1068	4	US-09-170-496D-129	Sequence 129, Ap
124	108	9.4	1193	4	US-08-899-112B-7	Sequence 7, Appli	197	90.8	7.9	1068	4	US-09-170-496D-231	Sequence 231, Ap
125	107.2	9.3	248	3	US-08-513-974B-300	Sequence 300, App	198	90.8	7.9	1161	1	US-08-153-848-31	Sequence 31, Appli
126	106.4	9.2	1690	4	US-08-665-034A-1	Sequence 1, Appli	199	90.8	7.9	1161	5	PCT-US93-11153-31	Sequence 31, Appli
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128	105.6	9.2	248	3	US-08-513-974B-301	Sequence 301, App	201	90.8	7.9	2254	3	US-09-299-843A-27	Sequence 27, Appli
129	105.6	8.9	1647	4	US-08-540-650B-6	Sequence 6, Appli	202	90.8	7.9	2254	4	US-09-088-337B-27	Sequence 27, Appli
130	102.2	8.9	1053	4	US-09-016-434-1423	Sequence 1423, Ap	203	90.8	7.9	2254	5	PCT-US93-11153-27	Sequence 27, Appli
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133	102	8.8	1116	4	US-08-720-565-5	Sequence 5, Appli	206	90.8	7.9	3119	4	US-09-088-337B-31	Sequence 31, Appli
134	101.2	8.8	1065	3	US-08-847-296B-2	Sequence 2, Appli	207	90.2	7.8	1083	4	US-09-131-827A-1	Sequence 1, Appli
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136	101.2	8.8	1193	4	US-08-720-565-3	Sequence 3, Appli	209	90.2	7.8	1979	3	US-08-446-669-3	Sequence 3, Appli
137	101.2	8.8	1201	4	US-09-016-434-1085	Sequence 1085, Ap	210	90.2	7.8	1979	4	US-09-023-655-1419	Sequence 1419, Ap
138	101.2	8.8	1201	4	US-09-023-655-905	Sequence 905, App	211	90.2	7.8	2232	5	PCT-US95-00476-3	Sequence 3, Appli
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141	101.2	8.8	1915	3	US-08-575-967A-3	Sequence 3, Appli	214	90.2	7.8	2232	4	US-09-016-434-1392	Sequence 1392, Ap
142	100.4	8.7	1158	4	US-09-023-655-992	Sequence 992, App	215	90.2	7.8	2232	4	US-09-023-655-1418	Sequence 1418, Ap
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145	100.4	8.7	2608	4	US-09-023-655-955	Sequence 955, App	218	89	7.7	1572	1	US-08-041-219A-5	Sequence 5, Appli
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147	97.2	8.4	980	4	US-09-218-467B-6	Sequence 6, Appli	220	88.2	7.6	1128	4	US-09-170-496D-201	Sequence 201, App
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149	97.2	8.4	1269	3	US-09-224-426-1	Sequence 1, Appli	222	88	7.6	1317	1	US-08-153-848-45	Sequence 45, Appli
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164	94	8.1	1872	5	PCT-US93-11153-39	Sequence 39, Appli	237	88	7.6	1737	3	US-09-104-296-3	Sequence 3, Appli
165	93.6	8.1	1101	4	US-09-170-496D-209	Sequence 209, App	238	88	7.6	1737	5	PCT-US94-06380-2	Sequence 2, Appli
166	93.4	8.1	2126	2	US-08-789-354-1	Sequence 1, Appli	239	87.8	7.6	1059	4	US-08-724-984A-3	Sequence 3, Appli
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169	93.4	8.1	2126	3	US-09-233-857-1	Sequence 1, Appli	242	87.8	7.6	1225	4	US-09-023-655-967	Sequence 967, App
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173	92.6	8.0	1119	4	US-09-170-496D-199	Sequence 199, App	246	87.8	7.6	1378	1	US-08-759-848-2	Sequence 2, Appli

247	87.8	7.6	1378	4	US-08-148-708-6	Sequence 6, Appl1	320	82	7.1	1107	4	US-09-595-549-3	Sequence 3, Appl1
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251	87.8	7.6	1477	4	US-08-833-752-2	Sequence 2, Appl1	324	81.8	7.1	1068	4	US-09-170-496D-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1

US-09-016-434-1417

Sequence 1417, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Sellhammer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

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CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

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? TELEPHONE: (650) 855-0555
? TELEFAX: (650) 845-4166
? INFORMATION FOR SEQ ID NO: 1417:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1182 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: GENBANK
? CLONE: 9532059
US-09-016-434-1417

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Query Match	99.3%	Score 1146;	DB 4;	Length 1182;
Best Local Similarity	99.6%	Pred. No. 7.7e-271;		
Matches 1149;	Conservative	0;	Mismatches 5;	Indels 0;

Qy	1	ATGGAACTCCCGATTCAGATCTTCCGCGGGGAGCGGGGCGCTCACTCGCGCCCGAGCGC	60
Db	14	ATGGAACTCCCGATTCAGATCTTCCGCGGGGAGCGGGGCGCTCACTCGCGCCCGAGCGC	73
Qy	61	TGCGTGCCTCCCAACAGCAGCGCGTGGTTCCCGGCTGGGCGGAGCCCGAGCAGCAAGCGC	120
Db	74	TGCGTGCCTCCCAACAGCAGCGCGCTGGTTCCCGGCTGGGCGGAGCCCGAGCAGCAAGCGC	133
Qy	121	AGGCGCGGCTCCGAGAGACGCGCAGCTGGAGCGCCGGCACATTCGCCGGCATCCCGGTC	180
Db	134	AGGCGCGGCTCCGAGAGACGCGCAGCTGGAGCGCCGGCACATTCGCCGGCATCCCGGTC	193
Qy	181	ATCATCACGGCGGCTCACTCCGAGTGTGCTGCGGGGCTTGGTGGGCAATCGCTGGTC	240
Db	194	ATCATCACGGCGGCTCACTCCGAGTGTGCTGCGGGGCTTGGTGGGCAATCGCTGGTC	255
Qy	241	ATGTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAAC	300
Db	254	ATGTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCATTTACATATTTAAAC	313
Qy	301	CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAAGATGCGTCACTTG	360
Db	314	CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAAGATGCGTCACTTG	373
Qy	361	ATGAATTCCTGGCTTTTGGGGATGTCGTGCGAAGATATGATTTCCATTGATTAAC	420
Db	374	ATGAATTCCTGGCTTTTGGGGATGTCGTGCGAAGATATGATTTCCATTGATTAAC	433
Qy	421	AACATGTTACACAGCATCTTCACTTGAACATGATGAGGGGACCGGTACATTGGCGGTG	480
Db	434	AACATGTTACACAGCATCTTCACTTGAACATGATGAGGGGACCGGTACATTGGCGGTG	493
Qy	481	TGCGACCCCGTGAAGGCTTTGGACTTCCGCACACCTTGAAGGCAAAAGATCATCATATC	540
Db	494	TGCGACCCCGTGAAGGCTTTGGACTTCCGCACACCTTGAAGGCAAAAGATCATCATATC	555
Qy	541	TGCATCTGCGTGTGTCATCTCTGTGGCATCTCTGCAATATGCTTGGAGGCAACAAA	600
Db	554	TGCATCTGCGTGTGTCATCTCTGTGGCATCTCTGCAATATGCTTGGAGGCAACAAA	613
Qy	601	GTCAGGGAAGAAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCGAGATGATGACTTACC	660
Db	614	GTCAGGGAAGAAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCGAGATGATGACTTACC	673
Qy	661	TGGTGGGACCTCTTCAATGAAGATCTGCGCTTCACTTTGACCTTGATGATCCGTCCTC	720
Db	674	TGGTGGGACCTCTTCAATGAAGATCTGCGCTTCACTTTGACCTTGATGATCCGTCCTC	733
Qy	721	ATCATCATGCTGTGCTACACCTGATGATCTGCGTCTCAAGAGCGTCGCGCTCTTCT	780
Db	734	ATCATCATGCTGTGCTACACCTGATGATCTGCGTCTCAAGAGCGTCGCGCTCTTCT	793
Qy	781	GCGTCCCGAGAAAGATGCGAAGCTGCGTAGATACCAAGATGCTGTGCTGTGGTGGTGG	840

Db	794	GGCTCCGAGAGAAAGATCGCAACCTGGGTAGATACACAACTGGTCTCTGGTGGTGTG	853
QY	841	GCAGTCTTCGTGCTGTGCTGAGATCCCACTTCCATATTCACTCTGGTGGAGGCTCTGGGG	900
Db	854	GGGGTTTTGATCTGTGCTGAGATCCCATTCATATTCATCTGGTGGAGGCTCTGGGG	913
QY	901	AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGATGGCTTTAGGCTAT	960
Db	914	AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGATGGCTTTAGGCTAT	973
QY	961	ACCAACAGTAGCTGAATCCCACTTCTAGGCGCTTTCTGATGAAACTTCAAGGGCGTG	1020
Db	974	ACCAACAGTAGCTGAATCCCACTTCTAGGCGCTTTCTGATGAAACTTCAAGGGCGTG	1033
QY	1021	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGAGACGGCAGAGCACTTAGCAGATC	1086
Db	1034	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGATGAGACGGCAGAGCACTTAGCAGATC	1099
QY	1081	CGAAATACAGTTCCAGAGATCTGCTTAACTCTGAGGGACATCGATGGGATGAAATTAACAGTA	1148
Db	1094	CGAAATACAGTTCCAGAGATCTGCTTAACTCTGAGGGACATCGATGGGATGAAATTAACAGTA	1153
QY	1141	TGACTAGTCGTGA	1154
Db	1154	TGACTAGTCGTGA	1167

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RESULT 2
US-09-341-446B-1
; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341.446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-446B-1

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Query Match	99.0%	Score 1143;	DB 4;	Length 1143;
Best Local Similarity	100.0%	Pred. No. 4.1e-270;		
Matches 1143;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGAGCTCCCCCATCCAGATCTTTCGCGGGGAGCCGGGCGCTTACTGTGGCGCCGAGGGCGC	60
Dd	1	ATGAGCTCCCCCATCCAGATCTTTCGCGGGGAGCCGGGCGCTTACTGTGGCGCCGAGGGCGC	60
QY	61	TGCGCTGCCCCCAACAGCAGCGCGCTGTGTTTCCCGGCTTGGGCTCGACCGACAGCAGCGC	120
Dd	61	TGCGCTGCCCCCAACAGCAGCGCGCTGTGTTTCCCGGCTTGGGCTCGACCGACAGCAGCGC	120
QY	121	AGCGCGGGCTCGAGGAGACGCGAGCTGGAGGCCGCGGCACATCTCCCGGCGCATTCCGGATC	180
Dd	121	AGCGCGGGCTCGAGGAGACGCGAGCTGGAGGCCGCGGCACATCTCCCGGCGCATTCCGGATC	180
QY	181	ATCATCAAGCGCGGTCTACTCTCGTAATGTTCCGTGCGGGCTTGGTGGGCAACTCGCTGGTC	240
Dd	181	ATCATCAAGCGCGGTCTACTCTCGTAATGTTCCGTGCGGGCTTGGTGGGCAACTCGCTGGTC	240
QY	241	ATGTTGCTATCATCCGATACCAAGAATGGAAGACAGCAACCAATTTATCATTTTAAC	300


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/
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 1275
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: RASL OR2
/ JS-09-341-446B-7

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Query Match	86.3%	Score 996.2;	DB 4;	Length 1275;
Best Local Similarity	92.8%;	Pred. No. 3.3e-234;		
Matches 1059; Conservative	0;	Mismatches 73;	Indels 9;	Gaps 1

QY	902	GCACCTCCCAAGACAGACAGCTGCTCTCCACAGTATTACTTTCGATTCGCGCTTAGGCTATA	961
Db	1004	GCACCTCCCAAGACAGACAGCTGCTCTCTCCAGTATTACTTTCGATTCGCGCTTAGGCTATA	106
QY	962	CCAAACAGTAGCCTGAATCCCAATCTCTACGCGCTTCTTGTATGATAAACTTCAAGCGGTGT	102
Db	1064	CCAAACAGTAGCCTGAATCCCAATCTCTACGCGCTTCTTGTATGATAAACTTCAAGCGGTGT	112
QY	1022	TCCGGGAATTCCTGCTTTCACCTGAAAGATGAGGATGAGCGGAGACCTAGCAGATCC	108
Db	1124	TCCGGGAATTCCTGCTTTCACCTGAAAGATGAGGATGAGCGGAGACCTAGCAGATCC	118
QY	1082	GAATATACAGTTCAGGATCTCTGCTTACCTGAGGACATCGATGGATGAATTAACCAAGTAT	114
Db	1184	GAATATACAGTTCAGGATCTCTGCTTACCTGAGGACATCGATGGATGAATTAACCAAGTAT	124
QY	1142	G 1142	
Db	1244	G 1244	

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RESULT 7
US-09-214-904-5
/ Sequence 5, Application US/09214904
/ Patent No. 663297
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
/ TITLE OF INVENTION: OF OPiate RECEPTORS IS MODIFIED
/ NUMBER OF SEQUENCES: 6
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/214,904
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/FR97/01282
/ FILING DATE:
/ APPLICATION NUMBER: FR 96.08810
/ FILING DATE: 15-JUL-1996
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1408 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 184..1323
/ US-09-214-904-5

Query Match      78.9%; Score 910.8; DB 4; Length 1408;
Best Local Similarity 86.8%; Pred. NO. 2.6e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0

QY      1 ATGAGACTCCCGATCCAGATCTTCGCGCGGAGCCGGGCGCTTACCTGCGCCCGGAGCGCC 60
Db      184 ATGAGATGCCCATTCAGATCTTCGAGAGAGATCCAGGCCCTTACTGCTCTCCAGTGTCT 243

QY      61 TGCTTGCCCCCAACAGACAGCGGCTGTGTTTCCCGGCTGGGCGGAGCCCGACAGCAAGGC 120
Db      244 TGCTTCTTCCCAACAGACAGCGCTTGTGTTCCCAACTGGGAGAGATCCGACAGTATGGC 303

QY      121 AGCGCGGCTCGAGAGAGCGCGCAGCTGGAGCCGCGGCACTTCCCGGCAATCCGGGTC 180
Db      304 AGTGTGGCTTAGAGAGATCAGACAGCTGGAGTCCGGGCACTTCTCCGGCAATCCCTGTT 363

QY      181 ATCTATCAGCGGCGTCTACTCCGTAGTGTTCGTGCGGAGCTTGTGGGCAACTCGCTGATC 240

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Db      364 ATCATCACGGCTGTACTCTGTGATTTGTGTGGGCTTGTGGGCAATCTCTGGTC 423
Qy      241 ATGTCGTGATCATCCGATACACAAAGATGAAGACGACCAACATTTACATTTTAA 300
Db      424 ATGTTTGCATATCCGATACACGAAGATGAAGACCGCAACCAATCATATTTTAA 483
Qy      301 CTGGCTTTGGGAGATGCTTTAGTTACTAACCAATGCCCTTCAGAGTAAGGCTTACTG 360
Db      484 CTGGCTTTGGGAGATGCTTTAGTTACTAACCAATGCCCTTCAGAGTAAGGCTTACTG 543
Qy      361 ATGAAATTCCTGGGCTTTTGGGGAGTGTGTGCAAGATAGTAATTTTCAATTACTAC 420
Db      544 ATGAAATTCCTGGGCTTTTGGAGATGTGTGCAAGATAGTCAATTTTCAATGACTAC 603
Qy      421 AACATGTTACCAAGCATCTTCACTTTGACATGATGAGCGGTGACCCGTACTTCCGCTG 480
Db      604 AACATGTTTACCAAGATTTTCACTTTGACATGATGAGGTGAGCCGCTACATTTGCTGTG 663
Qy      481 TGCCACCCCGGTGAAGGCTTTGGACTTCCGCAACCCCTTGAAGGCAAGATCATCATATC 540
Db      664 TGCCACCCCTGTGAAGGCTTTGGACTTCCGCAACCCCTTGAAGGCAAGATCATCATATC 723
Qy      541 TGCAATCTGGCTGCTTCTGCTCATCTGTGGCATCTGTGCAATAGTCTTTGAGGCAACAA 600
Db      724 TGCAATTTGGCTCTGGCATCATCTGTGGTATATCAGCGATAGTCTTTGAGGCAACAA 783
Qy      601 CTCAGGAAAGAGTGTGATGTCTTGAAGTCTCTTGCAGTTCCCAAGATGATCACTCC 660
Db      784 CTCAGGAAAGATGTGATGTCTTGAAGTCTCTTGCAGTTCCCAAGATGATCAATTTCC 843
Qy      661 TGGTGGGACCTTCTCATGAAGATGTGCGTCTTCTCATCTTTGCGCTTGTATCCCTGCTC 720
Db      844 TGGTGGGATCTCTTCTATGAAGATGTGTCTTCTTCTTCTTGTGCTTTGTATCTCCAGTCTTC 903
Qy      721 ATCATCATGCTGTCTGTAACCTGTGATGATCTGTGCTCAAGAGCGTCCGCTCTTCTCT 780
Db      904 ATCATCATGCTGTCTGTAACCTGTGATGATCTGTGCTCAAGAGTGTCCGCTCTCTGCT 963
Qy      781 GGCCTCCGAGAAAGATGCGAACCCTGGTGAAGATGACACAGATGCTGTGTGTGTG 840
Db      964 GGCCTCCGAGAAAGATGCGAAGATTTCCGCGGCAACCAAGCTGTGTGTGTGTGTG 1023
Qy      841 GCAGTCTTCTGCTGTCTGTGATCTCCATTCATCATATTTCTGTGTGAGAGCTCTGGGG 900
Db      1024 GCAGTCTTCTGATCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1083
Qy      901 AGCACTTCCCAAGACAGCTGTCTCTCCAGCTATTAATTTCTGTGATGCTTGAAGCTAT 960
Db      1084 AGCACTTCCCAAGACAGCTGTCTCTCCAGCTATTAATTTCTGTGATGCTTGAAGCTAT 1143
Qy      961 ACCAAGTAGCTGAATCCCAATTTCTCAAGCCTTTCTGTGAAGAAATTTAAACCGGTGT 1020
Db      1144 ACCAAGTAGCTGAATCCCAATTTCTGTGATGATGATGATGATGATGATGATGATGATG 1203
Qy      1021 TTCCGGGACTTCTGCTTCACTGAAGATGAGATGAGCGGCAAGACATGAGAGATC 1080
Db      1204 TTTAAGGACTTCTGCTTCCATTAAGATGAGATGAGCGGCAAGACATTAAGAGATT 1263
Qy      1081 CGAAATATAGTTCAAGATCTGTCTTAATCTGAGGAGCATGATGAGATGAATTAACAGTA 1140
Db      1264 AGAAATACAGTTCAAGATCTGTCTTAATCTGAGATGAGATGAGATGAATTAACAGTA 1323
Qy      1141 TGACTAGTGTGGA 1154
Db      1324 TGACTAGTGTGGA 1337

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RESULT 8
 US-08-147-592A-1
 ; Sequence 1, Application US/08147592A
 ; Patent No. 6096513
 ; GENERAL INFORMATION:

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; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 72210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 186..1325
; US-08-147-592A-1
;
; Query Match 78.9%; Score 910.8; DB 3; Length 1410;
; Best Local Similarity 86.8%; Pred. No. 2.6e-213;
; Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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Qy	301	TTGGCTTTGGGAGATGCTTATAGTATCTCAACACGATGCCCTTTCAGAGTACGGCTTACTTG	360
Db	486	CTGGCTTTGGGAGATGCTTATAGTATCTCAACACTATGCCCTTTCAGAGTCTGTCTACTTG	545
Qy	361	ATGAATTCCTGGCCTTTTGGGGATGTGCTGTGACAGATAGTAATTTCCATTGATTACTAC	420
Db	546	ATGAATTCCTGGCCTTTTGGAGATGTGCTATCCAGATATGTCTATTTCATTACTATCACTAC	605
Qy	421	AACATGTTACACAGATCTTCACTCCCTTGACCAATGAGAGCGGTGACCGCTACTTGGCCGG	480
Db	606	AACATGTTTACAGCATATTCACCTTGACCAATGAGAGTGTGACCGGTACTCTGTGG	665
Qy	481	TGCCACCCCGTGAAGGCTTTGGACTTTCGGCACACCCCTTGAAGGCAAAAGATCATCAATATC	540
Db	666	TGCCACCTCTGGAAGCTTTGGACTTTCGGCACACCTTTGAAGCAAAAGATCATCAACATC	725
Qy	541	TGCATCTGGCTGCTGTGCTCATCTGTGTGGACATCTGTCAATATGTCCTTGGAGGCAACAA	600
Db	726	TGCATTTTGGCTCTGGGCATCATCTGTGTGTATATAGGCAATGTCCTTGGAGGCAACAA	785
Qy	601	GTCAGGGAAGAGTGTGATGTCTATTAGTGTCTCTTGACAGTTCCCAATGATGATCACTCC	660
Db	786	GTCAGGGAAGATGTGATGTCTATTAGTGTCTCTTGACAGTTCCGATGATGATCAATTC	845
Qy	661	TGCTGGGAACTTCTTCATGAAAGATCTGCGTCTTTCATCTTGTGCTTGTGTATCCCTGTCTC	720
Db	846	TGCTGGGAACTTCTTCATGAAAGATCTGTGTCTTGTGCTTGTGTATCCCACTGTCTC	905
Qy	721	ATCATCATGCTGTGCTTACACCCCTGATGATCCGGGCTCAAGAGGTCCGGCTCTTCT	780
Db	906	ATCATCATGCTGTGCTTACACCTGATGATCTGGCGCTGAAGAGTGTCCGGCTCTGTCT	965
Qy	781	GAGTCCCGAGAAAGATCGCAACTCGGTGATGATCACCGACTGTCTGTGTGTGTG	840
Db	966	GAGTCCCGAGAAAGATCGCAAACTCGCGCGCATCACCAAGCTGTGTGTGTGTGTGT	1025
Qy	841	GCAGCTTCTGCTGTGCTGTGATCTCCCATTCATCATTCATCTCTGTGGAAGGCTTGGGG	900
Db	1026	GCAGCTTCTCATATGTGTGTGACCCCATTCATCATCTTATCTGTGTGAGGCTTGGGA	1085
Qy	901	AGCACTTCCACAGACACAGTGTCTCTTCCACAGCTATTACTTGTGATCGCTTATGAGCTAT	960
Db	1086	AGCACTTCCACAGACACAGTGTCTCTTCCACAGCTATTAATTTGTATGTGCTTGTGTTAT	1145
Qy	961	ACCAACAGTAGCTGTAATCCATTCTTAACGCTTTTCTTGATGAAAATTCAAGCGGTGT	1020
Db	1146	ACCAACACAGCTGTAATCTGTGTCTCATGTGCTTTCTGATGAAAATTCAAGCGGTGT	1205
Qy	1021	TTCCGGGACTTCTGTCTTTCACATGAAATGAGAGTGAAGCGGCACAGCACTGACAGATC	1080
Db	1206	TTTATGGGACTTCTGTCTTTCCTTATTAAGATGCAATGAGCGGCACAGCACTCAATATGATTT	1265
Qy	1081	CGAAATACAGTTACAGATCTGTCTTACCTGAGGGAATCGATGGGATGATTAACCAAGTA	1140
Db	1266	AGAAACACAGTTACAGATCTGTCTTCCATGAGAGATGTGGAGGAGATGAATTAACCAAGTA	1325
Qy	1141	TGACTAGTCGTGGA 1154	
Db	1326	TGACTAGTCGTGGA 1339	

RESULT 9
 US-08-292-694A-1
 Sequence 1, Application US/08292694A
 Patent No. 619686
 GENERAL INFORMATION:
 APPLICANT: BELL, GRAEME
 APPLICANT: REISINGE, TERRY
 APPLICANT: YASUDA, KAZUKI
 TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee

```

1 STREET: P. O. Box 4433
2 CITY: Houston
3 STATE: Texas
4 COUNTRY: USA
5 ZIP: 77210
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
11 SOFTWARE: Patentn Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/292,694A
15 FILING DATE: August 19, 1994
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/066,296
20 FILING DATE: 20 May 1993
21 CLASSIFICATION: 435
22 APPLICATION NUMBER: 08/100,694
23 FILING DATE: 30 July, 1993
24 CLASSIFICATION: 435
25 APPLICATION NUMBER: 08/147,592
26 FILING DATE: 5 No. 6319686ember 1993
27 CLASSIFICATION: 435
28 APPLICATION NUMBER: PCT/US94/05747
29 FILING DATE: 20 May 1994
30 CLASSIFICATION: 435
31
32 ATTORNEY/AGENT INFORMATION:
33 NAME: MARK B. WILSON
34 REGISTRATION NUMBER: 37,259
35 REFERENCE/DOCKET NUMBER: ARCD.140/WIM
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (512) 418-3000
38 TELEFAX: (713) 789-2679
39
40 TELEEX: 79-0924
41
42 INFORMATION FOR SEQ ID NO: 1:
43
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 1410 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49
50 MOLECULE TYPE: genomic DNA
51
52 FEATURE:
53 NAME/KEY: CDS
54 LOCATION: 186..1325
55 US-08-292-694A-1
56
57 Query Match 78.9%; Score 910.8; DB 4; Length 1410;
58 Beest Local Similarity 86.8%; Pred. No. 2.6e-213;
59 Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
60
61
62 1 ATGGACATCCCGATCCAGATCTTCCGCGGGGAGCGGGACCCTTACCTGCGCCGAGCGCC 60
63 Db 186 ATGAGATGCCCCCAATTCAGATTTCCGAGAGATCCAGGCCCTTACTGTCTCCAGTGTCT 245
64
65 61 TGCCTGCCCCCAACAGACAGCGGCTGGTTTCCCGGCTGGGCGGAGCCCGACAGCAAGCGC 120
66 Qy 246 TGCCTTCTCCCAACAGACAGCGTCTGGTTTCCCAACTGGGCAAGATCCGACATGTAATGCGC 305
67 Db 246 TGCCTTCTCCCAACAGACAGCGTCTGGTTTCCCAACTGGGCAAGATCCGACATGTAATGCGC 305
68
69 121 AGCGCCGGCTCGAGAGACGGGCACTGGAGCCCGGCACATCTCCCGGCCATCCCGGTC 180
70 Qy 306 AGTGTGGGCTCAGAGATCCAGCACTGAGTCCCGGCACATCTTCCGGCCATCCGTT 365
71 Db 306 AGTGTGGGCTCAGAGATCCAGCACTGAGTCCCGGCACATCTTCCGGCCATCCGTT 365
72
73 181 ATCATCAAGGCGGCTACTCCGATGTGTGCTGTGGGCTTGGTGGGCAATCGCTGGTC 240
74 Qy 366 ATCATCAAGGCGGCTACTCCGATGTGTGCTGTGGGCTTGGTGGGCAATCTCTGGTC 425
75 Db 366 ATCATCAAGGCGGCTACTCCGATGTGTGCTGTGGGCTTGGTGGGCAATCTCTGGTC 425
76
77 241 ATGTTCTGATCATCCGATACACAAGATGAGAGACAGCAACCAATTTACATATTTAAC 300
78 Qy 426 ATGTTCTGATCATCCGATACACAAGATGAGAGACAGCAACCAATTTACATATTTAAC 485
79 Db 426 ATGTTCTGATCATCCGATACACAAGATGAGAGACAGCAACCAATTTACATATTTAAC 485
80
81 301 CTGGCTTTGGCAGATGCTTTAGTTAGTACCAACATGCTCTTTCAGAGTACGCTTACTTG 360
82 Qy 301 CTGGCTTTGGCAGATGCTTTAGTTAGTACCAACATGCTCTTTCAGAGTACGCTTACTTG 360

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Db      486 CTGGCTTTGGACAGATCTTTGGTTACTACCACTATGCCCCCTTTGAGAGTGTCTACTATTG 545
Qy      361 ATGAATTCCTGGCTTTTGGGGATGCTGTGTGCAAGATGTAATTTCCATTGATTCTTAC 420
Db      546 ATGAATTCCTGGCTTTTGGAGATGCTGTGTGCAAGATGTAATTTCCATTGATTCTTAC 605
Qy      421 AACATGTTACCGACATCTTCACTTACCATATGATGAGGTGAGCCGCTACATTTGCGGTG 480
Db      606 AACATGTTACCGACATCTTCACTTACCATATGATGAGGTGAGCCGCTACATTTGCTGTG 665
Qy      481 TGGCAACCCCGTGAAGGCTTTGACCTTCCGACACCTTTGAAGGCAAAAGATCATCAATATC 540
Db      666 TGGCAACCCCGTGAAGGCTTTGACCTTCCGACACCTTTGAAGGCAAAAGATCATCAATATC 725
Qy      541 TGCATCTGGCTGTCTGTCTATCTGTGTCATCTGTGCAATGATCTGTGAGGCAACCA 600
Db      726 TGCATTTGGCTCTGTGCACTATCTGTGTCATCTGTGTCATCTGTGAGGCAACCA 785
Qy      601 GTCAAGGAAGACGTGATGTCATTTGAGTGTCTCTTGCAGTTCCAGATGATGACTACTTC 660
Db      786 GTCAAGGAAGATGTGATGTCAATGTAATGCTCTTGCAGTTCTCTGATGATGATGATTC 845
Qy      661 TGGTGGAGACTCTTCTATGAAAGATTCGCTCTTCTATTTTGGCTTCTGTATCTCTGCTCT 720
Db      846 TGGTGGAGACTCTTCTATGAAAGATTCGCTCTTCTATTTTGGCTTCTGTATCTCTGCTCT 905
Qy      721 ATCATCATCTGTCTGCTACACCTGATGATCTGCGTCTGCAAGAGGCTCGGCTCTTCT 780
Db      906 ATCATCATCTGTCTGCTACACCTGATGATCTGCGTCTGCAAGAGGCTCGGCTCTTCT 965
Qy      781 GGCTCCCGAAGAAAGATGCAACCTGCGTGAATTCACCAAGCTGCTGTGTGTGTG 840
Db      966 GGCTCCCGAAGAAAGATGCAACCTGCGTGAATTCACCAAGCTGCTGTGTGTGTG 1025
Qy      841 GCAATCTTCTGTCTGTCTGCTGCACTCCCATTCATATTCATCTGTGTGTGTGTG 900
Db      1026 GCAATCTTCTGTCTGTCTGCTGCACTCCCATTCATATTCATCTGTGTGTGTGTG 1085
Qy      901 AGCACTCTCCACAGACAGCTGCTCTCTCAGCTATTAATTTTGTGATGCGCTTAGGCTAT 960
Db      1086 AGCACTCTCCACAGACAGCTGCTCTCTCAGCTATTAATTTTGTGATGCGCTTAGGCTAT 1145
Qy      961 ACCAAGCTAGCTGAATCTTCTCTTCAAGCTTTCTTGTGAAACCTTCAAGCGGTGT 1020
Db      1146 ACCAAGCTAGCTGAATCTTCTCTTCTTCTTCTTGTGAAACCTTCAAGCGGTGT 1205
Qy      1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGAGTGGCGGCAAGCATAGCAGATC 1080
Db      1206 TTTCAGGACTTCTGCTTTTCCCTATTAAGATGCAATGAGCGGCAAGCATAGGATTT 1265
Qy      1081 CGAAATACAGTTCAAGATCTGCTTACCTGAGGAGCATGATGGAGTAATTAACAGTA 1140
Db      1266 AGAAACACAGTTCAAGATCTGCTTCCATGAGAGATGTGGAGGAGTAATTAAGCAGTA 1325
Qy      1141 TGACTAGTCTGTGA 1154
Db      1326 TGACTAGTCTGTGA 1339

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; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 72210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: N
; LOCATION: 607-608, 642-643, 896, 906
; IDENTIFICATION METHOD: N = A, C, G or T
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 102..986
; NAME/KEY: Xaa
; LOCATION: 169, 181, 265, 269
; IDENTIFICATION METHOD: Xaa = unknown
; US-08-147-592A-11

Query Match 75.5%; Score 871.2; DB 3; Length 1000;
Best Local Similarity 97.6%; Pred. No. 1.1e-203;
Matches 892; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Qy      244 TTCTGTATCATCCGATACCAAGATGAGAGCAAGCAACATTTTCAATATTTAACTTG 303
Db      87 TTCTTTTCTTTTGTATGATACCAAGATGAGAGCAAGCAACATTTTCAATATTTAACTTG 146
Qy      304 GCTTGGCAGATGCTTGAATTAATTAACCAAGATGAGAGCAAGCAACATTTTCAATATTTAACTTG 363
Db      147 GCTTGGCAGATGCTTGAATTAATTAACCAAGATGAGAGCAAGCAACATTTTCAATATTTAACTTG 206
Qy      207 AATTCTGGCTTTTGGGAGATGTGCTGTGCAAGATGTAATTTTCAATGATTTACTACAA 266
Db      424 ATGTTCACGACATCTTCACTTGAACATGATGAGGTGAGCCGCTACATTTGCGGTGTG 483
Qy      267 ATGTTCACGACATCTTCACTTGAACATGATGAGGTGAGCCGCTACATTTGCGGTGTG 326
Db      484 CACCCGTGAAGGCTTTGAGCTTCCGACACCTTGAAGGCAAAAGATCATCAATATTTCTG 543
Qy      327 CACCCGTGAAGGCTTTGAGCTTCCGACACCTTGAAGGCAAAAGATCATCAATATTTCTG 386
Db      544 ATCTGCTGTCTGTCTATCTGTGTGATCTTGTGCAATAGTCTCTTGAAGGCAACCAAGTC 603

```


OY	724	ATCATGCTGCTTAACACCTGATGATTCGCGTCCAGAGGTCOAGCTCTCTTCTGGC	783
Db	567	ATCATGCTGCTTAACACCTGATGATTCGCGTCTCAGANNGTCCGACTCTTCTGGC	626
OY	784	TCCGAGAGAAAGATCGCAACCTGCGTAGATCACCAACTGTGCTGTGTGTGTGCA	843
Db	627	TCCGAGAGAAAGATGNNCAACTGCGTAGATCACCAACTGTGCTGTGTGTGTGCA	686
OY	844	GTCTTCGAGCTGTGTGACCTCCATTAACAATTAATCTGTGTGTGTGTGTGTGTGCA	903
Db	687	GTCTTCGAGCTGTGTGACCTCCATTAACAATTAATCTGTGTGTGTGTGTGTGTGCA	746
OY	904	ACCTCCACAGACAGCTGCTCTCTCCAGATTAATCTTGTGCATGCGCTTAGCTATACC	963
Db	747	ACCTCCACAGACAGCTGCTCTCTCCAGATTAATCTTGTGCATGCGCTTAGCTATACC	806
OY	964	AACAGTACCTGGAATCCATTCTCTAGGCTTTCTTGATGAAAATTCAAGCGGTGTTT	1022
Db	807	AACAGTACCTGGAATCCATTCTCTAGGCTTTCTTGATGAAAATTCAAGCGGTGTTT	866
OY	1024	CGGCACTTCTGCTTCCACTGAGATGATGAGATGAGCGGACAGACATAGCAGATCCGA	1083
Db	867	CGGCACTTCTGCTTCCACTGAGATGATGAGATGAGCGGACAGACATAGCAGATCCGA	926
OY	1084	AATAAGTTGAGATTCCTGCTTAACCTGAGGACATCGATGG--GATGAATAAACAGTA	1140
Db	927	AATAAGTTGAGATTCCTGCTTAACCTGAGGAGATCGATGGATGATGAATAAACAGTA	986
OY	1141	TGACTAGTCGTGA 1154	
Db	987	TGACTAGTCGTGA 1000	

RESULT 12
US-08-430-286A-1
Sequence 1, Application US/08430286A
Patent No. 6225080
GENERAL INFORMATION:
APPLICANT: Uhl, George R.
APPLICANT: Epler, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,286A
FILING DATE: 28-Apr-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A843-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2135 base pairs
TYPE: nucleic acid
STANDARDS: single

```

;          TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA to mRNA
;
; ORIGINAL SOURCE:
;
; ORGANISM: Rattus rattus
;
; IMMEDIATE SOURCE:
;
; CLONE: mu receptor cDNA
;
DS-08-430-286A-1

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Query Match	38.8%	Score 448;	DB 3;	Length 2135;
Best Local Similarity	67.0%;	Pred. No. 4.1e-100;		
Matches 669;	Conservative 0;	Mismatches 320;	Indels 9;	Gaps 2;

QY	110	ACAGCAACGGGAGGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGGCAACATCTCCCGG	169
Db	167	ACGCGACCGGGCTTTGGGGGGAACGACAGCCTGTGCTCTACACCGGACGCCCTTCATGTG	226
QY	170	CCATCCGGTCATCATCACGGCGGTCTACTCCGTAAGTTCGTGCTGGGCTTGGTGGCA	229
Db	227	TCACAGCATTTACCATCATGTGGCCCTTACTCTATCGTGTGTGTGGGGCTCTTCGGAA	286
QY	230	ACTGCTGCTGTCATGTTGGTATCATTCGGATACCAAGATGAAAGACAGCAACCAACTT	289
Db	287	ACTTCCTGGTCATGTATGTATGTAAATACACAAAATGMAATCCTGCCACCAACATCT	346
QY	290	ACATATTTAACTGGCTTTGGAGAGATCTTGTAGTTACTTACCAACCATCCCTTCAGAGTA	349
Db	347	ACAATTTTCAACCTTTGCTCTGTGGACAGCCCTTTAGGACCAAGTACATGCTCCTTCAGAGTG	406
QY	350	CGGCTACTTGAATGAAATCTCTGGCCTTTTGGGGAATGTGCTGTGCAAGATAGTAATTTCCA	409
Db	407	TCAACTACCTGAATGGGAACATGGCCCTTCGGAAACCACTCTCTGMAATCTGTATCTTCAA	466
QY	410	TTGATTACTCAACATGTTTACCAGCAATCTTCACTTGACATATAGCGTGAACGCT	469
Db	467	TAAATTACTACAACTGTTTACCGACAGATTTACACCTCTGTGCAACATAGCTGGACCGCT	526
QY	470	ACATTTGCCGTGTGCACCCCGTGAAGGCTTTGGACTTTCGCAACACCTTGAAGGCAAGA	529
Db	527	ACATTTGTGCTGTCCACCCAGTCAAAAGCCCTGTGAATTTCCGTATCCCGGAAATCCAAA	586
QY	530	TCATCAATATCTGATCTGGCTGTGCTGTCTCATCTGTGTGGCATCTGCAATAGTCCCTG	589
Db	587	TCGTCAACGCTGTCAACTGTGATCTCTCTTCTGCGCATGCTGTGCTGTATATGTTCAATGG	646
QY	590	GAGGCACCAAAATGTCAGGGAAGAAGCTGATGCAATGAGTCTCTTGACAGTCTCCAGATG	649
Db	647	CAACCAACAAATTCAGGACAGGGGTCT-----CATAGATTCACCCCTCACGTTCTCCACC	700
QY	650	ATGACTACTCTGTGTGGGACCTTTTCATGAAAGATCTGGCTTCATCTTTGGCCTTCGTGA	709
Db	701	CAACTGTGTACTGGGAAGAACTGTCTC---AAATTCGTGTCTTATCTTGTGCTTCAATCA	757
QY	710	TCCCTGTCTCATCATCATCTGTCTGTCTACAACCTGTATGATCTGCGTCTCAAGAGCTGCC	769
Db	758	TGCGGAGCTCATCATCATCTGTGTGTGTTAGGGCTGTATGATCTTACGACTCAAGAGGCTTC	817
QY	770	GGTCTCTTTCTGGCTCTCCGAGAGAAAGATGCAACTGTGTAGATATCCAGACTGTCTCC	829
Db	818	GCATGCTATCGGGCTCTCAAGAAAGAAAGACAGGAATCTGGCAGAGATCACCCGGATGTGTGC	877
QY	830	TGTGTGTGTGTGACGTCTGTCTGTCTGTGTGCACTCCATCTCAATATTCATCTGTGTGG	889
Db	878	TGTGTGTGTGTGTATTTATTTATCTGTCTGTGACCCCCATCCATCTTAGTATCATCTCA	937
QY	890	AGGCTCTGGGAGACCTCTCCACAGACAAGCTGTCTCTTCAGCTATTACTTCTGCATCG	949
Db	938	AAGCGCTATTCACGATTCAGAAACCAATTCAGACCGTTCCTGGCACTTCTGCACATGG	997
QY	950	CCCTTAGGCTATACCAACAGTAGCTGAATCCCATCTTCTAAGGCTTCTTGTATGAAAGACT	1009
Db	998	CTTTGGGTATACGAAGACAGTGTGCTGTAAATCTCAAGTTCTTTAGCGCTTCTGTGATGAAGACT	1057
QY	1010	TCAGGCGGTGTTCCGGGACTTCTGTGCTTTCACCTGAAGATGAGAGTGAAGCGGCGAAGCA	1069

DB 1058 TCAAGCAGATGCTTCAAGAGAGTTCGTGATCCCAACCTGCTCCAGATCGAAGCAAAACT 1117
QY 1070 CTAGCAGAGTCCGAATATACAGTTCAAGATCTGCTTAC 1107
DB 1118 CCATCGAGTCGTCAGAACACTAGGGAACATCCCTCC 1155

RESULT 13

US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; US-08-889-108-1

Query Match 38.7%; Score 446.4; DB 3; Length 1618;

Best Local Similarity 66.9%; Pred. No. 9.2e-100; Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 110 ACAGCAAGCGACGCGCGCTCGAGGACGCGCAGCTGGAGCCCGCGCATCTCCCGG 169
DB 350 ACCGACCGGGCTTGGCGGAAACGACGCTGTGCTTCAGACCGGAGCCCTTCATGG 409
QY 170 CCATCCGGTCAATCAACGCGGCTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGCA 229
DB 410 TCACAGCCATATACATCAATGCGCCCTCTACTATGCTGTGTAGTGGGCTCTTCGGA 469
QY 230 ACTGCTGATCATGTCGTGATCATCCGATACCAAAAGTGAAGCAGCAACCAATTT 289
DB 470 ACTTCTGATCATGATGATGATTTGAAGTACCAAAATGAAGACGCGACCAACATCT 529
QY 290 ACATATTAACCTGCTTGGCAGATGCTTTAGTTACTACAACCAATGCGCTTTCAGAGTA 349
DB 530 ACATTTCAACTTCTCTGCGGACGAGCGCTTAGGACCACTGACTGCCCTTTCAAGATG 589

QY 350 CGGTCTACTGTGATGATTCCTGCGCTTTGGGATGTGCTGTGCAAGATGTAATTTCA 409
DB 590 TCAACTACTGTATGGGAACATGGCCCTTGGAACCATCTCTGCAAGATGATCTCA 649
QY 410 TTGATTTACTACAACATGTTCAACAGCATCTTCACTTGAACATGATGACGCTG 469
DB 650 TAGATTACTACAACATGTTCAACAGCATTTACCTCTGCAACATGACGCTG 709
QY 470 ACATTCGCGTGTGCAACCCCGTGAAGCTTGGACTTCCGACACCTTGAAGCAAGA 529
DB 710 ACATTCGCTGTGCGACCAAGCAAGCCCTGATTCGATCCGCCCAATGCAAAA 769
QY 530 TCATCAATATCTGCACTGCTGCTGTGCTATCTTTGGCATCTCTGAAATAGTCTTG 589
DB 770 TCGTCAAGCTGTGCACTGATCTCTCTTCTGCAATGCTGCTGCTTAATGTTATG 829
QY 590 GAGCACCAAGTCAAGGGAAGACGTGATGATGATGATGATGATGATGATGATGATG 649
DB 830 CAACCAAAATACAGGACGGGCTC-----CATGATTTGACACCTCAGTTCTCCAC 883
QY 650 ATGACTACTCTGTGGGACCTCTTCATGATGATGATGATGATGATGATGATGATG 709
DB 884 CAACCTGATCTGGGAGAACCTGCTC-----AAATCTGTGTCTTTATCTTCGCTTCATCA 940
QY 710 TCCCTGCTCTATCATCTGCTGCTCAACCCGATGATCTGCTGCTCAAGAGCTCC 769
DB 941 TCCCATCTCTCATCACTGCTGTGATGATGATGATGATGATGATGATGATGATGATG 1000
QY 770 GGCCTCTTCTGCTGCTCCGAGAAAGATGCAACCTGCTGATGATGATGATGATGATG 829
DB 1001 GCATCTATCTGGGCTTCCAAAGAAAGACAGAACTGTGGCAGATTCACCGGATGCTC 1060
QY 830 TGTGTGTGTGTCAGTCTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
DB 1061 TGTGTGTGTGTCAGTCTTATTTATGCTGCTGGAACCCCATTCACATCTCATCATCA 1120
QY 890 AGCTCTGGGAGACCTTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGATG 949
DB 1121 AAGCCTCATCAAGATTCAGAAACCAATTCAGACCGTTTCTGGGACCTTCTGATG 1180
QY 950 CCTTAGGCTATACCAAGATGAGCTGAAATCCATCTCTCAAGCTTCTTGAAGAACT 1009
DB 1181 CTTTGGGTTACAGAAACGCTGCTGAAATCCAGTTCTTTAGCCTTCTCGATGAAACT 1240
QY 1010 TCAAGCGGTGTTTCCGGAATCTTGTCTTTCACCTGAAGATGAGATGAGCGGACAGCA 1069
DB 1241 TCAAGCAGATGCTTCAAGAGATCTGCTATCCCAACCTGCTCCAGATCGAAGCAAGAAACT 1300
QY 1070 CTAGCAGATCCGAATATACAGTTCAAGATCCGCTTAC 1107
DB 1301 CCATCGAGTCGTCAGAACACTAGGGAACATCCCTCC 1338

RESULT 14

US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25

QY 110 ACAGCAAGCGACGCGCGCTCGAGGACGCGCAGCTGGAGCCCGCGCATCTCCCGG 169
DB 350 ACCGACCGGGCTTGGCGGAAACGACGCTGTGCTTCAGACCGGAGCCCTTCATGG 409
QY 170 CCATCCGGTCAATCAACGCGGCTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGCA 229
DB 410 TCACAGCCATATACATCAATGCGCCCTCTACTATGCTGTGTAGTGGGCTCTTCGGA 469
QY 230 ACTGCTGATCATGTCGTGATCATCCGATACCAAAAGTGAAGCAGCAACCAATTT 289
DB 470 ACTTCTGATCATGATGATGATTTGAAGTACCAAAATGAAGACGCGACCAACATCT 529
QY 290 ACATATTAACCTGCTTGGCAGATGCTTTAGTTACTACAACCAATGCGCTTTCAGAGTA 349
DB 530 ACATTTCAACTTCTCTGCGGACGAGCGCTTAGGACCACTGACTGCCCTTTCAAGATG 589

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cdna)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3

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Query Match      38.7%; Score 446.4; DB 3; Length 1618;
Best Local Similarity 66.9%; Pred. No. 9.2e-100;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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110 ACAGCAAGCGGCGCGGCTGCGAGGACGCGGAGCTGGAGCGCGCGGCAATCTCCCGG 169
350 ACCGACCGGGGTTGGCGGAAAGACAGCTGTGCTTCAAGCGCGGAGCTTTCATGG 409
170 CCATCCCGGTCATCATCGCGGCTCTACTCCGTAAGTTCGTCGCGGCTTGGTGACA 229
410 TCACAGCATTAACATCATGAGGCTCTACTGATGTGTGTGTGTGTGTGTGTGTGTGT 469
230 ACTGCTGTGATGATGCTGTGATCATCCGATACACAAAGATGAGACAGACCAATTT 289
470 ACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
290 ACATATTTAACCTGCTTGGAGATGCTTGTAGTACTACAAACATGCTTTCAGAGTA 349
530 ACATTTTAACTTGTCTGTGCAAGCGCTTAAAGCAGTACACTGCTTTTCAAGTGTG 589
350 CGGTCTACTGATGATTTCTGCGCTTTTGGGAGTGTGCTGTGCAAGATGATTAATTTCA 409
590 TCAACTACCTGATGGAAACATGCGCTTCGGAACCATCTCTGCAAGATGATGATCTCAA 649
410 TTGATTTACAAACATGTTCAACGACATCTTCACTTGAACATGATGAGCTGAGCGCT 469
650 TAGATTTACAAACATGTTCAACGACATTTACCTCTGCAACATGAGCTGAGCGCT 709
470 ACATGCGGTGTGCAAGCGCTTGAAGGCTTGAACCTTGGACCTTGAAGGCAAGA 529
710 ACATTTGCTGTGCAAGCGCTTGAAGGCTTGAACCTTGGACCTTGAAGGCAAGA 589
530 TCATCATATTTGCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 589
770 TCGTCAACGCTGCAACATGATGCTCTTCTTCTGCAATGCTGTGCTGTGATGTTGATGG 829
590 GAGGACCAAGTAGGAGGAAACGTCATGATGATGATGATGATGATGATGATGATGATG 849
830 CAACCAACAAATATACAGGAGGAGGCTC-----CATAGATGACACCTCAAGCTTCCACC 883
650 ATGACTACTCTGTGTGAGGAGCTTTCATGAGATGCTGTGCTTTCATGCTTTCGTA 709
884 CAACCTGTGATGAGGAGGAGGAGGCTC-----AAAATCTGTGTGTGTGTGTGTGTGTGT 940
710 TCCCTGTCTCATCATCATGCTGTGCTGATACACCTGATGATGCTGCTTCAAGAGCGTCC 769

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Db      941 TCCGATCTCATATCATCTGTGTGTACGGCTTGATGATCTTACGACTCAAGAGCGTTC 1000
Qy      770 GGCCTCTTTTGGGCTCCCGAGAGAAAGATCCAACTGCGTAGGATCCAGACTGGTCC 829
Db      1001 GCATGCTTATCGGGGCTCCAAAGAAAGAGACAGAAATCTGCGAGGATCACCGGATGGTGC 1060
Qy      830 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
Db      1061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
Qy      890 AGGCTCTGAGGAGACCTCCACAGACAGCTGCTCTCTCAGCATTAATCTTGCATTCG 949
Db      1121 AAGGCTGATATCATATTCAGAAACACATTTAGACCGTTTCTTGGACCTTGTGCATTTG 1180
Qy      950 CTTAGGCTATATACCAAGATAGCTGATCCGATCTTCTTACGCTTTCTTGATGAAAAT 1009
Db      1181 CTTGGGTTTACAGCAAGAGCTGCTGATTCAGATCTTTTACGCTTCTTGATGAAAAT 1240
Qy      1010 TCAAGCGGTGTTCGGGACTTCTGCTTTCATCTGAAGATGAGATGAGAGCGGAGCA 1069
Db      1241 TCAAGCGATGCTTCAAGAGATTCGATCCCAACCTGCTCCAGATGGAACAGCAAACT 1300
Qy      1070 CTACGAGATCCGAATATCAAGTTCAGATCTCTGCTTAC 1107
Db      1301 CCACTCGATCTCTTCAGAACTAGGAGACATCTCTCC 1338

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RESULT 15
US-08-120-601B-1
Sequence 1, Application US/08120601B
Patent No. 6235496

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GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
METHODS
NUMBER OF INVENTION: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,601B
FILING DATE: 13-Sep-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1407
US-08-120-601B-1

```

```

Query Match      38.7%; Score 446.4; DB 3; Length 1618;
Best Local Similarity 66.9%; Pred. No. 9.2e-100;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```

```

QY 110 ACAGCAAGGCGAGCGCGGCTGAGAGACGCGAGCTGAGAGCGCGGCAATCTCCCGG 169
DB 350 ACCGCAACCGGCTTGCGGGGAAAGACAGCTGCTGCTTCAAGACGGGAGCTTTCATGG 409
QY 170 CCATCCCGGTCAATCAACGCGGCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 229
DB 410 TCACAGCCATTAACATCATGCGCTCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
QY 230 ACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289
DB 470 ACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
QY 290 ACATATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
DB 530 ACATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
QY 350 CGGCTACTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 409
DB 590 TCACTACTGATGGGAAATGCGCTTGGAAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 410 TTGATTTACTAACAATGCTTCAACAGATCTTCACTTCAACATGATGAGCGTGGACGCT 469
DB 650 TAGATTACTAACAATGCTTCAACAGATCTTCACTTCAACATGATGAGCGTGGACGCT 709
QY 470 AATATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
DB 710 AATATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 530 TCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
DB 770 TGTCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
QY 590 GAGGCAACAAGTCAAGGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
DB 830 CAACCAACAATTAAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
QY 650 ATGATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
DB 884 CAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
QY 710 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
DB 941 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
QY 770 GCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
DB 1001 GCATGCTATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060
QY 830 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
DB 1061 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
QY 890 AGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
DB 1121 AAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1180
QY 950 CCTTGAAGCTTAAACAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009
DB 1181 CTTTGGGCTTAAACAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1010 TCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1069
DB 1241 TCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
QY 1070 CTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1107
DB 1301 CCACTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1338

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RESULT 16
US-08-120-601B-3
; Sequence 3, Application US/08120601B

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; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1232
; US-08-120-601B-3

Query Match 38.7%; Score 446.4; DB 3; Length 1618;
Best Local Similarity 66.9%; Pred. No. 9, 2e-100;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 110 ACAGCAAGGCGAGCGCGGCTGAGAGACGCGAGCTGAGAGCGCGGCAATCTCCCGG 169
DB 350 ACCGCAACCGGCTTGCGGGGAAAGACAGCTGCTGCTTCAAGACGGGAGCTTTCATGG 409
QY 170 CCATCCCGGTCAATCAACGCGGCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 229
DB 410 TCACAGCCATTAACATCATGCGCTCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
QY 230 ACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289
DB 470 ACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
QY 290 ACATATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
DB 530 ACATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
QY 350 CGGCTACTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 409
DB 590 TCACTACTGATGGGAAATGCGCTTGGAAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 410 TTGATTTACTAACAATGCTTCAACAGATCTTCACTTCAACATGATGAGCGTGGACGCT 469
DB 650 TAGATTACTAACAATGCTTCAACAGATCTTCACTTCAACATGATGAGCGTGGACGCT 709
QY 470 AATATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
DB 710 AATATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 530 TCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589

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QY	950	CTTAGGGTATACCAACAGTAGACCTGGATCCATCTCTAGAGCCTTTCTTAGAAACT	1009
Db	1181	CTTTGGGTAAACGACACAGCTGCTCGAATCCAGTTCCTTAGCGCTCTCGATGAAACT	1240
QY	1010	TCAAGCGGTGTTTCCGGAGACTTTCGCTTCCACTGAATGAGATGAGCGCAGAGCA	1069
Db	1241	TCAAGCGATGCTTCAGAGAGTTTCGCATCCCACTCGTCCACGATCGAACAGCAAACT	1300
QY	1070	CTAGCAGATCCGAATACAGTTCAGATTCCTGTTCAC	1107
Db	1301	CCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCC	1338

RESULT 18

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PCT-US94-10358-3
Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
PCT-US94-10358-3

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	Query Match	38.7%	Score 446.4	DB 5	Length 1618
	Best Local Similarity	66.9%	Pred. No. 9,2e-100		
	Matches 668	Conservative 0	Mismatches 321	Indels 9	Gaps 2
QY	110 ACAGCAAGCGACGCCCGGCTCGAGAGACGCCACGTGAGGCCGGCGCATCTCCCGG				
DB	350 ACCGACACGGGGCTTGACCGGGAAAGACAGCCTGTGCCTTGAACCGCACCCCTTCATGG				
QY	170 CCATCCCGGTATCATCAACGGGGCTTACTCCGTAGTCTTCTCTGGGCTTGGGGGA				
DB	410 TCACAGCCATTACCATCATCAGGCGCCCTTACTCATGTGTGTAGTGGGCTTTCGAA				
QY	230 ACTGGCTGGTATCTTTCGTGATCATCCGATTACAAAGTTGAAGACGAAACCAATTT				
	289				

Db	470	ACTCTCGTGCATGTATGTGATTGTGAAGATACCAAAATGAAAGACTGCCAACATCT	529
Oy	290	ACATATTTAACTGGCTTTGGCAATGCTTTAGTTACTACAACATGCCCTTTAGAGTA	349
Db	530	ACATTTTCAACCTTGTCTGTGGCAACGCCCTTAAAGGACAGTACACTGCCCTTTAGAGTG	589
Oy	350	CGGCTACTGATGAATATCTCGGCTTTTGGGAGATGCTGTGCAAGATAGTAATTTCCA	409
Db	590	TCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCTCTGCAAGATCGTATCTCA	649
Oy	410	TTGATTACTACAAATGTTCAACGACATTTTCACCTTTGACCATGATGAGCTGACCGCT	469
Db	650	TAGATTACTACAAATGTTCAACGACATTTTCACCTCTGCACCATGAGCGTGAACGCT	709
Oy	470	ACATTTGCGATGGCAACCCGTGAAGCTTTGACCTCCGACACCCCTGAAGGCAAGA	529
Db	710	ACATTTGCTGTGCACCCAGTCACAAACCCCTGGATTTCCGTAACCCCGAATGCAAAA	769
Oy	530	TCATCAATATCTGCATCTGGCTGTGTCGTATCTGTGGACATCTGCATATGCTCTTG	589
Db	770	TCGTCAAGCTCTGCAACTGGATCTCTCTTCTGTGCATCGGTCCTGTATATGTTCAATG	829
Oy	590	GAGGCACCAAGTAAAGGAAGACGTGCATGTCATTTGATGTCTCTTGCACTTCCCAATG	649
Db	830	CAACCACAAAATAAAGGACAGGGATC-----CATAGATTGACCTCAAGTTCACAC	883
Oy	650	ATGACTACTCTGTGTGGGACCTCTTTCATGAAGATCTGCGTTCATCTTTGSCCTTGTGA	709
Db	884	CAACCTGTACTGGGAACCTGCTC---AATACTGTGCTTTATCTTGCTTTCAATCA	940
Oy	710	TCCTGTCTCATCATCATGTGTCTGTACACCTGATGATCTCGGTCTCAAGAGCTCC	769
Db	941	TGCCGATCTCATCATCATGTGTGTGTTAAGGCCCTGATGATCTTACGACTCAAGAGCTTC	1000
Oy	770	GGCTCTTTCTGGTCTCCCGAGGAAGATGSCAACCTGCGTAGGATACACGACATGGTCC	829
Db	1001	GCATGCTATCGGCTTCCAAAGAAAGACAGGAATCTGCGCAGATCAACCGGATGTGC	1060
Oy	830	TGTGTGTGTGGCAGTCTTGCTGTCTGTGAGACTCCCATTCACATATTCATCTGTGTGG	889
Db	1061	TGGTGTGTGTGGCTGTATTTATCGTGTGTGAGACCCCATTCACATCATGATCATATCA	1120
Oy	890	AGGCTCTGGGAGACCTCCCAACAGCACAGTGTCTCTCAAGTATTACTTTCGACATCG	949
Db	1121	AAAGGCTGATCCAGATTCAGAAACCAATTTCAAGACGGTTTCTGGACATCTTGCAATG	1180
Oy	950	CCTTAGGCTATACCAACAGTAGCTGTGATCCCATTTCTCTACGCTTTCTGATGAAACT	1009
Db	1181	CTTTGGGTACGAAACAGCTGCTGTATCCAGTTCTTTAGCTTCTGTGATBAAACT	1240
Oy	1010	TCAAGCGGTGTTCCGGAATCTTGCTTTTCCACTGAAGATGAGATGAGCGGACAGCA	1069
Db	1241	TCAAGCATGCTTCAGAGAGTTTGCATATCCCAACCTGTCTCAGATCGAACAGCAAACT	1300
Oy	1070	CTAGCAGATGCCAAATACAGTTAGGATCTGCTTAC	1107
Db	1301	CACTCTGATGCTGCAGAACACTAGGAACATCTCTCC	1338

RESULT 19

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US-08-889-108-7
: Sequence 7, Application US/08889108
: Patent No. 6103492
:
: GENERAL INFORMATION:
:
: APPLICANT: Yu, Lei
:
: TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
:
: NUMBER OF SEQUENCES: 17
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Arnold, White & Durkee
:
: STREET: P. O. Box 4433
:
: CITY: Houston
:
: STATE: TX
:
: COUNTRY: USA

```

```

1      ZIP: 77210-4433
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: Floppy disk
4      COMPUTER: IBM PC compatible
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6      SOFTWARE: PatentIn Release #1.0, Version #1.25
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/889,108
9      FILING DATE:
10     CLASSIFICATION:
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: 08/305,518
13     FILING DATE:
14     ATTORNEY/AGENT INFORMATION:
15     NAME: Wilson, Mark B.
16     REGISTRATION NUMBER: 37,259
17     REFERENCE/DOCKET NUMBER: INDA005\WIM
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: 512-418-3000
20     TELEFAX: 512-474-7577
21     INFORMATION FOR SEQ ID NO: 7:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 1610 base pairs
24     TYPE: nucleic acid
25     STRANDEDNESS: single
26     TOPOLOGY: linear
27     MOLECULE TYPE: CDNA
28     US-08-889-108-7

```

Query Match	37.7%;	Score 434.8;	DB 3;	Length 1610;
Best Local Similarity	66.3%;	Pred. No. 6.3e-97;		
Matches 660; Conservative	0;	Mismatches 327;	Indels 9;	Gaps 2

OY	92	CCGGCTGGGCGAGACC	CGAAGCAAGGAGGGCGGCTCGGAGGAGCGCGAGCTGGAGC	151
Db	363	CCGACCATCGGCTCCGACCGGACCGACCTTGGCGGGAGACAGCCTGGCCCTCCGA	4222	
OY	152	CCGGCACATCTCCCGGCGCATCCGGTCATCATCAAGCGGCTTACTCCGTAAGTGTG	2111	
Db	423	CCGGCAGTCCCTCCATGATCAAGGCATACGATCATGGCCCTCTACTCATCGTGTGG	482	
OY	212	TCTGGGCTTGGTGGGCACTCGCTGTGTCATGTTGTGATCATCCGATACCAAAATGA	2711	
Db	483	TGGTGGGCTCTTCGAAACTTCCTGTGATGATGTAATGTGTCAGATACCAAGATGA	5422	
OY	272	AGACAGAACCAACATTTACATATTAACTGGCTTGGGAGATGCTTAACTCTCA	3311	
Db	543	AGACTGCAACCAACATCTACATTTTAACTTGTCTGTGGCAAGTCCCTTACCAACATGA	6022	
OY	332	CCATGCCCTTTCAGAGTACGCTCTACTTGATGAATTCCTGGCTTTGGGAGTGTCT	3911	
Db	603	CCCTGCCCTTCAGAGTGTGAATTTACTTAATGGGAACATGGCAATTGGAACATCTTT	6622	
OY	392	GCAAGATAGTAATTTCCATTGATCTACACAATGTTCAACAAGATCTTCACTTGACA	4511	
Db	663	GCAAGATAGTACTTCATAGATTAATCTAATACATGTTCAACAAGATTTCACTCTGCA	7222	
OY	452	TGATGAGCGTGAACCGCTCATTTGGCGGTGTCACCCGTAAGGCTTGGACTTCCGA	5111	
Db	723	CCATGAGTGTGATTCATCATTTGACGTGTGCACCCCTGTCAAGGCTTGTGATTTCCGA	7822	
OY	512	CACCTTTGAAGGCAAAATCATCAATATCTGCATCTGGCTGTGTGCTCATCTTGGCA	5711	
Db	783	CTCCCCGAATGCAAAATTAATCATGTGTGAACTGGAATCTCTCTTCCAGCAATTGTC	8422	
OY	572	TCTCTGCATATGCTCTTGGAGCAACCAAGTCAGGAAGAGCTGATGTCAATTGAGTCT	6311	
Db	843	TTCTGTATATGTTCAAGGCTACAAACAAATAACAGCAAG-----TTCCATAGATGTA	896	
OY	632	CTTGGAGTTCACAGATGATGATCACTCTGTGGGACCTTTGATGAATCTGGCTCT	6911	
Db	897	CACTAACATTTCTCATTCACCACTGTACTGGGAAACCTGCG--TGAAGTCTGTGTT	953	

Qy	692	TCATCTTTGCCCTTGGTANCCCTGCGCCATCATCATATGTCGTCAGAACCCGATGATGCC	751
Db	954	TCATCTTTGCCCTTCAATATGCGAGTGTCAATCATTAACCTGTGCTATGAGCTGATGATCT	1013
Qy	752	TGCGCTCAAGAGCCGTCCGGCTCCTTTCTTGCGCTCCGAGAGAAAAGATGCAACCTGCGCTA	811
Db	1014	TGCGGCTCAAGAGTGTCCGCAATGCTCTCTGGGCTCAAGAAAAGGACAGAAATCTTGCAG	1073
Qy	812	GGATTAACCAAGACTGGATCCTGGTGGTGGTGGCAATCTTGTGCTGCTGGAATCCCATTC	871
Db	1074	GGATTAACCAAGATGGTGGTGGTGGTGGGCGGTGTGTTTCATGCTGCTGGAGACTCCCATTC	1133
Qy	872	ACATATTCATCTCGGTGGAGGCTCGGGGAGACACTCCACAGACAGTCTCTCTCCCA	931
Db	1134	ACATTTACGTCAATCATTTAAAGCTTTGGTTACAAATCCAGAAACTACGTTCCAGACTGTTT	1193
Qy	932	GCTATTACTTCGTGATCGCTTAGGCTATACCAACAGTAGGCTGAATCCATTCCTACAG	991
Db	1194	CTTGGCACTTCGTGATTTGCTCTAGGTTTACAAACAGCTGCTCAACCCAGTCTTTATG	1253
Qy	992	CCTTTCTTGAATGAACCTTCAAGCGGATTTCCGGACCTTCTGCTTTCACCTGAAGATGA	1051
Db	1254	CATTTCTGAATGAACCTTCAAGAGATGCTTCAAGAGATTTCTGTATCCCAACTCTTCCA	1313
Qy	1052	GGATGAGCGGCGAGGACCTAGACAGAGTCCGAATA	1087
Db	1314	ACATTTAGCAACAAACTCCACTGGAATTCGTCCAG	1349

RESULT 20
PCT-US94-10358-7

Sequence 7, Application PC/TUS9410358

GENERAL INFORMATION:
APPLICANT:

```

; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wh

STREET: P. O. Box 4433
CITY: Houston

STATE: Texas

; COUNTRY: USA
; ZIP: 77210

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; COMPUTER READAB
; MEDIUM TYPE:

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COMPUTER: IBM
OPERATING SYSTEM: OS/360

OFFERING IS
SOFTWARE: PA
CUT DOWN 100%

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; CURRENT APPLICATION DATE
; APPLICATION NUMBER:

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; FILING DATE: Concurrent
 ; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICANT NUMBER: 08/1320

FILED DATE: 13 SEPTEMBER 1993

ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.

REGISTRATION NUMBER: 3
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000

TELEPHONE: (312) 710-5000
TELEFAX: (713) 789-2679

TELEX: 79-0924
; INFORMATION FOR SEQ
;

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; SEQUENCE CHARACTERISTIC
; LENGTH: 1610 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single

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; CIPHERTEXT: single
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; TOPOLOGY: linear
;
; WORDS: 128

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MOLECULE TYPE: CDNA
PCT-US94-10358-7

Query Match	37
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Query Match 37.7%; Score 434.8; DB 5; Length 1610;

Query Match 37.7%; Score 434.8; DB 5; Length 1610;

Best Local Similarity 66.3%; Pred. No. 6.3e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACAAAGGAGCGCGGCTCGGAGGAGCGGACCTGGAGC 151
Db 363 CCGGACCAATCGGCTCGGAACCCGACCGACCTGGGAGAGACAGCCGTGCTCCGA 422
QY 152 CCGGCGACATCTCCCGGCGATCCGGATCATACGCGGCTCACTCCGAGTGTG 211
Db 423 CCGGAGTCCCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
QY 212 TCGTGGGCTTGGTGGGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
Db 483 TGGTGGGCTTGGTGGGAACTTCTGGTCTGATGATGATGATGATGATGATGATGATG 542
QY 272 AGACAGCAACCAATTTACATTTTAACTTGGCAGATGCTTTAGTTACTACA 331
Db 543 AGACTGCCACCAACATTTTCACTTTTCACTTGGCAGATGCTTTAGCCACAGTA 602
QY 332 CCATGCCCTTTCAGATAGGCTCTGATGATGATGATGATGATGATGATGATGATGATG 391
Db 603 CCTGCCCTTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 662
QY 392 GCAAGATAGTAATTTCCATTTGATTTACTACAATGTTCCAGCATCTTCACTTGACA 451
Db 663 GCAAGATAGTATCTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 722
QY 452 TGATAGAGGTGAGCGGCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
Db 723 CCATAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
QY 512 CACCTTTGAAGGCAAAATCATCATATCTGATGATGATGATGATGATGATGATGATG 571
Db 783 CCCCCGAAAGGCAAAATTTATCATATGCTGCACTGATGCTCTCTTCAAGCATTTGG 842
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGACGTGATGATGATGATG 631
Db 843 TTCCTGATATGTTTATGCTGATACAAATAACAGCAAG-----TTCATAGATTTGA 896
QY 632 CTTTGACAGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db 897 CACTTAACATTTCTCATCCAACTGATGATGATGATGATGATGATGATGATGATGATG 953
QY 692 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
Db 954 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1013
QY 752 TGGCTCTGAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
Db 1014 TGGCTCTGAAGAGTCCGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1073
QY 812 GGATCAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
Db 1074 GGATCAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1133
QY 872 ACATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 1134 ACATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1193
QY 932 GCTATTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 1194 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
QY 992 CTTTCTTGTATGAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAAGATG 1051
Db 1254 CAATTCTGATGAAACTTCAAAAGATGCTTCAAGAGATTTCTGTATCCCAACTCTTCCA 1313
QY 1052 GGATGAGCGGAGAGCACTAGCAGATGCTCGAATA 1087
Db 1314 ACATTTGAGCAACAAACTCCACTGAAATTCGTCA 1349

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RESULT 21

US-08-188-275A-1
; Sequence 1, Application US/08188275A

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; Patent No. 6258556
; GENERAL INFORMATION:
; APPLICANT: Unl, George R.
; APPLICANT: Wang, Jia-Bei
; APPLICANT: Persico, Antonio
; APPLICANT: Johnson, Peter S.
; TITLE OF INVENTION: CDNA and Genomic Clones Encoding Human
; TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-3487
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,275A
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-449P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2160
; OTHER INFORMATION: /label= cDNA
; OTHER INFORMATION: /note= "cDNA encoding human mu opiate receptor"
; US-08-188-275A-1

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Query Match 37.7%; Score 434.8; DB 3; Length 2160;

Best Local Similarity 66.3%; Pred. No. 7e-97;

Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACAAAGGAGCGCGGCTCGGAGGAGCGGACCTGGAGC 151
Db 337 CCGGACCAATCGGCTCGGAACCCGACCGACCTGGGAGAGACAGCCGTGCTCCGA 396
QY 152 CCGGCGACATCTCCCGGCGATCCGGATCATACGCGGCTTACTCCGATGATGTTG 211
Db 397 CCGGAGTCCCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 456
QY 212 TCGTGGGCTTGGTGGGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
Db 457 TGGTGGGCTTGGTGGGAACTTCTGGTCTGATGATGATGATGATGATGATGATGATG 516
QY 272 AGACAGCAACCAATTTACATTTTAACTTGGCAGATGCTTTAGTTACTACA 331
Db 517 AGACTGCCACCAACATTTTCACTTTTCACTTGGCAGATGCTTTAGCCACAGTA 576
QY 332 CCATGCCCTTTCAGATAGGCTCTGATGATGATGATGATGATGATGATGATGATGATG 391
Db 577 CCTGCCCTTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 636

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QY 392 GCAAGATGTAATTTCATTGATTACTACAACTGTTACACGACATCTTACCTTGACCA 451
DB 637 GCAAGATGTAATTTCATTGATTACTACAACTGTTACACGACATCTTACCTTGACCA 451
QY 452 TGATGACGCGGACGCGTACGCGTGGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511
DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756
QY 512 CACCTTTGAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 571
DB 757 CTCGCCGAATGCGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 816
QY 572 TCTGTCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
DB 817 TTCCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 870
QY 632 CATTGACGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 871 CACTAACATTTCTCTCATCCACCTGTTACTGGGAAAACCTCG---TGAAGATCTGTGTT 927
QY 692 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 928 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 987
QY 752 TGGGTCTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 811
DB 988 TGGGTCTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1047
QY 812 GGATGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
DB 1048 GGATGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1107
QY 872 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
DB 1108 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
QY 932 GCTATTACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
DB 1168 CTGGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1227
QY 992 CTTTCTTGAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
DB 1228 CATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1287
QY 1052 GGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1087
DB 1288 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323

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RESULT 22
US-09-351-198-1
; Sequence 1, Application US/09351198
; Patent No. 6335168
; GENERAL INFORMATION:
; APPLICANT: Kireek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischefield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226N
; CURRENT APPLICATION NUMBER: US/09/351,198
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

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; NAME/KEY: misc feature
; LOCATION: (2063)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2091)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
US-09-351-198-1

```

```

Query Match 37.7% Score 434.8; DB 4; Length 2162;
Beet Local Similarity 66.3%; Pred. No. 76-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 151
DB 337 CCGAGCCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 396
QY 152 CCGGCGACATTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 211
DB 397 CCGGCGACATTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 456
QY 212 TCGTGGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 271
DB 457 TGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 516
QY 272 AGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 331
DB 517 AGACTGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 576
QY 332 CCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 391
DB 577 CCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
QY 392 GCAAGATGTAATTTCATTGATTACTACAACTGTTACACGACATCTTACCTTGACCA 451
DB 637 GCAAGATGTAATTTCATTGATTACTACAACTGTTACACGACATCTTACCTTGACCA 496
QY 452 TGATGACGCGGACGCGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 511
DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756
QY 512 CACCTTTGAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 571
DB 757 CTCGCCGAATGCGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 816
QY 572 TCTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
DB 817 TTCCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 870
QY 632 CTTTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 691
DB 871 CACTAACATTTCTCTCATCCACCTGTTACTGGGAAAACCTCG---TGAAGATCTGTGTT 927
QY 932 TCACTTTGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
DB 992 TCACTTTGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
QY 992 TCACTTTGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
DB 1228 CATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1287
QY 1052 GGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1087
DB 1288 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323

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REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1379:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9452072
US-09-016-434-1379

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Query Match      37.7%; Score 434.8; DB 4; Length 2162;
Best Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAAGGAGCGCGCTCGAGAGACGGCGAGCTGGAGC 151
DB 337 CCGACCCATGCGGTCCGAAACCGACCACTGGCGGAGAGACAGCTGTGCTCCGA 396
QY 152 CCGGCAATCTTCCCGGCAATCCGGTATCATACGGCGGTCTTACCTCGTAGTGTG 211
DB 397 CCGGAGTCCCTCCATGATCAGGCGCATCAGATCATGGCCCTTACTCATCGTGTGG 456
QY 212 TCGTGGGCTTGGTGGCACTGCTGTCATGTGTGATCATCCGATACAAAGATGA 271
DB 457 TGGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGATG 516
QY 272 AAGACAGCAACAACTTATCATATTTAACTGCTTGGCAGATCTTATGATTAACA 331
DB 517 AGACTGCCACCAACTCTACATTTTCACTTCTGCTGCAATGCTTATGCAACAGTA 576
QY 332 CCATGCCCTTTAGAGTACGGTCTACTGATGATTTCTGGCTTTTGGGAGTGTGCT 391
DB 577 CCTGCGCTTCAGAGTGTGAATTACTTATGGAACATGGGCACTTGGAAACCATCTT 636
QY 392 GCAGATAGTATTTTCAATGATTTACTCAACATGTCACGACATCTTCACTTGAACA 451
DB 637 GCAAGATGATGATCTCCATAGTATCTTAAATTTTCAACGACATTTTCACTTGTGA 696
QY 452 TGATAGGCTGAGACGGCTACATTTGCGGTGCGACCCGTAAGGCTTGAATTCGCA 511
DB 697 CCATGAGTGTGATGATACATTTGCAAGTCTGCAACCTGTCAAGGCTTAAATTTCCGTA 756
QY 512 CACCTTGAAGGCAAGATCATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 571
DB 757 CTCCCGGAAATGCCAAATTTATCAATGCTGCACTGGATCTCTTTCACGCAATGGTC 816
QY 572 TCTTGCATAGTCTTGGAGGACCAAGTCAGGAAGAGCTGATCTGATTTAGTGTCT 631
DB 817 TTCCTGATGTTTCAATGCTACAAACAAATACAGCAAG-----TTCATATAGTGA 870
QY 632 CCTTGCATTTCCAGATGATGATCTCTGCTGGGAACTCTTCAATGAAGTCTGCTGCT 691
DB 871 CACTAACATTTCTTCATCAACCTGGTACTGGGAAACCTG---TGAAGATCTGTGTT 927
QY 692 TCATTTTGGCTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
DB 928 TCATTTTGGCTTGTGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
QY 752 TGGCTTCAAGAGCGTCCGCTCTTCTTGGCTCCGAGAGAAAGATCGCAACCTGGCTA 811
DB 988 TGGCTTCAAGAGCGTCCGCTCTCTGCTGCTCAAGAGAAAGAGAGCAAGAAATTTGAA 1047
QY 812 GGATCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 1048 GGATCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931

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DB 1108 ACATTTAGTATCATTTAAAGCTTGGTTACATCCAGAAACTACAGTTCAGCTGTTT 1167
QY 932 GCTATTACTTGTGATGCTCTTAAAGCTTAACTAACAGATGAGCTGATCCATTTCTACG 991
DB 1168 CTGGCACTTGTGATGCTCTTAAAGCTTAACTAACAGATGAGCTGATCCATTTCTACG 1227
QY 992 CTTTCTTGAATGAATCTTAAAGGCTTTCGGGACTTGTGCTTCTTCACTGAAGATGA 1051
DB 1228 CATTTGTGAATGAATCTTAAAGGCTTTCGGGACTTGTGCTTCTTCACTGAAGATGA 1287
QY 1052 GGATGAGCGGCGAGAGCACTAGAGAGTCCGAATA 1087
DB 1288 ACATGAGCAACAAACTCCACTGGAATTCGTGACA 1323

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RESULT 25
US-09-355-709C-7
Sequence 7, Application US/09355709C
Patent No. 6538120
GENERAL INFORMATION:
APPLICANT: Max-Deibrock-Centrum fur Molekulare Medizin
TITLE OF INVENTION: Genomic Sequences of Human -opioid Receptor Gene ...
FILE REFERENCE: 101195-15
CURRENT APPLICATION NUMBER: US/09/355,709C
CURRENT FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: DE 197 03 925.1
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 2162
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Human Genomic
OTHER INFORMATION: Clone
OTHER INFORMATION: CDNA encoding human opiate receptor
NAME/KEY: unsure
LOCATION: (2063)
OTHER INFORMATION: n = unknown
NAME/KEY: unsure
LOCATION: (2091)
OTHER INFORMATION: n = unknown
US-09-355-709C-7

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```

Query Match      37.7%; Score 434.8; DB 4; Length 2162;
Best Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAAGGAGCGCGCTCGAGAGACGGCGAGCTGGAGC 151
DB 337 CCGACCCATGCGGTCCGAAACCGACCACTGGCGGAGAGACAGCTGTGCTCCGA 396
QY 152 CCGGCAATCTTCCCGGCAATCCGGTATCATACGGCGGTCTTACCTCGTAGTGTG 211
DB 397 CCGGAGTCCCTCCATGATCAGGCGCATCAGATCATGGCCCTTACTCATCGTGTGG 456
QY 212 TCGTGGGCTTGGTGGCACTGCTGTCATGTGTGATCATCCGATACAAAGATGA 271
DB 457 TGGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGATG 516
QY 272 AAGACAGCAACAACTTATCATATTTAACTGCTTGGCAGATCTTATGATTAACA 331
DB 517 AGACTGCCACCAACTCTACATTTTCACTTCTGCTGCAATGCTTATGCAACAGTA 576
QY 332 CCATGCCCTTTAGAGTACGGTCTACTGATGAATTTCTGCGCTTTTGGGAGTGTGCT 391
DB 577 CCTGCGCTTCAGAGTGTGAATTACTTATGGAACATGGGCAATTTGGAAACCATCTT 636
QY 392 GCAAGATAGTATTTTCAATGATTTTCAACATGTTTCAACGATCTTCACTTGAACA 451
DB 637 GCAAGATAGTATTTTCAATGATTTTCAACATGTTTCAACGATCTTCACTTGAACA 696

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Oy	452	UGATGAGGTGGAACGGTCAATTCGCGTGTGCAACCCCGTGAAGGCTTTGGACTTCGCGA	511
Db	697	CCATAGTGTGATGATACATTCGACGTGCGACCCCTTCGAAAGGCTTAGATTTCCGTA	756
Oy	512	CACCCCTTGAGGCAAGATCATCATATATCTGCATCTGCGTGTGTCATCTGTGTGGA	571
Db	757	CTCCCCGAAATGCCAAAATATCATATGTCTGCAATCGATATCCTCTCTTACGACATTGGTC	816
Oy	572	TCTCTGCATAATGTCCTTTGAGGCAACCAAGTCAGGAGAGAGCGTCGATGTCAATTAGTGTCT	631
Db	817	TTCCGTGATATGTTCAATGAGCTTACCAACAAAATATACAGGCAAGG-----TTCCATATGATTTGA	870
Oy	632	CCTTGACAGTCCCAATGATGACTACTCCTGCTGGGACCTCTTCATGAAATGATGTGCTCT	691
Db	871	CACTAACATTTCTCTCATCCAACCTGGTACTGGGAAAACTCG--TGAAATCTGTGTTT	927
Oy	692	TCATCTTTGCTTCGTGATCCCTGTGCTCATCATCATCTGTCTGTACACCCGTGATGATCC	751
Db	928	TCATCTTGCCCTTCATTTATGCGACAGTCTCATTTACCGTGTGCTATGGAATGATGATCT	987
Oy	752	TGCGTCTCAAGAGCGTCCGGCTCTCTTTCTGCTCTCCGAGAGAAAGATGCAACTGCGTA	811
Db	988	TGCGGCTCAAGAGTGTCCGCAATGCTCTCTGCGCTCCAAAAGGACAGAGAAATCTTCGAA	104
Oy	812	GGATACACAGACTGTCCTGTGTGTGTGTGTGTGGACAGTCTGTCGTCTGTGGAATCCCATTC	871
Db	1048	GGATACACAGATGT	1107
Oy	872	ACATATTCATCCTGTGTGAGGCTCTGTGGGAGACCTCCACAGACAGCTGCTCTTCCGA	931
Db	1108	ACATTTAGCTATCATTTAAAGCTTGTTGTTACATCCGAAATCTAGCTTCAGACCTGTTT	116
Oy	932	GCTATTAATCTTGTGATTCGCTTAGGCTATATACCAACAGTAGCTGAATCCCATTTCTTACG	991
Db	1168	CTTGGACATCTGCAATTCGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG	122
Oy	992	CCTTCTTGATGAAAACTTCAGACGGGTGTTCCGGGACTCTGCTTCCATGGAAGATGA	105
Db	1228	CATTTCGTGATGAAAACTTCAGACGATGCTTACAGAGATGTTCTGTATCCACCTCTTCCA	128
Oy	1052	GGATGAGCGGCGAGACACTACAGAGATGCCGAATA	1087
Db	1288	ACATTGAGCAACAAAATCTCACTCGAATTCGTCA	1323
RESULT 26			
US-09-761-962A-3			
Sequence 3, Application US/09761962A			
Patent No. 6500927			
GENERAL INFORMATION:			
APPLICANT: Memorial Sloan-Kettering Cancer Center			
TITLE OF INVENTION: MULTIPLE SPLICE VARIANTS OF THE MU-OPIOD RECEPTOR GENE			
FILE REFERENCE: 830002-2000.2			
CURRENT APPLICATION NUMBER: US/09/761,962A			
CURRENT FILING DATE: 2001-01-17			
PRIOR APPLICATION NUMBER: 09/743,872			
PRIOR APPLICATION NUMBER: PCT/US99/15974			
PRIOR FILING DATE: 1999-07-15			
NUMBER OF SEQ ID NOS: 46			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 3			
LENGTH: 1334			
TYPE: DNA			
ORGANISM: Mus musculus			
US-09-761-962A-3			

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FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-761-962A-11

Query Match      37.5%; Score 432.4; DB 4; Length 1365;
Best Local Similarity 65.8%; Pred. No. 2.3e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCGGCGGCTGGAGGACGGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGAGCCAGCCTGTGCTCAGA 244
QY 152 CCGGCAATCTCCCGGCAATCCGGTATCATCAAGCGGTCTTACTCCGTAAGTTGG 211
DB 245 CCGGCAAGCCCTTCAATGATCAGGCCATCACCATATGCGCTTATCTATCGTGTG 304
QY 212 TGGTGGCTTGGTGGCAATCGCTGTGATGTTGCTGATCATCCGATACAAAGATGA 271
DB 305 TGGTGGCTTGGTGGCAATCTGCTGTATGATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGCAACCAATTTACATATTTTAACTGGCTTGGAGAGCTTTAGTACTACAA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACTTGTCTGCAAGATCCCTTAGCATTACA 424
QY 332 CCATGCCCTTTAGAGTACGCTTACTTGTATGAATTCCTGCGCTTTTGGAGATGTGCTGT 391
DB 425 CGCTCCCTTTAGAGTATCTACTGATGATGATGATGATGATGATGATGATGATGATG 484
QY 392 GCAAGATGATATTTTCAATGATTTACTAACAATGTTACACAGCACTTTTCACTTGAACA 451
DB 485 GCAAGATGATATCTCAATGATTTACTAACAATGTTACACAGCACTTTTCACTTGAACA 544
QY 452 TGATGAGCGTGAGCCGCTACATTTGCGTGTGCAACCCGCTGAAAGCTTTGACCTTCCGA 511
DB 545 CCATAGAGTGAACCGCTACATTTGCGTGTGCAACCCGCTGAAAGCTTTGACCTTCCGA 604
QY 512 CACCTTGAAGCAAGATCATATATCTGATTTGCTGTGCTGTGCTGTGCTGTGCTGTG 571
DB 605 CCCCCGAAATGCAAAATGTCATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 664
QY 572 TCTGTCAATAGTCTTGTGAGGACCAAAAGTCAGGGAAGAGTGTGATGATGATGATG 631
DB 665 TGCCGCTATGTTTCAATGCAACCAAAATGACGAGGAGGTC-----CATAGTTGCA 718
QY 632 CTTTGAGTTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 719 CCGTCAAGTCTCTCATCCCAATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 692 TCATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 776 TCATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
QY 752 TGGCTCTCAAGAGCGTCCGGCTCTTTTGTGCTCCGAGAGAAAGATGCAACCTGGGTA 811
DB 836 TACGACTCAAGAGTGTGCGATGCTGTGCGCTCCAAAGAAAGAGAGAGAGAGAGAGAG 895
QY 812 GGAATCAACAGACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 871
DB 896 GGAATCAACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 955
QY 872 ACATATTCATCTGTGAGGCTGTGGGAGAGCACTCCACAGAGCAAGCTGTCTCTCCA 931
DB 956 ACATCTATGTATCATCAAGCACTGATCAAGATTTCCAGAAACACTTTCCAGAGCTGTT 1015
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QY 932 GCTATTACTTGTGATGCGCTTAAAGCTATTAACCAAGATAGCTGAATCCATTTCTTACG 991
DB 1016 CCGGCACTTCTGATGATGCTTGGGTTTACCAAAAGAGTGTGCAACCCAGTTCTTATG 1075
QY 992 CTTTCTTGAAGAAACTTCAAGGCGTGTTCGGGACTTGTGCTTCCACTGAAGATGA 1051
DB 1076 GCTTCTGATGAATAACTTCAAGAGATGTTTAAAGAGTCTGATCCCAACTTCTTCCA 1135
QY 1052 GAATGAGCGGAGAGCACTAGCAGAGTCCGAATTAAGTTACAGATC 1099
DB 1136 CAATGCAACAGCAAAACTGCTGCTGCAATCCGTCAAAACACTAGGAAAC 1183

RESULT 28
US-09-761-962A-1
; Sequence 1, Application US/09761962A
; Patent No. 650927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICE VARIANTS OF THE MU-OP10ID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-761-962A-1

Query Match      37.5%; Score 432.4; DB 4; Length 1423;
Best Local Similarity 65.8%; Pred. No. 2.3e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCGGCGGCTGGAGGACGGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGAGCCAGCCTGTGCTCAGA 244
QY 152 CCGGCAATCTCCCGGCAATCCGGTATCATCAAGCGGTCTTACTCCGTAAGTTGG 211
DB 245 CCGGCAAGCCCTTCAATGATCAGGCCATCACCATATGCGCTTATCTATCGTGTG 304
QY 212 TGGTGGCTTGGTGGCAATCGCTGTGATGTTGCTGATGATGATGATGATGATGATGATG 271
DB 305 TGGTGGCTTGGTGGCAATCTGCTGTATGATGATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGCAACCAATTTACATATTTTAACTGGCTTGGAGAGCTTTAGTACTACAA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACTTGTCTGCAAGATCCCTTAGCATTACA 424
QY 332 CCATGCCCTTTAGAGTACGCTTACTTGTATGAATTCCTGCGCTTTTGGAGATGTGCTGT 391
DB 425 CGCTCCCTTTAGAGTATCTACTGATGATGATGATGATGATGATGATGATGATGATG 484
QY 392 GCAAGATGATATTTTCAATGATTTACTAACAATGTTACACAGCACTTTTCACTTGAACA 451
DB 485 GCAAGATGATATCTCAATGATTTACTAACAATGTTACACAGCACTTTTCACTTGAACA 544
QY 452 TGATGAGCGTGAGCCGCTACATTTGCGTGTGCAACCCGCTGAAAGCTTTGACCTTCCGA 511
DB 545 CCATAGAGTGAACCGCTACATTTGCGTGTGCAACCCGCTGAAAGCTTTGACCTTCCGA 604
QY 512 CACCTTGAAGCAAGATCATATATCTGATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 571
DB 605 CCCCCGAAATGCAAAATGTCATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 664
QY 572 TCTGTCAATAGTCTTGTGAGGACCAAAAGTCAGGGAAGAGTGTGATGATGATGATG 631
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Db      665 TGCCTGTAATGTTCAATGSCAACCAAAATACAGGAGGAGT-----CATAGATTGCA 718
Qy      632 CCTTGAGTTCACAGATGATGACTCTGAGTGGGACCTCTTCAATGAGATCTGCTCT 691
Db      719 CCTCAAGTCTCTCAATCCCAATGATCTGAGAGAACTGCTC---AAATCTGTGCT 775
Qy      632 TCATCTTTCCTGCTGATCTCTGCTCTCATCATCTCTGCTTACACCTTGATGATCC 751
Db      776 TCATCTTTCCTGCTTCAATGAGGAGTCTCTCATCATCTGTGTATGATGATGATCT 835
Qy      752 TCCGCTCAAGAGCGTCCGCTCTTCTGCTCTCCGAGAGAAAGATCGCAACTTCGTA 811
Db      836 TACGACTCAAGAGTGTCCCAATGCTGTGCGGCTCCAAAGAAAGACAGAACTTCGCGCA 895
Qy      812 GGATACACGACATGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      896 GGATACACCGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
Qy      872 ACATATTCATCTGCTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
Db      956 ACATCTATGTCTCATCAAGACATGATCATGATTCAGAAACACCTTTCAGAGCTGTT 1015
Qy      932 GCTATTTACTTCTGATCGCTTATAGCTATACCAACAGTAGCTGAATCCATTTCTTACG 991
Db      1016 CCTGCACTTCTGATGCTTGTGCTTGTGTTACAAACAGCTGCTGAACCCAGTTCTTATG 1075
Qy      992 CTTTCTTGATGAAATCTTCAAGCGGTGTTCCGGAATCTTCTGCTTCTGATGAAATGA 1051
Db      1076 CTTTCTTGATGAAATCTTCAAGCGGTGTTTAGAGAGTTCTGCAATCCCACTTCTCTCA 1135
Qy      1052 GGATGAGGCGAGAGCACTAGACAGATGCGAAATACAGTTACAGTTCAGATC 1099
Db      1136 CAATGACAGCAAAACTCTGCTCAATCTGCTCAAACTGAGGAAAC 1183

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RESULT 29
US-09-761-962A-16
; Sequence 16, Application US/09761962A
; Patent No. 6500927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICING VARIANTS OF THE MU-OP10ID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; PRIORITY FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-16

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```

Query Match      37.5%; Score 432.4; DB 4; Length 1610;
Best Local Similarity 65.8%; Pred. No. 2,4e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;
Qy      92 CCGGCTGGGCGAGCCGACAGCAACGAGCGCGGCTCGGAGGACGCGAGCTGAGAC 151
Db      401 CCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGAGCCAGCTGTGCTCCACMA 460
Qy      152 CCGGACACATCTCCCGGCGATCCGCGTATCATCAACGCGGCTTACTCCGATGTTGCG 211
Db      461 CCGGAGCGCTTCCATGATGATCAAGGACATCAATATGCGCTTATCTGATGATG 520
Qy      212 TGTGTGGCTTGTGTGGCAATCGCTGTGTATGTTGTGATCAATCCGATACCAAGATGA 271
Db      521 TAGTGGGCTCTTGTGAAATCTTGTGTGTATGTATGTATGATATACCAAAATGA 580
Qy      272 AAGACGAAACAAATTTATCATATTTAATCTGCTTGTGCAATGCTTATGTTACATACA 331

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```

Db      581 AAGTCCGACCAACCAATCTAATTTTCAACCTTGTCTGTGCAATGCTTAGCAGATGACA 640
Qy      332 CCATGCGCTTTTCAAGATGATGCTTACTGATGATTAATTCCTGCGCTTTTGGGATGCTGT 391
Db      641 CCGTCCCTTTCAAGATGTTAATCTGATGGAACGAGGCTTGTGAAACATCTCTCT 700
Qy      392 GGAAGATGATATTTCCATGATTAATCAATGATGATCAACATGATGATGATGATGATGAT 451
Db      701 GCAAGATGATGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 760
Qy      452 TGATGAGGCTGAGCGCTTACATTTGCGTGTGCAACCCCGTGAAGGCTTGTGATCCGCA 511
Db      761 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 820
Qy      512 CACCTTGAAGGCAAAATCATCAATATATGATGATGATGATGATGATGATGATGATGATG 571
Db      821 CCCCCGAAATGCCAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 880
Qy      572 TCTTGCAATATGCTTGTGAGGCAACCAAGTCAAGGAAAGACGTGATGATGATGATGATG 631
Db      881 TGCCTGTAATGTTCAATGCAACCAAAATACAGGAGGAGT-----CATAGATTGCA 934
Qy      632 CTTGCACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db      935 CCTCAAGTCTCTCATCTCCACATGATGATGATGATGATGATGATGATGATGATGATGATG 991
Qy      692 TCATCTTTCCTGCTGATCTCTGCTGTCTCATCATGATGATGATGATGATGATGATGATG 751
Db      992 TCATCTTTCCTGCTTCAATGCTGCTGTCTCATCATGATGATGATGATGATGATGATGAT 1051
Qy      752 TGCCTGTAAGAGCGTCCGCTCTTCTGTGCTCCGAGAAATATGCAACCTGAGTGA 811
Db      1052 TACGACTCAAGAGTGTGCGATGCTGTGCGGTCCAAAGAAAGACAGAACTGCGCA 1111
Qy      812 GGATCAGCAGATGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1112 GGATCAGCAGATGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1171
Qy      872 ACATATTCATCTGCTGAGAGCTCTGAGGAGACCTCCACAGACAGCTGCTCTCTCA 931
Db      1172 ACATCTATGATCATCAAGACATGATCAAGATTCAGAAACCACTTTCAGAGCTGTT 1231
Qy      932 GCTATTTACTTCTGATCGCTTATAGCTATACCAAGATGATGATGATGATGATGATGATG 991
Db      1232 CTTGCACTTCTGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291
Qy      992 CTTTCTTGATGAAATCTTCAAGCGGTGTTCCGGAATCTTCTGCTTCCAGTGAAGATGA 1051
Db      1292 CTTTCTTGATGAAATCTTCAAGCGGTGTTTAGAGAGTTCTGATCTCCAACTTCTCTCA 1351
Qy      1052 GGATGAGCGGAGAGCACTAGACAGATGCGAAATACAGTTACAGTTCAGATC 1099
Db      1352 CAATGACAGCAAAACTCTGCTCAATCTGCTCAAACTGAGGAAAC 1399

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RESULT 30
US-09-761-962A-9
; Sequence 9, Application US/09761962A
; Patent No. 6500927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICING VARIANTS OF THE MU-OP10ID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; PRIORITY FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1729

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SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-4

Query Match 37.2%; Score 429.2; DB 4; Length 1542;
Best Local Similarity 65.6%; Pred. No. 1.4e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGGCTCGAGAGACGCGAGCTGAGC 151
DB 185 CCGAGCCAGTGGGGTCTTAACCGGAGCGGGCTTGGGGAGAGCCAGCCTGTGGCTCAGA 244
QY 152 CCGGCAACATCTCCCGGCGCATCCGGTCATCATCAAGCGGGCTTACCTCGTAGTGTG 211
DB 245 CCGGAGCGCTTCAATGTCAGAGCCATCAACATATGAGCCCTCTATTCATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCAACTGCGTGTGATGTTGATCAATCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCTGTCATGTATGTATGTAAGATATACCAAAATGA 364
QY 272 AGACAGCAACCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTATGTTACTACA 331
DB 365 AGACTGCCAACCAACTTACATTTTCAACCTTGTCTGGCAGATGCTTACGCACTAGCA 424
QY 332 CCATCCCTTTTACAGTACGGCTTCTGATGAATTCCTGGCTTTTGGGAGTGTGCT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTAGTGGAAACGTCGCTTTTGGAAACATCTCT 484
QY 392 GCAAGATGTAATTTCCATTTGATTTACTAACAATGTTACCGAGATCTTCACTTGAACA 451
DB 485 GCAAGATGTAATTTCCATTTGATTTACTAACAATGTTACCGAGATCTTCACTTGAACA 544
QY 452 TGATGAGCGTGAGACCGGTACATTTGCGTGTGCAACCCCGTGAAGGCTTTGACCTTCCGA 511
DB 545 CCATGAGTGTAGACCGGTACATTTGCGTGTGCAACCCCGTGAAGGCTTTGACCTTCCGA 604
QY 512 CACCTTTGAAGCAAGATTCATCATATCTGATCTGCTGTCTGTCTGATCTGTGGCA 571
DB 605 CCCCCGGAATGCAAAATTTGTCATGTGTGACATGATCTCTCTTCTGCAATTTGCTC 664
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATGCAATTTGAGTCT 631
DB 665 TGCCGTATATGTTATGGAACACCAAAATACAGGCAAGGGTCTC-----CATAGTTGCA 718
QY 632 CTTGCACTTCCAGATGATGATCTCTCTGTTGGGACCTCTTCAATGAAGTCTGCGTCT 691
DB 719 CCTTCACGTTCTCTCATCCCAACATGTACTGGAGAACCTGTCTC---AAATCTGTGCT 775
QY 692 TCATCTTTGCTCTGTGATTCCTGTCTCTCATCATATGTCGTCTGACACCTGATGATCC 751
DB 776 TCATCTTTGCTCTGTGATTCCTGTCTCTCATCATATGTCGTCTGATGATGATCT 835
QY 752 TGCGCTCAAGAGCGTCCGCTCTCTTGTGGCTCCGAGAGAAAGATGCAACCTGCGTGA 811
DB 836 TAGGACTCAAGAGTSTCCGATGCTGTGGGCTCCAAAGAAAGAGAGAACTGTGGCA 895
QY 812 GGAATCAACGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGAATCAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
QY 872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 956 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
QY 932 GCTATTAATCTTGATCGCTTTAGGCTATACCAACAGTAGCTGAATCCATTCTTACG 991
DB 1016 CTTGCACTTCTGATGCTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 992 CTTTCTTGTGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
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DB 1076 GCTTCTGATGATAAACTTCAAGATGTTTATAGAGTTTGTGATCCCACTTCTTCCA 1135
QY 1052 GATGAGCGGCGAGAGCACTAGCAGAGTCCGAATPACATTTACAGATC 1099
DB 1136 CAATCGAACACAAAACCTGTGCTGAAATCCGTCAAAACACTAGGGAAC 1183
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RESULT 34

US-08-387-707-15
; Sequence 15, Application US/08387707
; Patent No. 6265563
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,707
; FILING DATE: 10-SEP-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-387-707-15

Query Match 37.2%; Score 429.2; DB 3; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.6e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

```
QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGGCTCGAGAGACGCGAGCTGAGC 151
DB 374 CCGAGCCAGTGGGGTCTTAACCGGAGCGGGCTTGGGGAGAGCCAGCCTGTGGCTCAGA 433
QY 152 CCGGCAACATCTCCCGGCGCATCCGGTCATCATCAAGCGGGCTTACCTCGTAGTGTG 211
DB 434 CCGGAGCGCTTCAAGTGTACAGCATCAACATCATGAGCCCTCTATTCATGTGTGTG 493
QY 212 TCGTGGGCTTGGTGGCAACTGCGTGTGATGTTGCTGATCATCGATACCAAGATGA 271
DB 494 TAGTGGGCTCTTGGAACTTCTGTCATGTATGTATGTAAGATATACCAAAATGA 553
QY 272 AGACAGCAACCAACATTTACATATTTAACTGGCTTTGGGAGATGTTAGTTACTACAA 331
DB 554 AGACTGCCAACCAACTTACATTTTCAACCTTGTCTGGGAGATGCTTACGCACTAGCA 613
QY 332 CCATGACCTTTCAAGATGATGATCTGATGAATTCCTGACCTTTTGGGAGTGTGCT 391
DB 614 CGCTGCCCTTTCAGAGTGTAACTTACCTGATGTGAAAGTGTGCGCTTTGGAAACATCTCT 673
QY 392 GCAAGATGTAATTTCCATTTGATTTACTACAAATGTTCAACAGCATCTTACCTTGAACA 451
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Db      674  GCAAGATCGTGAATCTCAATAGACTACTAGCAACATGTTCAACAGTATCTTCAACCTCTGCA 733
Qy      452  TGATAGAGCGTGAACCGCTACATTCGCGTGTGCCACCCCGTGAAGGCTTGGACTTCCGA 511
Db      734  CCATAGATGTAGACCGCTACATTCGCGTGTGCCACCCCGTGAAGGCTTGGACTTCCGA 793
Qy      512  CACCTTGAAGCAAAAGATCATCATATATCTGCACTGTGCTGTGCTGATCTGTGGCA 571
Db      794  CCCCCGAAATGCCAAATTTGTCAATGTCTGCACTGATCCTCTCTTCTGCAATTTGTC 853
Qy      572  TCTGTCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGTCATTTAGTGTCT 631
Db      854  TCCCGTATGTTCATAGGCAACCAAAATACAGGACGGGATC-----CATAGATTGA 907
Qy      632  CCTTGAAGTCCCAAGATGATGACTACTCTGTGTGGGACCTCTTTCATGAAGATCTGCTCT 691
Db      908  CCTCAAGTCTCTCATCCACATGATGATCTGGAGAACCTGCTC---AAAATCTGTGTCT 964
Qy      692  TCATCTTTCCTTGGATCCGCTGCTCATCATCTGCTGCTCAACCCCTGATGATGCTC 751
Db      965  TCATCTTTCCTTTCATCATGCGGACCTCATCATCTGCTGCTCAACCCCTGATGATGCTC 1024
Qy      752  TCGCTCTCAAGACGCTCCGCTCTCTTCTGCTCCGAGAGAAAGATCCGAACCTGCTGA 811
Db      1025  TACAGCTCAAGAGTGTCCGATGCTGTGCGGGCTCAAAAGAAAGACAGAAACCTGCGCA 1084
Qy      812  GGATCAACCAAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1085  GGATCAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Qy      872  ACATATTCATCTGCTGGAGGCTCTGCGGAGACCTCCACAGACAGCTGCTCTGCTCA 931
Db      1145  ACATCTATGTCTATCATCAAGACATGATCAAGATTCAGAAACCATTTTCCAGATCTTTC 1204
Qy      932  GCTATTAATCTTGCATGCGCTTGAAGCTATACCAACAGTACCTGATCCCATTTCTCTAG 991
Db      1205  CTTGGACATCTTGCATGCGCTTGAAGCTATACCAACAGTACCTGATCCCATTTCTCTAG 1264
Qy      992  CTTTCTTGTATGAAATCTTCAAGCGGTGTTCCGGGACCTTCTGCTTCCATCTGAAATGA 1051
Db      1265  CTTTCTTGTATGAAATCTTCAAGCGGTGTTCCGGGACCTTCTGCTTCCATCTGAAATGA 1324
Qy      1052  GGATGAGGCGAGAGCACTAGACAGTCCGAAATCACTGATCCAGATC 1099
Db      1325  CAATGACAGCAAACTGCTCGATCGATCGTCAAAACACTAGGGAAC 1372

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; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-405-271A-15

Query Match      37.2%; Score 429.2; DB 4; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.6e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

Qy      92  CCGGCTGGCCGAGCCCGACAGCAACGAGCGCGGCTCGGAGAGCGCGCACTGGAGC 151
Db      374  CCGACCCATGCGGTCTTAACCGAGCGGCTTGGCGGAAAGACAGACCTGTGCTTCA 433
Qy      152  CCGGCAATCTCCCGGCGCATCCGATCATCAACGCGGATCTACTCCGATGTTG 211
Db      434  CCGGAGCCCTTTCATGCTCAGACGATCAGATGACGCTTCTATTTCTATCTGTGTG 493
Qy      212  TGTGTGGCTGTGGGCAACCTGCTGTGATGTTGTGTATCATCCGATACAGAAAGATGA 271
Db      494  TAGTGGGCTCTTGTGAAACCTTCTGCTCATATGATGATTAAGATTAACCAAAATTA 553
Qy      272  AGACGCAACCAATTTTACATATTAACCTGCTTGGCAATGTTAGTTACATCA 331
Db      554  AGACTGCCAACAACATTAATTTTCACTTGTGCTGCAATGCTTGAACATCTTCA 613
Qy      332  CCATCCCTTTCAGAGTACGCTCTTGAATGATTAATTCGAGCTTGGGAGTGTGCTGT 391
Db      614  CGCTGCCCTTTCAGAGTGTATCTATCTATGATGGAACGTTGCTTGGAAACATCTCT 673
Qy      392  GCAAGATGTAATTTTCATGATTAATCAACATGTTCAACAGATCTTACCTTGAACA 451
Db      674  GCAAGATGTAATTTTCATGATTAATCAACATGTTCAACAGATCTTACCTTGAACA 733
Qy      452  TGATAGAGTGAACCGCTATATTCGCTGTGTGCAACCCCGTGAAGCTTGGACTTCCGA 511
Db      734  CCATAGATGTAGACCGCTATATTCGCTGTGTGCAACCCCGTGAAGCTTGGACTTCCGA 793
Qy      512  CACCTTGAAGCAAAAGATCATCATATATCTGATCTGCTGTGCTGATCTGTTGGA 571
Db      794  CCCCCGAAATGCCAAATTTGTCAATGTCTGCAATGATCCTCTCTTCTGCAATTTGTC 853
Qy      572  TCTGTCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGTCATTTAGTGTCT 631
Db      854  TCCCGTATGTTCATAGGCAACCAAAATACAGGACGGGATC-----CATAGATTGA 907
Qy      632  CCTTGAAGTCCCAAGATGATGACTACTCTGTGTGGAACCTTTCATGAAGATCTGCTCT 691
Db      908  CCTCAAGTCTCTCATCCACATGATGATGGAAGAACCTGTCTC---AAAATCTGTGTCT 964
Qy      692  TCATCTTTCCTTGGATCCGCTGCTCATCATGATGATGCTGCTGCTCAACCCCTGATGATGCTC 751
Db      965  TCATCTTTCCTTTCATCATGCGGACCTCATATCACTGTGTGTTATGACTGATGATCTT 1024
Qy      752  TCGCTCTCAAGACGTCGCGCTCTTTCGCTCCGAGAGAAAGATGCAACCTGCTGA 811
Db      1025  TACAGCTCAAGAGTGTCCGATGCTGTGCGGGCTCAAAAGAAAGACAGAAACCTGCGCA 1084
Qy      812  GGATCAACCAAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1085  GGATCAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Qy      872  ACATATTCATCTGCTGGAGGCTCTGCGGAGACCTCCACAGACAGCTGCTCTCTCA 931

```

RESULT 35
 US-08-405-271A-15
 Sequence 15, Application US/08405271A
 Patent No. 6432652
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 APPLICANT: KEITH, DUANE E.
 TITLE OF INVENTION: OPIOID RECEPTOR GENES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/405,271A
 FILING DATE: 14-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

Db 1145 ACATCTATGTCAATATCAAAAGACCTGATCCAGATTCCAGAAAACCACTTCCAGACTGTT 1204

Qy 932 GCTATTACTTCTGCATCGCTTTAGGCTATACCAACAGTAGTCCGTGAATCCATTCTTAAG 991

Db 1205 CCTGGCACTTCGCAATTCCTTTGGGTTACAAAACAGTGCCTGAACCCAGTTCTTTATG 1264

Qy 992 CCTTTCTTGATGAAAACCTTCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGA 1051

Db 1265 CGTTCCTGGATGAAAACCTTCAACAGCATTTTTAGAGAGTCTCGATCCCACTTCCCTCA 1324

Qy 1052 GGATGGAGCGGACGACCTAGACAGAGTCCGAAATACAGTTCAAGATC 1099

Db 1325 CAATGGAACAGCAAAACTCTGCTCAATCCGTCAAAACACTTAGGGATC 1372

```

1      RESULT 36
2      US-08-411-859-1
3      / Sequence 1, Application US/08411859
4      / Patent No. 5985600
5      / GENERAL INFORMATION:
6      / APPLICANT: EVANS, CHRISTOPHER J.
7      / APPLICANT: KEITH JR., DUANE E.
8      / APPLICANT: EDWARDS, ROBERT H.
9      / TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
10     / TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
11     / TITLE OF INVENTION: PHARMACEUTICALS
12     / NUMBER OF SEQUENCES: 15
13     / CORRESPONDENCE ADDRESS:
14     / ADDRESSEE: Morrison & Foerster
15     / STREET: 755 Page Mill Road
16     / CITY: Palo Alto
17     / STATE: California
18     / COUNTRY: USA
19     / ZIP: 94304-1018
20     / COMPUTER READABLE FORM:
21     / MEDIUM TYPE: Floppy disk
22     / COMPUTER: IBM PC compatible
23     / OPERATING SYSTEM: PC-DOS/MS-DOS
24     / SOFTWARE: Patent In Releasee #1.0, Version #1.25
25     / CURRENT APPLICATION DATA:
26     / APPLICATION NUMBER: US/08/411,859
27     / FILING DATE:
28     / CLASSIFICATION: 424
29     / PRIOR APPLICATION DATA:
30     / APPLICATION NUMBER: US 07/929,200
31     / FILING DATE: 13-AUG-1992
32     / ATTORNEY/AGENT INFORMATION:
33     / NAME: LITHGOW, TIMOTHY J.
34     / REGISTRATION NUMBER: 36,856
35     / REFERENCE/DOCKET NUMBER: 22000-20526.00
36     / TELECOMMUNICATION INFORMATION:
37     / TELEPHONE: 415-813-5600
38     / TELEFAX: 415-494-0792
39     / TELEX: 706141
40     / INFORMATION FOR SEQ ID NO: 1:
41     / SEQUENCE CHARACTERISTICS:
42     / LENGTH: 1829 base pairs
43     / TYPE: nucleic acid
44     / STRANDEDNESS: single
45     / TOPOLOGY: linear
46     / FEATURE:
47     / NAME/KEY: CDS
48     / LOCATION: 29..1144
49     / US-08-411-859-1

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	Query Match	Best Local Similarity	Score	DB 2	Length
	67.6%	36.1%	422.6	1829	
			Pred. No. 63e-94		
	Matches 634	Conservative 0	Mismatches 299	Indels 12	Gaps 2
Oy	93	CGGCTGGGCCAGGCCGACGACGAGCGCGGCTCGGAGGACGCGCAGCTGGAGCC	152		
Ob	91	CGGCTTTTCCGAGCGCTTTCCCGAGCGCGGCGGCATCGTCGGGATGCGCGGAGCCG	150		

RESULT 37
US-08-387-707-7
Sequence 7, Application US/08387707
Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,707
FILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 29..1144
US-08-387-707-7

Query Match 36.6%; Score 422.6; DB 3; Length 1829;
Best Local Similarity 67.1%; Pred. No. 6.3e-94;

Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

93 CGGCTGGGCGGACCGGACGACGAGCGGCGGCTGGAGAGACGCGACCTGGAGCG 152
91 CGCCTTCCGAGCGCTTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150
153 CGGCGACATCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212
151 TAGTGCCTCTGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 210
213 CGTGGGCTTGGTGGGCGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 272
211 AGTGGGCGCTTGGGCGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 270
273 GACAGCAACCAACATTTACATATTTAACCTGGCTTGGGAGATGCTTTAGTTACTACA 332
271 GACCGCCACCAACATCTACATCTTCAATCTGGCTTGGGAGATGCTTGGGAGATG 330
333 CATGCCCTTTCAGAGTACGCTTCTTCTTGAATTCCTGGCTTTTGGGAGATGCTGTG 392
331 GCTGCCCTTTCAGAGCGCGCAAGTACTTGTATGAAACGTGGCGGTTGGGAGATGCTGTG 390
393 CAAGATAGTAATTTCCATTTGATTACTACAAAGTGTTCACAGACATCTTCACTGACAT 452
391 CAAGGCTGTCTCTCATTTGACTACTACAAAGTGTTCATACATCTTCACTGACATCT 450
453 GATGAGCGTGAACCGCTACATGCGGTGGGACACCGCGGAGAGGCTTGGAGCTTCCGAC 512
451 GATGAGCGTGAACCGCTACATGCGGTGGGACACCGCGGAGAGGCTTGGAGCTTCCGAC 510
513 ACCCTTGAAGGCAAGATCATATATATCTGATCTGGCTGTCTGTCTGTCTGTGGCAT 572
511 ACCAGCCCAAGGCGCAAGTGTATATATGATCTGGGCTTGGGCTTCAAGGTGTGGGAT 570
573 CTCTGCATATGCTTGGAGGACCAAACTCAGGGAAGCGTCGATGTTCATGATGATGCTC 632
571 CCCCATCATGCTCATGAGGAGTGAACCAACCGGAGATGATGAGTATGATGATCTCTCA 630
633 CTTCGAGTTCCAGATGATGATGATCTCTCTGATGAGGACCTTCAAGAGATCTGCGTCT 692

DB 631 GTTCCCAAGTCC-----CAGCTGTACTGGGACACTGTGACCAAGATCTGCGTGT 681
QY 693 CATCTTGGCTTGGTATGATCCCTGCTCTCATCATCTGCTGTCTACACCTCATATCTCT 752
DB 682 CCTCTTGGCTTGGTATGATCCCTGCTCTCATCATCTGCTGTCTACACCTCATATCTCT 741
QY 753 GCGTCTCAAGAGCGGCGGCTCTTCTTGGCTCCGAGAGAAAGATTCGCAACCTGGGTAG 812
DB 742 GCGCTTGGCGAGCGGCGGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 801
QY 813 GATCAACCAAGTGTCTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 872
DB 802 CATCAAGCGCATGCTGT 861
QY 873 CATATTCATCTGCTGTGAGGCTCTGTGGG---AGCATCTCCACAGACAGCTGTCTCTC 929
DB 862 CATCTTGTGATGCTGTGAGCGCTGTGTGAGCATCATTCGCGCGGCGGCGGCGGCGG 921
QY 930 CAGCTATTACTTGTGATGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 989
DB 922 CGCAGTGCACCTGTGATGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 981
QY 990 CGCCTTCTGTGATGAAACCTTCAAGCGGCTGTGTTCGCGGAGCTTCTG 1034
DB 982 CGCCTTCTGTGAGCAAGAACTTCAAGCGGCTGTGTTCGCGGAGCTTCTG 1026

RESULT 38

US-08-405-271A-7
Sequence 7, Application US/08405271A

Patent No. 6432652

GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.

TITLE OF INVENTION: OPIOID RECEPTOR GENES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & ROESTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/405,271A

FILING DATE: 14-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20526.22

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500

TELEPHONE: (202) 887-0763

TELEX: 90-4030 MRSNFORSMH

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 29..1144
US-08-405-271A-7

Query Match 36.6%; Score 422.6; DB 4; Length 1829;
Best Local Similarity 67.1%; Pred. No. 6.3e-94;

Matches	634; Conservative	0; Mismatches	299; Indels	12; Gaps	2;
Qy	93 CGGCTGGGCGGAGCCCGGACAGCAAGGACGCGCGGCTGGAAGACGCGACCTGGAGCC				152
Db	91 CGCCTTCCGAGGCGCTTCCCGACGCGGCGCGCATGCGGGGTCCCGGAGCCCG				150
Qy	153 CGGCGACATCTCCCGGCGCATCCGGTCAATCAACGGGGCTACTTCCGTAGTGTCT				212
Db	151 TAGTGCTGTCTCCCTGCGCTTCCGACGCGCGCATCCGCGCTTACTCGGCTGTGCGC				210
Qy	213 CGTGGGCTTGTGGGCACTCGTGTGATGTTTCTGTATCATCCGATACAAAGATGA				272
Db	211 AGTGGGGCTTCTGGGCACTGTCTGTATGTTTGGCATGTCCGGTACCAAAATGA				270
Qy	273 GACAGCAACCAATTATATATTTAACTGGCTTTGGCAAGTCTTTAGTTACTAAC				332
Db	271 GACCGGCACCAATCTATCATCTTCAATCTGGCTTTGGCTGTAGTGGCCACAGCAC				330
Qy	333 CATGCCCTTCAAGAGTACGCTCACTGTATGAATTCCTGGCCCTTTGGGGATGTGCTG				392
Db	331 GCTGCCCTTCAAGAGGCGCAAGTACTGTATGAAGAAAGTGGCCGTTTGGAGCTGCTG				390
Qy	393 CAAGATAGTAATTTCCATTGATTACTACAAAGTTCACAGCATCTTCACTTGACAT				452
Db	391 CAAGGCTGTCTCTCATTTGACTACTACAAAGTTTCACTAGCATCTTCACTTGACAT				450
Qy	453 GATGAGCGGTGACCGCTATATGCGGTGTCACCCCGTGAAGGCTTTGGATTTCCGAC				512
Db	451 GATGAGCGGTGACCGCTATATGCTGTCTGTCATCTGTCAAAAGCCCTTGGACCTT				510
Qy	513 ACCCTTGAAGGCAAAAGATCATATATCTGATCTGGCTGTGTGATCTTGTGGCAT				572
Db	511 ACCAGCCAAAGGCAAGCTGATCATATATATGATCTGGGCTTTGGCTTCAAGTGTG				570
Qy	573 CTCTCAATAGTCTCTTGAAGGCAACCAAGTCAAGGAAAGTGTATGATGATGCTC				632
Db	571 CCCCATCATAGTCAATGAGGAGTACCAACCCCGGATGGTGAAGTATGATGATCTCA				630
Qy	633 CTGGAAGTCCCAATGATGATCTCTCTGGTGGGACCTCTTCAAGAAATGTGGTCTT				692
Db	631 GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAAGATCTGGTGT				681
Qy	693 CATCTTGGCTTCTGTATCTCTGTCTGATCATCTGCTGATCAACCCGTATGATCTT				752
Db	682 CTTCTTGGCTTCTGTATCTCTGTCTGATCATCTGCTGATCAACCCGTATGATCTT				741
Qy	753 GGTCTCAAGAGGCTCCGCTCTCTTCTGGCTCCGAGAGAAAGTGTGCAACTGTGAG				812
Db	742 GCGCTGGCGAGCGCTGCTGTCTGCTGTCCAAAGAGAAAGACCCGACGCTGCGGCG				801
Qy	813 GATCAGCAGACTGTCTGTGGTGGTGGAGCTTGTGCTGTGCTGGAATCCCATTC				872
Db	802 CATCAGCGCATGTGTGTGGTGGTGGAGCCCTTGTGTGTGTGTGTGTGTGTGTGT				861
Qy	873 CATATTCATCTGTGTGAGGCTCTGGGG---AGCAGCTTCCACAGCAGCTGTCTCTC				929
Db	862 CATCTTGT				921
Qy	930 CAGCTATTAATTTCTGTGATCTGCTTATAGGCTTATACCAAGTATGCTGAATTCCT				989
Db	922 CGCAGTGAACCTGTGATGTGGCTGGGGCTAGCGCAACGAGCCCTCAACCGGTTCT				981
Qy	990 CGCCTTCTGTATGAAACTTCAAGCGGTGTTCGCGGAGCTTCTG 1034				
Db	982 CGCCTTCTGTATGAAACTTCAAGCGGTGTTCGCGGAGCTCTG 1026				

RESULT 39
US-09-214-904-3
; Sequence 3, Application US/09214904
; Patent No. 6632977
; GENERAL INFORMATION:
; APPLICANT:

;; TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
;; TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
;; NUMBER OF SEQUENCES: 6
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/214,904
;; FILING DATE:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR97/01282
;; FILING DATE:
;; APPLICATION NUMBER: FR 96.08810
;; FILING DATE: 15-JUL-1996
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2218 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 58..1173
;; US-09-214-904-3

Query Match 36.6%; Score 422.6; DB 4; Length 2218;
Best Local Similarity 67.1%; Pred. No. 6.8e-94;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

Qy	93 CGGCTGGGCGGAGCCCGGACAGCAAGGACGCGCGGCTGGAAGACGCGACCTGGAGCC					152
Db	120 CGCCTTCCGAGGCGCTTCCCGACGCGGCGCAATGCGGTGCGGAGGCGCG					179
Qy	153 CGGCGCATCTCCCGGCGCATCCCGGTCATCATCAGGCGGTCTACTCCGATGTTGCT					212
Db	180 TAGTGCTGTCTCTGCTGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTG					239
Qy	213 CGTGGGCTTGTGGGCAACTCGTGTGATCTGCTGATCATCGATCATCGATCAACAAATGA					272
Db	240 AGTGGGCTTCTGGGCAAGGCTGTGTGATGTTGGATGTTGGATGTTGGATGTTGGAT					299
Qy	273 GACAGCAACCAATTTATATTTAACTGGCTTTGGCAAGTCTTTATGTTACTAAC					332
Db	300 GACGCGCAACCAATTTATATTTAACTGGCTTTGGCAAGTCTTTATGTTACTAAC					359
Qy	333 CATGCCCTTCAAGAGTACGCTCTACTGATGAATTCCTGGCCTTTTGGGGATGTGCTG					392
Db	360 GCTGCCCTTCAAGAGGCGCAAGTACTGATGGAAGCGTGGCTTTGGCGAGCTGCTG					419
Qy	393 CAAGATAGTAATTTCCATTGATTACTAACATGTTTCAACGAGATCTTCACTTGACAT					452
Db	420 CAAGGCTGTGCTCTCCATTGATCTACTAACATGTTTCAATGACATCTTCACTTGAC					479
Qy	453 GATGAGGTGAGACCGCTACATTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT					512
Db	480 GATGAGGTGAGACCGCTACATTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT					539
Qy	513 ACCCTTGAAGGCAAAAGATCATATATCTGATCTGGCTGTGCTGCTGCTGCTGCTG					572
Db	540 ACCAGCAAGGCGCAAGTATCATATATGATCTGGGTCTTGGCTTCAAGTGTGCGGT					599
Qy	600 CCCCATATGATGATGAGCAAGTACCAACCCCGGAGTGTGAGTGTGATGATGATG					659
Db	633 CTGCAATAGTCTTGTGAGGCAACAAAGTCAAGGAAAGTGTGATGATGATGATG					692
Qy	660 GTTCCCAAGTCC-----CAGCTGTATCTGGGCACTGTGACCAAGATCTGCGGTT					710
Db	693 CATCTTGGCTTCTGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG					752

Db 711 CCTCTTGGCTTCGTGTCGCGATCTCATCTACAGGTCGTATAGGCTCATGTACT 770
Qy 753 GGGTCTCAAGAGCGTCGGCTCTTTCTGTGCTCCGAGAGAAAGATCGAACCTGTGTAG 812
Db 771 GGGCTTCGCGACGTCGTCTGTCTCCGGTTCCAAAGAGAAAGACCGGAGCTGTGGCG 830
Qy 813 GATCAACGAGTCGTCTGT 872
Db 831 CATCAAGCGCATGT 890
Qy 873 CATATTCATCTGT 929
Db 891 CATCTTCGTCATGT 950
Qy 930 CAGCTATTAATCTGT 989
Db 951 CGCACTGACACCTGT 1010
Qy 990 CGCCTTTCTGTATGAAGAACTTCAAGCGGTGTTCGGGACTTCTG 1034
Db 1011 CGCCTTCTGAGAGAACTTCAAGCGGTGTTCGGGACTTCTG 1055

RESULT 40
US-08-432-174A-1
; Sequence 1, Application US/08432174A
; Patent No. 6562587
; GENERAL INFORMATION:
; APPLICANT: KIEFER, BRIGITTE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
; FILE REFERENCE: EX9209-US
; CURRENT APPLICATION NUMBER: US/08/432,174A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)...(1174)
US-08-432-174A-1

Query Match 36.6%; Score 422.6; DB 4; Length 2219;
Best Local Similarity 67.1%; Pred. No. 6,8e-94;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

Qy 93 CGGCTGGGCGAGCCCGACAGCAACGCGAGCGCGGCTCGAGAGACGCGAGCTGGAGCC 152
Db 121 CGCCTTCCCAAGCGCTTCCCGAGCGCGCGCCCAATGCGTGGGCTCGCGGAGCCCG 180
Qy 153 CGCGCAATCTCCCGCGCATCCCGGTATCATACAGGCGGTCTCTCTGTGTGTGTGT 212
Db 181 TAGTGCCTGCTCGCGCTTCCCGCATCGCATCAACGCGCTCTACTCGCTGTGTGTGT 240
Qy 213 CGTGGGCTGT 272
Db 241 AGTGGGCGCTTGGGCAAGT 300
Qy 273 GACAGCAACAACTTATACATTTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
Db 301 GACCCGCAACAACTTATACATTTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Qy 333 CATGCCCTTTGAGAGAGGTCTACTGTATGAATTCGGGCTTTTGGGGATGTGTGTGT 392
Db 361 GCTGCCCTTCCAGAGGCGCAAGTCTGTATGAGAAAGTGGCGGTTTGGAGCTGTGTGT 420
Qy 393 CAAGATAGTAATTTTCATTTACTATACAAATGTTCACAGCATTTTCACTTGTACCAT 452
Db 421 CAAGGCTGTGTCTCATTTAGTACTAGCAAACTGTTCATACATTTTCACTTGTACCAT 480

Qy 453 GATGAGCGTGAACCGCTACATTTGCGGTGTGTCACCCCGGTAAGGCTTTTGGACTTCGAC 512
Db 481 GATGAGCGTGAACCGCTACATTTGCGGTGTGTCACCCCGGTAAGGCTTTTGGACTTCGAC 540
Qy 513 ACCCTTGAAGGCAAGATCATCAATATTCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
Db 541 ACCAGCCAAAGGCAAGCTGTATATATATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 573 CTCTGCAATAGTCTTTGAGAGCAACAAAGTCAAGGAAAGCTGTGTGTGTGTGTGTGTGT 632
Db 601 CCCCATCATGT 660
Qy 633 CTGTGAGTTCCCAATGATGATCTACTCCCTGGGAGACCTTTCAAGAAATGTGTGTGTGT 692
Db 661 GTTCCCAAGTCTC-----CAGCTGTACTGGGAACTGTGACCAAGATCTGTGTGT 711
Qy 693 CATCTTTCGCTTGT 752
Db 712 CCTCTTTGCTTGT 771
Qy 753 GGGTCTCAAGAGCGTCCGCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
Db 772 GCGCTTGGGACGTCGCTGT 831
Qy 813 GATCAACGAGCTGT 872
Db 832 CATCAAGCGCATGT 891
Qy 873 CATATTCATCTGT 929
Db 892 CATCTTCGTCATGT 951
Qy 930 CAGCTATTAATCTGT 989
Db 952 CGCACTGACACCTGT 1011
Qy 990 CGCCTTTCTGTATGAAGAACTTCAAGCGGTGTTCGGGACTTCTG 1034
Db 1012 CGCCTTCTGAGAGAACTTCAAGCGGTGTTCGGGACTTCTG 1056

RESULT 41
US-08-147-592A-3
; Sequence 3, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435

FEATURE:
NAME/KEY: CDS
LOCATION: 12..1127
US-08-292-694A-3

Query Match 36.6%; Score 422.6; DB 4; Length 2272;
Best Local Similarity 67.1%; Pred. No. 6.9e-94;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

93 CGGCTGGGCGAGCCCGACAGACAGGAGCGCGCGCTGAGAGACGCGAGCTGAGCC 152
74 CGCCTTCCCAAGCGCTTCCAGCGCGGCGCCCAATGCTGGGGGTGCGCGGAGCCG 133
153 CGCGCAATCTCCCGCGCATCCCGGTATCATACGGGGCTTACTCCGTATGTGTGT 212
134 TAGTCCCTGCTCCCTGCGCTGAGCCATGCGCATACCGGCTCTACTCGGCTGTGTGCGC 193
213 CGTGGGCTTGGTGGGCAACTCGCTGATCATGTTGATCATCCGATACAAAGATGAA 272
194 AGTGGGGCTTCTGGGCAAGCTGCTGTATGTTGGCATGTCCGGTACCAAAATTGAA 253
273 GACAGCAACCAACATTTATATATTTAACCTGGCTTTGGCAAGTGTCTTATGTTACTAAC 332
254 GACCGCAACCAACATCTATCATCTTCATCTGGCTTTGGCTGATGGCTGGCCACAGCAC 313
333 CATGCCCTTTAGAGTAGCGGTCTACTTGTATGAAATTCCTGGCTTTGGGGATGTGTGTG 392
314 GCTGCCCTTCCAGACGCGCAAGTACTGTATGAAACGTGGCCGTTTGGGAGACTGTGTG 373
393 CAAGATAGTATTTGATTTGATTTACTATCAACAGTTCACAGCATCTTACCTTGACAT 452
374 CAGGCTGTGCTCTCTCACTTACTACTACAACTGTTCATCTACATCTTCACTCACTCACT 433
453 GATGACGCTGACCGCTACATTTGCGGTGACACCCCGTGAAGGCTTTGGAATTCGCGAC 512
434 GATGACGCTGACCGCTACATTTGCGGTGACACCCCGTGAAGGCTTTGGAATTCGCGAC 493
513 ACCCTTGAAGGCAAGATCATATATCTGCACTCTGCTGCTGTGTCTATCTGTGGCAT 572
494 ACCAGCCAAAGGCAAGCTGATCATATATATGCACTCTGGGCTTTCAGGCTGTGGGGT 553
573 CTCTGCAATAGTCTCTGGAGGACCAAGTCAAGGGAAGAGTGTATGATGAGTGTCT 632
554 CCCCATCTATGTCATGTCAGTACCCAAACCCCGGATGTGCACTGTATGATGCTCA 613
633 CTTCGAGTTTCCAGATGATGATCTACTCTCTGTGGGACCTCTTCAATGAAGTCTGGCTTT 692
614 GTTCCCAAGTCC-----CAGCTGTGATCTGGGACCTGTGACCAAGATCTGGGTGT 664
693 CATCTTTGCTTCTGTGATCCCTGTCTCTATCATCATGCTGTCTACACCTGTATGATCT 752
665 CCTCTTTGCTTCTGTGATCCCTGTCTCTATCATCATGCTGTCTACACCTGTATGATCT 724
753 GGTCTCAAGAGCGCTCCGCTCTTCTGTGGCTCCGAGAGAAAGATTCGCAACTGCGTAA 812
725 GGGCTTGGGAGCGGTGCTGTGTCTGTGCTGCTGCTCAAGAGAAAGACCGGAGCTTGGGCG 784
813 GATCAACCAAGTGTCTGT 872
785 CATCAAGGCAATGT 844
873 CATATTCATCTGT 929
845 CATCTTGTGATCTGT 904
930 CAGCTATTAATCTGT 989
905 GCGACTGACCTGT 964
990 GCGCTTTCTTGT 1034
965 GCGCTTTCTGAGAGAACTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009

RESULT 43
US-09-761-962A-12
Sequence 12, Application US/09761962A
Patent No. 6500927
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: MULTIPLE SPLICE VARIANTS OF THE MU-OPIOID RECEPTOR GENE
FILE REFERENCE: 830002-2000.2
CURRENT APPLICATION NUMBER: US/09/761.962A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743.872
PRIOR APPLICATION NUMBER: PCT/US99/15974
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 1346
TYPE: DNA
ORGANISM: Mus musculus
US-09-761-962A-12

Query Match 35.6%; Score 411; DB 4; Length 1346;
Best Local Similarity 65.7%; Pred. No. 3.8e-91;
Matches 663; Conservative 0; Mismatches 335; Indels 11; Gaps 4;

92 CGGCTGGGCGAGCCCGACAGCAACGAGCGCGCTCGAGAGACGCGAGCTGGAGC 151
185 CCGACCAATGCGGCTCTAAACGACAGGGGCTTGGGAGGCCACAGCTGTGCTCAGA 244
152 CGGCAATATCTCCCGGCACTCCGGTATCATACAGCGGCTTACTCCGATGTTGCG 211
245 CCGGACGCTTCCATGTCATGTCACAGCATCACCATATGAGCCCTTATTTATGCTGTG 304
212 TCGTGGGCTTGGTGGGCAACTCGCTGTATGTTGATGATCATCCGATACCAAGATGA 271
305 TAGTGGGCTCTTGGAACTTCCGTGATATGATATGATATGATATGATATGATATGAT 364
272 AGACAGCAACCAACATTTATATTTAACTGCTTTGGCAGATGCTTTAGTTACTACA 331
365 AGACTGCAACCAACATTTATATTTAACTGCTTTGGCAGATGCTTTAGCTAGCACTAGA 424
332 CCATGCCCCCTTCAAGTACGCTCTATGATGAAATTCGAGGCTTTGGGAGTGTGTGT 391
425 GCGTCCCTTTCAGAGTGTAACTATGATGAGGAACGTTGGGAAATCTCTCT 484
392 GCAAGATGATATTTCCATGATTTACTACACATGTTCAACGATCTTCACTTGACCA 451
485 GCAAGATGATATTTCAATGATTTAGCTTACACATGTTCAACGATCTTCACTTGACCA 544
452 TGATGAGGTGAGCGGTACATTTGCTGTGTGACACCCCGTGAAGGCTTTGACCTTCCGA 511
545 CCATAGATGATGAGCGGTACATTTGCTGTGTGACACCCCGTGAAGGCTTTGACCTTCCGA 604
512 CACCTTGAAGGCAAGATCATATATCTGATCTGTGCTGTGTGTGTGTGTGTGTGTGT 571
605 CCCCCGAAATGCAAAATGTGATGTGTGAACTGTCTCTCTCTGTGCAATTTGTC 664
572 TCTGTCAATAGTCTTGTGAAGGCAACAAAGTCAAGGGAAGACGTGATGATCATTTGAGTGT 631
665 TGCCGTATATGTTATGAGCAACCAAAATACAGGCAAGGCTC-----CATAGATGGA 718
632 CTTTGAAGTTCAGATGATGATCTACTCTGTGTGGACCTTTCATGAAGATCTGTGT 691
719 CCGTACGCTTCTCATCCACATGATGTGGAAGAACTGTCTC---AAAATCTGTGTCT 775
632 TCACTTTGCTCTGTGATCCCTGTCTCATCATATGATGTCTGTGCAACCCGATGATCTC 751
776 TCACTTTGCTCTGTGATCCCTGTCTCATCATATGATGTCTGTGCAACCCGATGATCTC 835
752 TGCGTCTCAAGAGCTCGGCTCTTTTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
836 TAGGACTCAAGAGTGTCCGATGCTGTGTGGGCTCCAAAGAAAGACAGAACTGTGCGCA 895

Db 1197 CCGGACGTGACGATGTCTGACCGGTGGCAGCATTTGCCAAGA 1241

RESULT 49
US-09-976-594-171
Sequence 171, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 171
LENGTH: 3205
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 222181.1
US-09-976-594-171

Query Match 34.1%; Score 393.4; DB 4; Length 3205;
Best Local Similarity 65.1%; Pred. No. 1.1e-86;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCGCATCCGGTCACTATCAAGCGGTCTACTCGTAAGTGTGT 212
DB 380 CCGCTTCTGCGCTCCGCGCTAAGGTACCACTGTGGGCTCTTACCTGCGCGTGTGT 439
QY 213 CGTGGCTGTGTGGCACTCGCTGTATGTTCTGTATCAATCCGATACACAAAGATGA 272
DB 440 CGAAGGCTCTCGGGAACTGCTGTATGATGATCTCTCAAGCAGCACCACAAATGA 499
QY 273 GACGACAAACCAATTTACATTTAACTGGCTTTGGCAAGTGTCTTACTTACAC 332
DB 500 GACAGCCACCAATATTTACATCTTTAACTGGCCCTGCGCCGACACTCTGCTCTGAC 559
QY 333 CATGCCCTTTCAGATGAGTCTACTGTATGAAATCTGCGCTTTGGGAAATGCTGTG 392
DB 560 GCTGCCCTTTCAGGACGAGATCTCTGCGCTTTGGGCTTTGGGAAATGCGCTGTG 619
QY 393 CAAGATGATTAATTTCCATTTACTTACAAACATGTTCAACAGCATCTTACCTTGACAT 452
DB 620 CAAGACATGATTTGCACTTACTTACAAACATGTTCAACAGCATCTTACCTTGACAT 679
QY 453 GATGAGCGTGAACCGCTACATTTGCGGTGCAACCCCGTGAAGGCTTTGACTTCCGAC 512
DB 680 CATGAGTGTGATGCTGTATGATCCATCTGCAACCCCATCCGTGCGCTGAGTCCGAC 739
QY 513 ACCCTTGAAGCAAGATCATCAATATCTGATCTGCTGTGCTGTGATCTGTGGCAT 572
DB 740 GTCCAGCAAGCCCGCTGATATGTGCAATCTGCGCTGTGCTGTGCTGTGCTGTGCT 799
QY 573 CTCTGCAATGATCTTTGAGGACCAAGATGAGGAAAGCTGATGATGATGATGCTC 632
DB 800 TCCCGTTCATATGAGGCTCGGCAAGTCTC-----GAGATGAAGATCGATGCTC 853
QY 633 CTTCGATTTCCCAATATGATCTCTGTGTGGAACCTTTTCAATGAATCTGTGCTTT 692
DB 854 GATGAGATGCTTCAATCCCTCAGGATTAAC---TGGGCGCGGATGTTTGCATCTGATCTT 910
QY 693 CATCTTCTCTTGTGATCTCTGTCTCATCATCATGCTGTCTACACCTGATGATCTCT 752
DB 911 CTTCTTCTCTTCAATGCTGCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 970
QY 753 GCGTCTCAAGAGCTCGGCTCTTTTGTGCTTCCGAGAAAGATGCAACCTGTGCTAG 812

Db 971 GCGGCTCGGTGAGTCCGCTCTGCTGTGGGCTCCCGAAGAAAGACCGGAACCTCGGCG 1030
QY 813 GATCACGAGTGTCTGT 872
DB 1031 CATCATCTGCTGT 1090
QY 873 CATATTCATCTGT 932
DB 1091 GGTCTGT 1150
QY 933 CTATTAATCTTGCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1151 TGTGGCTTGTGCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1210
QY 993 CTTTCTGTGATGAAATCTTCAAGCGGTGTTTCCGGAATCTTGTCTTCACTGAAGATG 1052
DB 1211 CTTCCTGTGATGAAATCTTCAAGCGGTGTTTCCGGAATCTTGTCTGTGATCTGCT 1270
QY 1053 GATGAGCGCGAGAGCACTAGCAGATCCGGAATATCAATTGAGGA 1097
DB 1271 CCGGACGTGACGATGTCTGACCGCGTGTGCGCAGCATTTGCCAAGA 1315

RESULT 50
US-09-761-962A-2
Sequence 2, Application US/09761962A
Patent No. 650927
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: MULTIPLE SPLICER VARIANTS OF THE MU-OPIOD RECEPTOR GENE
FILE REFERENCE: 830002-2000.2
CURRENT APPLICATION NUMBER: US/09/761,962A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1238
TYPE: DNA
ORGANISM: Mus musculus
US-09-761-962A-2

Query Match 33.6%; Score 387.6; DB 4; Length 1238;
Best Local Similarity 67.8%; Pred. No. 2e-85;
Matches 575; Conservative 0; Mismatches 264; Indels 9; Gaps 2;

QY 252 CATCCGATTAACAAGATGAAGACAGCAACCAATTAATATTAACCTGCTTGGC 311
DB 179 CTTAGATATTAACAAGATGAAGATGACAGCAACCAATTAATTAACCTGCTTGGC 238
QY 312 AGATGCTTTAGTACTTAAACAATGCTGCTTTCAAGATGACGCTTACTTGAATTCCTG 371
DB 239 AGATGCTTTAGTACTTAAACAATGCTGCTTTCAAGATGACGCTTACTTGAATTCCTG 298
QY 372 GCCCTTTGGGAGT 431
DB 299 GCCCTTTGGGAGT 358
QY 432 CAGCATCTTACCTTGCATGATGAGCGTGAACCGCTTACATTTGCGTGTGCAACCCGCT 491
DB 359 CAGTATTTACCTTGCATGATGAGCGTGAACCGCTTACATTTGCGTGTGCAACCCGCT 418
QY 492 GAAGCTTTGAGCTTCCGCAACCTTTGAAGGCAAGATCATGATATGCTGTGCT 551
DB 419 CAAGGCTTGAATTTCCGTAACCCCGAATGCAAAATGTCATATGCTGCAACTGGAT 478
QY 552 GCTGTCTCATCTGT 611
DB 479 CTTCTTCTTGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
QY 612 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 671

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Db      536  ---GGGATCCATGATGACACCTCAGCTTCTCATCCACATGAGTATGGGAGACCT 592
Qy      672  CTTGATGAAGATCTGGCTTTTATCTTTGCTTGGATCCCTGCTTATCATCATGCT 731
Db      593  GCTC---AAATCTGTGCTTCATCTTCCCTTTCATCATGACCGGCTTCATCATCTGT 649
Qy      732  CTGCTACACCCCTGATGATCTGCTGCTCAAGAGCGTCCGGCTCTTTCTGGCTCCGAGA 791
Db      650  GTGTTATGAGACTGATGATCTTACGACTCAAGAGTGTCCGATGCTGTGGGCTCCAAAGA 709
Qy      792  GAAAGATGCAACTCTGCTGATGATACACAGACTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db      710  AAAGACAGAAACCTGCGAGATACACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
Qy      852  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db      770  TGTCTGCTGAGACCCCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 829
Qy      912  CAGCAGAGTGTCTCTCCAGCTATTTACTTTCGATCCGCTTACGCTATACCAAGATAG 971
Db      830  AACCATTTCCAGACTGCTTTTCTGCACTTCTGCACTGCTGCTGCTGCTGCTGCTGCT 889
Qy      972  CCTGATCCCATTTCTCTACGCTTTCTTGTGATGATAAACTTCAAGCGGTGTTCCGGGACT 1031
Db      890  CCTGAACCAAGTCTTTATGCTGCTCTGATGATAAACTTCAACGATGTTTATGAGAGTT 949
Qy      1032  CTGCTTTCCACTGAAGATGAGATGAGAGCGGAGAGCACTAGCAGAGTCCGAATATACGT 1091
Db      950  CTGCATCCCACTTCTCTCCCAATGAGAACAGAAACTCTGCTGCAATCCGTCAAACAC 1009
Qy      1092  TCAGATC 1099
Db      1010  TAGGAAAC 1017

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RESULT 51
US-09-761-962A-5
; Sequence 5, Application US/09761962A
; Patent No. 6500927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICED VARIANTS OF THE MU-OPIOD RECEPTOR GENE
; FILE REFERENCE: 830002-2000 2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-5

```

```

Query Match      33.6%; Score 387.6; DB 4; Length 1257;
Best Local Similarity 67.8%; Pred. No. 2e-85;
Matches 575; Conservative 0; Mismatches 264; Indels 9; Gaps 2;

```

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Qy      252  CATCGATACACAAAGATGAGAGCAACCACTTTACATTTAACTTGGCTTGGC 311
Db      179  CCTGAGATATACCAAAATGAAACCTGCCACCAACATCTACATTTTCAACCTTGTCTGCG 238
Qy      312  AGATGCTTATGATCTACCAACCATGCTTTCAGAGTACGCTCTACTGATGAATTCCTG 371
Db      239  AGATGCTTATGATCTACCAACCATGCTTTCAGAGTACGCTCTACTGATGAATTCCTG 298
Qy      372  GCTTTTGGGAGTGTGCTGTGCAAGATGATATTTTCATGATTTACCAACATGTTAC 431
Db      299  GGCCTTTGGAAACATCTCTGCAAGATGATGATCTCAATAGACTACTCAACATGTTAC 358

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Qy      432  CAGCATCTTCACTTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTGACCCCGT 491
Db      359  CAGTATCTTCACTCTGACCATGATGATGAGCGCTACATTTGCCGTGACCCCGT 418
Qy      492  GAAAGCTTTGATCTTCCGACACCCCTTGAAGGCAAAATCATCAATATCTGATCTGCT 551
Db      419  CAAGCCCTGAGATTTCCGTACCCCGGAAATGCCAAATTTGCAATGCTGCAACCTGAT 478
Qy      552  GCTGTCTCATCTGTGGATCTCTGCAATAGTCTTGGAGGACCAAAAGTGAAGGAGA 611
Db      479  CCTCTCTTCTGCAATGATGCTGCTCCGCTATGTTCAATGCAACCAAAATACAGGA--- 535
Qy      612  CTGATGATCTATGATGCTCTCTTCCAGATTTCCCAATGATGATGATGATGATGATGAT 671
Db      536  ---GGGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
Qy      672  CTTGATGAAGATCTGCTGCTTCTCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db      593  GCTC---AAATCTGTGCTTCATCTTCCGCTTTCATCATGACCGGCTTCATCATCATCT 649
Qy      732  CTGCTACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Db      650  GTGTTATGAGACTGATGATCTTACGACTCAAGAGTGTCCGATGCTGCTGCTGCTGCT 709
Qy      792  GAAAGATGCAACTCTGCTGATGATCAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db      710  AAAGACAGAAACCTGCGAGATACCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
Qy      852  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db      770  TGTCTGCTGAGACCCCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 829
Qy      912  CAGCAGAGTGTCTCTCCAGCTATTTACTTTCGATCCGCTTACGCTATACCAAGATAG 971
Db      830  AACCATTTCCAGACTGCTTTTCTGCACTTCTGCACTGCTGCTGCTGCTGCTGCTGCT 889
Qy      972  CCTGATCCCATTTCTCTACGCTTTCTTGTGATGATAAACTTCAAGCGGTGTTCCGGGACT 1031
Db      890  CCTGAACCAAGTCTTTATGCTGCTCTGATGATAAACTTCAACGATGTTTATGAGAGTT 949
Qy      1032  CTGCTTTCCACTGAAGATGAGATGAGAGCGGAGAGCACTAGCAGAGTCCGAATATACGT 1091
Db      950  CTGCATCCCACTTCTCTCCCAATGAGAACAGAAACTCTGCTGCAATCCGTCAAACAC 1009
Qy      1092  TCAGATC 1099
Db      1010  TAGGAAAC 1017

```

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RESULT 52
US-08-889-108-16
; Sequence 16, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
US-08-889-108-16

Query Match 32.7%; Score 377.6; DB 3; Length 1567;
Best Local Similarity 63.9%; Pred. No. 6e-83;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCGCATCCCGGTGATCATACGCGGCTTCTCCGTAAGTGTCTG 212
DB 292 CGCTTCTCCGCGCTTGACATCAAGGTACCATCGTGGGCTTCTGAGCTGTGTGAT 351
QY 213 CGTGGGCTTGTGGGCAACTGCGTGTATGTTCTGTATCATCCGATACACAAAGATGA 272
DB 352 CGGGGGGCTCTCGGGGAAGTGCCTGTATGATGATCTCTCGAGCAGACCAAGATGA 411
QY 273 GACAGCAACCAATTATTAATTTAACTTGGCAATGCTTTAGTTACTACAC 332
DB 412 GACAGCTACCAATTATTAATTTAACTTGGCAATGCTTTAGTTACTACAC 471
QY 333 CATGCCCTTGAAGTACGCTTACTTGAATTCCTGGCTTTGGGAGATGTCTGTG 392
DB 472 ACTGCCCTTCAAGGACAGACATCTTACTGCGCTTGGCCATTTGGGAATGCACTGTG 531
QY 393 CAAGTAAATTTCTATTGATTACTACAACTGTTACACAGATCTTCACTTGAACCAT 452
DB 532 CAAGCTGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 591
QY 453 GATGAGCGTGAACGCTTCAATTGCGGTGCCACCCCGTGAAGGCTTTGACTTCGAC 512
DB 592 CATGAGCGTGAACGCTTCAATTGCGGTGCCACCCCGTGAAGGCTTTGACTTCGAC 651
QY 513 ACCCTGAAGGCAAGATCATCAATATCTGCATCTGCTGTCTGTCTGTCTGTCTGT 572
DB 652 ATCCAGCAAGGCCAGGCTGTTAATGTCGCAATAGGCGCTTGAAGTGTGTG 711
QY 573 CTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAGACGCTCATTTGATGTGCTC 632
DB 712 TCCTGTGCTCATGATGCTTCAAGCAAGT-----GGAATGAAGATGAGTGTCT 765
QY 633 CTTCGAGTTCCCAATGATGATCTACTCTGTGTGGACCTTTCATGAAGATCTGCTGT 692
DB 766 GGTGAGATCCCTGCGCTTCAAGCAATATTTGGGG---CCCTGATATTCGCACTGCA 822
QY 693 CATCTTGGCTTCTGATCCCTGCTCTCATATATCTCTGCTTCAACCTGATGATCTCT 752
DB 823 CTTTTCCTTTCATCATCTCCCTGCTGATCATCTCTGCTTCAACCTGATGATCTCT 882
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTCCGAGAGAAATGCACTGCGTAG 812
DB 883 ACGACTTCTGTGTCT 942
QY 813 GATACCAAGACTGTCTGT 872
DB 943 TATCACTGACTGT 1002

QY 873 CATATTCATCTGTGTGAAGGCTTGGGAGACCTCCACAGCAGAGCTCTCTCCAG 932
DB 1003 GGTGTGTCTCTGTGTGAAGGCTTGGGAGCTTCCAGCAGAGTGTGAATGATGATG 1062
QY 933 CTATTAATCTTGTGATCCGCTTGAAGCTTATCAAGAGTATGAGTATGATCTCTTAC 992
DB 1063 CTGTGCTTCTGTGACAGGCTTGGGCTTATGCAAGGTTGTCTCATCTCTCTATGC 1122
QY 993 CTTTCTGTATGAATACTTCAAGCGGTGTTCCGGAATCTTCTGCTTTCATGAAGATG 1052
DB 1123 TTTCTGTATGAATACTTCAAGCGCTTCTGCTTGAAGGTTGTCTGCTGCTGCTG 1182
QY 1053 GATGAGCGGAGAGCACTGACAGATCCGAAATACATGATGATCTCTG 1102
DB 1183 CGGAGATGAGGTTTCTGTATGCTGTGTGGAGCATTTGCCAAGATGTTG 1232

RESULT 53
PCT-US94-10358-16
Sequence 16, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
PCT-US94-10358-16

Query Match 32.7%; Score 377.6; DB 5; Length 1567;
Best Local Similarity 63.9%; Pred. No. 6e-83;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCGCATCCCGGTGATCATACGCGGCTTCTCCGTAAGTGTCTG 212
DB 292 CGCTTCTCCGCGCTTGACATCAAGGTACCATCGTGGGCTTCTGAGCTGTGTGAT 351
QY 213 CGTGGGCTTGTGGGCAACTGCGTGTATGTTCTGTATCATCCGATACACAAAGATGA 272

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Db      352 CGGGGGGCTCCGGGAACTGCTGTATGATGATCCTCAGGACACCAAGTGA 411
Qy      273 GACAGCAACCAACATTTACATATTTAACTGCTTGGCAAGTCTTAACTACAAAC 332
Db      412 GACAGCTACCAACATTTACATATTTAACTGCTTGGCAAGTCTTAACTACAAAC 471
Qy      333 CATGACCTTTGAGATGAGTGTACTGTATGAAATTCCTGGGCTTTTGGGGAATGCTG 392
Db      472 ACTGCGCTTCCAGGCAAGACATCTACTGAGGCTTCTGGCCATTTGGAAATGACTG 531
Qy      333 CAAGATAGTAAATTTCCATGATTTACTACAAATGTTCAACAGCATCTTCACTTACAT 452
Db      532 CAAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
Qy      453 GATGAGCGTGAACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Db      592 CATGAGCGTGAACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
Qy      513 ACCCTTGAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
Db      652 ATCCAGCAAGCGCCAGGCTGTTAAATGAGCCATATGAGCCCTTGGCTTCACTGCTG 711
Qy      573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGCTGATGATGATGATGATG 632
Db      712 TCCTGCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGCTGATGATGATGATG 765
Qy      633 CTTCGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
Db      766 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
Qy      693 CATCTTGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 752
Db      823 CTTTTCCTTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Qy      753 GCGTCTCAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
Db      883 AGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
Qy      813 GATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
Db      943 TATCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Qy      873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
Db      1003 GGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
Qy      933 CTATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
Db      1063 CCGTGGCTTCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
Qy      993 CTTTCTGATGAAACCTTCAAGCGGTGTTCCGGGACTTCTGCTTCACTGAAGATG 1052
Db      1123 TTTCTGATGAGACTTCAAGCGGTGTTCCGGGACTTCTGCTTCACTGAAGATG 1182
Qy      1053 GATGAGCGGCAAGACATGAGAGTCCGAATACAGTCAAGATCCG 1102
Db      1183 CCGGAGATGAGCGGTGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1232

```

RESULT 54
US-08-454-549-1

Sequence 1, Application US/08454549
Patent No. 5863324
GENERAL INFORMATION:
APPLICANT: EPLER, C. Mark
APPLICANT: OZEMBERGER, Bradley A.
APPLICANT: HILMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Darby & Darby, P.C.

```

; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
;
; US-08-454-549-1
;
; Query Match 32.7%; Score 377.6; DB 2; Length 2706;
; Best Local Similarity 63.9%; Pred. No. 7.4e-83;
; Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

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Qy      133 CGGGCAATCTCCCGGCGATCCCGGTGATATCAAGCGGCTTACCTGATGTTGCT 212
Db      226 GCGCTTCTGCGCCCTTGAGCTCAAGGTCAACATGCTGAGGCTTACTGCTGCTGCT 285
Qy      213 CGTGGGCTTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
Db      286 CGGGGGGCTCCGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
Qy      273 GACAGCAACCAACATTTACATATTTAACTGCTTGGCAAGTCTTAACTACAAAC 332
Db      346 GACAGCTACCAACATTTACATATTTAACTGCTGCTGCTGCTGCTGCTGCTGCT 405
Qy      333 CATGCGCTTTCAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
Db      406 ACTGCGCTTTCAGAGGCAAGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
Qy      393 CAAGATAGTAAATTTCCATGATTTACTACAAATGTTCAACAGCATCTTCACTTACAT 452
Db      466 CAAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 525
Qy      453 GATGAGCGTGAACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Db      526 CATGAGCGTGAACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
Qy      513 ACCCTTGAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
Db      586 ATCCAGCAAGCGCCAGGCTGTTAAATGAGCCATATGAGCCCTTGGCTTCACTGCTG 645
Qy      573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGCTGATGATGATGATGATG 632
Db      646 TCCTGCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGCTGATGATGATGATGATG 699
Qy      633 CTTCGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
Db      700 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756

```



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; Sequence 1, Application US/08676351C
; Patent No. 6046026
; GENERAL INFORMATION:
; APPLICANT: EPFLER, CECIL
; APPLICANT: OZENERGER, BRADLEY
; APPLICANT: HULMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A818US1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Rat
; US-08-676-351-1

Query Match      32.3%; Score 372.8; DB 3; Length 2706;
Best Local Similarity 63.6%; Pred. No. 1,1e-81;
Matches 604; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGCCATCCGGTCAATCAACGGGGGTCTACCTCCGATGTTGCT 212
DB 226 CGCCTTCCTCCGCTTGACATCAAGTCAACATCGGGGCTCTACTTGCTGTGCT 285
QY 213 CCGTGGCTTGGGGCACTCGCTGTCATGTTGTCATCCGATACACAAAGTAA 272
DB 286 CGGGGGGCTCCGGGGAACCTGCTGTCATGTCATCCAGGACACCAAGATGA 345
QY 273 GACGACCAACCAATTTACATATTTAACTGCGCTTTGGAGATGCTTACTATAAC 332
DB 346 GACACTACCAATTTACATATTTAACTGCGCTTTGGAGATGCTTACTATAAC 405
QY 333 CATGCCCTTTCAGAGTACGCTTACTGTAATTCCTGGCTTTGGGAGTGTCTGTG 392
DB 406 ACTGCCCTTTCAGGACACAGACATCTACTGCGCTTTGGGAGTGTCTGTG 465
QY 393 CAAGATTAATTTTCATGATTACTATCAACATGTTACACACATCTTCACTTACCAT 452
DB 466 CAAGCTGTCATGTCATGACTACTACCAACATGTTTACACACATCTTCACTGACGC 525
QY 453 GATGACGCTGACCGCTACATGCGGTGACCAACCGCGTGAAGCTTTGGAATTCGAC 512
DB 526 CATGACGCTGACCGCTATGCTGCTATGTCACACCTTACCTGCTGATGTTGAC 585
QY 513 ACCCTTGAAGGCAAGATCATATATCTGATCTGCGCTGTGCTCATCTGTTGGCAT 572
DB 586 ATCCAGCAAAAGCCGAGGTGTAATGTCGCAATATGGGCTTGGCTTGAATGCTG 645
QY 573 CTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAAAGCTGATGTCATGAGTCTC 632
DB 646 TCCTGTTCGATCATGAGGTTTCAGACAAAGT-----GGAAGATGAAGATGAGTGCCT 699
QY 693 CTTCGAGTTCCAGATGATGACTACTCCTGATGGGACCTCTTCAAGAAATCTGGTCTT 692
DB 700 GGTGAGATCTCTGCGCTCAGAGACTATTTGGG---CCCTGATATTCGCAATCTGATCTT 756
QY 693 CATCTTGTGCTTCTGATCTCTGCTCTCATCATCTGCTCAACCTGATGATCTCT 752
DB 757 CTTTTTTTCTTCATCATCTCTGCTGATCATCTCTGCTCAAGCTCATGATTCG 816
QY 753 GGTCTCAAGAGCTCCGCTCTTTCTGCTCCGAGAAAGATCGACACTGCTGAG 812
DB 817 AGGACTTCGTGTGTCCTGCTCTTCAGGCTCCGGGGAAGGACCGAAACCTCGGGG 876
QY 813 GATCACAAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872

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DB 877 TATCACTGCACTGATGCTGTAGTGTGGCTGTGTTTGGGGCTGCTGGACGCTGTGCA 936
QY 873 CATATTCAATCTGTGTGGAGGCTTGTGGGAGACCTTCCACAGACAGCTGCTCTCCAG 932
DB 937 GGTGTGTTCTCGGTTCAGAGCTGTGGTTCAGCAGGTATGAGACTGACAGTTGCCAT 996
QY 933 CTATTACTTTCGATCGCTTATAGGCTATACCAAGTAGAGCTGAATCCATCTCTAGC 992
DB 997 CCGGCTTTCGACAGCCCTGAGCTATGTCAACAGTTGTCTCAATCCATCTCTATGC 1056
QY 993 CTCTTGTATGAAAATTCAAGCGGTGTTTCGGGACTTCTGCTTTCATGAGATGAG 1052
DB 1057 TTCTCTGATGAGAACTTCAAGGCTGCTTATGAAAGTTCTGCTGCTGCTGCTGCTGCA 1116
QY 1053 GATGAGCGCGACAGACTTACGAGAGTCCGAATACAGTTCAGATCTCG 1102
DB 1117 CCGGAGATGACGAGTTTGTGATCGTGTGCGGAGCATTCACAGATGTTG 1166

RESULT 57
US-08-149-093A-3
; Sequence 3, Application US/08149093A
; Patent No. 5658783
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
; TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
; TITLE OF INVENTION: Opioid Receptor Gene and Uses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,093A
; FILING DATE: 06-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658783nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-149-093A-3

Query Match      31.9%; Score 368; DB 1; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1,3e-80;

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Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGGCGCATCTCCCGGCGCATCCCGGTCAATCAGGCGGCTACTCCGTAGTTCCT 212
DB 301 CGCCTTCTGCCCCCTTGAAGTCAAGGTCAACATCGGGGCTCATCTGGCTGTGCAT 360
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGATGTTCTGATCATCCGATACAAAGATGAA 272
DB 361 CGGGGGGCTCCGGGGAACTGCTGTGATGATGATGATGATGATGATGATGATGAA 420
QY 273 GACAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 332
DB 421 GACAGTACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 480
QY 333 CAGGCGCTTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 392
DB 481 ACTGCTTTCAGGGGCAAGACATCTACTGAGCTTTCAGGCTTTCAGGCTTTCAG 540
QY 393 CAGAGTATGATTTTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 452
DB 541 CAAAGCTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 600
QY 453 GATGAGCGTGAACCGCTACATTTGCGGTGCAACCCCGTGAAGCTTTGACTTCCG 512
DB 601 CATGACCGTGAACCGCTATGTGTATGTCACACCTTATCCGTGCTGTGATGTT 660
QY 513 ACCCTTGAAGCAAGATCATCATATATGATCTGAGCTGTGCTGTGCTGTGCTG 572
DB 661 ATCCAGCAAGGCCCGCTGTTAATGTGGCCATATGGGCTTTCAGTGTGTTGGT 720
QY 573 CTCTGCAATAGTCTTGAAGGCAACAAAGTCAAGGAAAGATGATGATGATG 632
DB 721 TCCTGTGCAATAGTCTTGAAGGCAACAAAGTCAAGGAAAGATGATGATG 774
QY 633 CTGAGAGTTCAGAGTGAATGATGATGATGATGATGATGATGATGATGATG 692
DB 775 GGTGAGAGTTCAGAGTGAATGATGATGATGATGATGATGATGATGATGATG 831
QY 693 CATCTTTCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 752
DB 832 CCTTTTTCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 891
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTGCTCCGAGAGAAAGATGCAAC 812
DB 892 ACGACTGTGGGTGTCGCTGCTCTTCAAGGCTCCGGGAGAAAGATGCAAC 951
QY 813 GATCAACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 872
DB 952 TATCACTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1011
QY 873 CATATTCATCTGTGAGAGCTGTGAGAGCACTCCACAGACAGCTGTGCTGTG 932
DB 1012 GGTGTGTCTGTGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 1071
QY 933 CTATATCTTTCAGATGCTTTCAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 992
DB 1072 CCGTGTCTTTCAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 1131
QY 993 CTTCCTTTCAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 1052
DB 1132 TTTCTTCAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 1191
QY 1053 GATGAGCGGAGAGCACTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 1102
DB 1192 CGGGAGATGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 1241

RESULT 58
US-08-911-245-3
Sequence 3, Application US/08911245

Patent No. 5821067
GENERAL INFORMATION:
APPLICANT: Bunzow, James R

APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,245
FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin B
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-911-245-3

Query Match 31.9%; Score 368; DB 1; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGGCGCATCTCCCGGCGCATCCCGGTCAATCAGGCGGCTACTCCGTAGTTCCT 212
DB 301 CGCCTTCTGCCCCCTTGAAGTCAAGGTCAACATCGGGGCTCATCTGGCTGTGCAT 360
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGATGTTCTGATCATCCGATACAAAGATGAA 272
DB 361 CGGGGGGCTCCGGGGAACTGCTGTGATGATGATGATGATGATGATGATGATGAA 420
QY 273 GACAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 332
DB 421 GACAGTACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 480
QY 333 CAGGCGCTTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 392
DB 481 ACTGCTTTCAGGGGCAAGACATCTACTGAGCTTTCAGGCTTTCAGGCTTTCAG 540
QY 393 CAGAGTATGATTTTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 452
DB 541 CAAAGCTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 600

QY 1053 GATGAGGGGAGAGACACTAGAGAGTCCGAATACAGTTGAGATCTG 1102
Db 1192 CCGGAGATGACGAGTTTCTGATGCTGCGAGCATGCGCAAGAGATGTTG 1241

RESULT 61

US-09-170-331-3

/ Sequence 3, Application US/09170331C
/ Patent No. 6028175
/ GENERAL INFORMATION:
/ APPLICANT: Bunzow, James R
/ APPLICANT: Grandy, David K.
/ TITLE OF INVENTION: A No. 6028175el Mammalian Methadone-Specific Opioid Receptor
/ TITLE OF INVENTION: Gene and Uses
/ FILE REFERENCE: 93-311-C
/ CURRENT APPLICATION NUMBER: US/09/170,331C
/ CURRENT FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1452
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (182)..(1282)
US-09-170-331-3

Query Match 31.9%; Score 368; DB 3; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1,3e-80;

Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCATCATCACGGCGCTCTACCTCCGATGTTGCT 212
Db 301 CGCCTTCCGCGCCCTTGAGCTCAAGTGCACATCGGGGCTCATCTTGCTGCTGCTAT 360
QY 213 CCGTGGCTTGGTGGGCACTCGCTGCTCATCTTCTGATCATCCGATACAAAGATGAA 272
Db 361 CCGGGGGCTCCCTGGGAACTGCTGCTCATCTGATGCTCATCTTCAGAGACCCAAAGATGAA 420
QY 273 GACAGCAACCAACATTTTACATTTTAACTGCTTGGAGATGCTTAACTACTACAAC 332
Db 421 GACAGCTACCAACATTTTACATTTTAACTGCTTGGAGATGCTTAACTACTACAAC 480
QY 333 CATGCCCTTTCAGAGTACGCTGCTACTGATGAAATCTTGGCCCTTGGGAGATGCTGTG 392
Db 481 ACTGCCCTTTCAGAGTACGCTGCTACTGATGAAATCTTGGCCCTTGGGAGATGCTGTG 540
QY 393 CAAGATGATTAATTTTCACTGATTTACTACAACATGTTTACAGACATCTTCACTTGAACAT 452
Db 541 CAAGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 600
QY 453 GATGAGCGGAGCGGCTACATTCGCGTGGCCACCCCGTGAAGGCTTGGACTTCCGAGC 512
Db 601 CATGAGCGTGAAGCGGCTATGCTGCTATCTGCGACCTTATCCGCTTGAATGTTCCGAC 660
QY 513 ACCCTTGAAGGCAAGATCATCATATATCTGATCTGCTGCTGCTGCTCATCTTGGGAT 572
Db 661 ATTCAGCAAAAGCCAGGCTGTTAATGTTGCGCATATGAGGCGCTTGGCTTGAATGTTG 720
QY 573 CTCTGCAATATGCTCTTGAAGGCAACCAAGTCAAGGAGACGTCGATGTCATTTGATGCTC 632
Db 721 TCTCTGTCATCATCATGAGGTTTCAAGCAAGT-----GGAAGATGAAAGATGAGTGGCT 774
QY 633 CTTCGAGTTCCAGATGATGATCTACTCCGATGAGGAGCTTTCATGAGATGCTGCTT 692
Db 775 GGTGAGATCTCTGCGCCCTCAGAGCTATTTGGG---CCCTGATTCGCCATCTGATCTT 831
QY 693 CATCTTGGCTTCTGATCTCTGCTCTCATTCATTCATTCATTCATTCATTCATTCATTCAT 752
Db 832 CTTTCTTCTCTCATCATCATCTCTGCTGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 891

QY 753 GCGTCAAGAGACCGTCCGGCTCTCTTCTGCTCCCGAGAGAAAGATCCGACCTGCTAG 812
Db 892 ACGACTTGTGTGTGCTCCGCTCTGCTTCAAGGCTCCCGAGAGAGACCGAAACTCTGCGG 951
QY 813 GATCACCAAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
Db 952 TATCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
QY 873 CATATTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
Db 1012 GGTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
QY 933 CTATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
Db 1072 CTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
QY 993 CTTTCTGATGAAAACCTTCAAGCGGCTGTTCCGAGCTTCTGCTTTCATGAGATGAG 1052
Db 1132 TTTCTGATGAGAACTTCAAGCGCTGCTTGAAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCA 1191
QY 1053 GATGAGCGGAGAGACTAGAGAGTCCGAATACAGTTGAGATCTG 1102
Db 1192 CCGGAGATGACGAGTTTCTGATGCTGCGAGCATGCGCAAGATGTTG 1241

RESULT 62

US-09-510-473-3

/ Sequence 3, Application US/09510473

/ Patent No. 6280973

/ GENERAL INFORMATION:

/ APPLICANT: Bunzow, James R

/ APPLICANT: Grandy, David K

/ TITLE OF INVENTION: A No. 6280973el Mammalian Methadone-Specific

/ TITLE OF INVENTION: Opioid Receptor Gene and Uses

/ NUMBER OF SEQUENCES: 7

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Banner & Allegretti, Ltd.

/ STREET: 10 South Wacker Drive, Suite 3000

/ CITY: Chicago

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60606

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/510,473

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/149,093

/ FILING DATE: 06-NOV-1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: No. 6280973nan, Kevin E

/ REGISTRATION NUMBER: 35,303

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 312-715-1000

/ TELEFAX: 312-715-1234

/ TELE: 910-221-5317

/ INFORMATION FOR SEQ ID NO: 3:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1452 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA

/ FEATURE:

/ NAME/KEY: 5'UTR

/ LOCATION: 1..181

/ FEATURE:

NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-09-510-473-3

Query Match 31.9%; Score 368; DB 3; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

153 CGCGACATCTCCCGGACATCCCGGATCATCAACGGGGGTCTACTCGGTATGTTGCT 212
DB 301 CCGCTTCCGCGGCTTGGATCAAGGTCAACATCGGGGCTCATCTTGGCTGTGCAAT 360
QY 213 CGTGGGCTTGGTGGCACTCGCTGTCTATGTTGCTGATCATCCGATCAACAAGATGA 272
DB 361 CCGGGGGCTCTGGGGAACTGCTGTCTATGATGATCTCTCAAGAACCCAAATGA 420
QY 273 GACAGCAACCAATTATATATTTAATCTGCTTGGAGATGCTTTAGTTACTACAA 332
DB 421 GACAGCAACCAATTATATATTTAATCTGCTTGGAGATGCTTTAGTTACTACAA 480
QY 333 CATGCCCTTTCAGAGTACGCTCTACTTGTATGAATCTGCGCTTTGGGGATGCTGTG 392
DB 481 ACTGCCCTTTCAGAGGCAAGACATCTCTACTGCGCTTGGCCATTTGGAAAGCACTCTG 540
QY 393 CAAGATAGTAAATTTCCATTTGATTTACTACAAATGTTACACAGCATCTTCACTTGACCAT 452
DB 541 CAAGATAGTAAATTTGATTTGATTTACTACAAATGTTTACAGCACTTTTACTGACCGC 600
QY 453 GATGAGCGGACGCGCTCATTTGCGGTGGCAACCCCGTGAAGGCTTTGATTCGGAC 512
DB 601 CATGAGCGTGAACCGCTATGTTGCTATCTGCAACCTTACCGTGCCTTGTATGTTGAGC 660
QY 513 ACCCTTGAAGGCAAGATCATATATCTGATCTGCGCTGTGCTGATCATCTGTTGCGAT 572
DB 661 ATCCAGAAAGCCAGGCGTTAAATGTTGGCAATAGGGCCCTGGCTTCAAGTGTGGTGT 720
QY 573 CTCTGCAATATGCTCTTGGAGGCAACAAATGCAAGGAAAGCTGATGTCATGATGTC 632
DB 721 TCCTGTGTCATCATGAGGTTGACCAAGT-----GGAAATGAAGATGCAAGTGCCT 774
QY 633 CTGCAATTCACAGTATGA CTACTCGGATGGGACCTCTTCAATGAAGATGCTGTGCT 692
DB 775 GGTGAGATTCCTGCGGCTCAGAGCTATTTGGG---CCCTGATTCGCGCATCTGATCTT 831
QY 693 CATCTTTCCTTGTGATCTCTGCTCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB 832 CTTTTCCTTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCGCTCCCGAAGAAAGATGCAACCTGCGTAG 812
DB 892 ACGACTTCGTGAGTCCGCTGCTTCAAGGCTCCCGGAGAAAGACCGAAACCTGCGCG 951
QY 813 GATCAACAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
DB 952 TATCACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
QY 873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
DB 1012 GGTGTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071
QY 933 CTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
DB 1072 CTGCGCTTCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
QY 993 CTTCCTTGATGAAATCTCAAGCGGTGTTCCGGGACTTCTGCTTCCATGGAAGATGAG 1052
DB 1132 TTTCCTTGATGAAATCTCAAGCGGTGTTCCGGGACTTCTGCTTCCATGGAAGATGAG 1191
QY 1053 GATGAGCGGACAGCACTGACAGATCCGAATATGATTCAGGATCTG 1102

DB 1192 CCGGAGATGCAAGTTTCTGATCTGTGCGGACGATTCGAAGATGTTG 1241
RESULT 63
US-09-916B-3
Sequence 3, Application US/09048916B
Patent No. 6406866
GENERAL INFORMATION:
APPLICANT: Grandy et al.
TITLE OF INVENTION: Method of screening a compound for binding to MSOR
FILE REFERENCE: 49888
CURRENT APPLICATION NUMBER: US/09/048,916B
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 08/514,451
PRIOR FILING DATE: 1995-08-11
PRIOR APPLICATION NUMBER: 08/149,093
PRIOR FILING DATE: 1993-11-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1452
TYPE: DNA
ORGANISM: Rattus sp.
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(181)
NAME/KEY: CDS
LOCATION: (182)..(1282)
NAME/KEY: 3'UTR
LOCATION: (1283)..(1452)
US-09-916B-3

Query Match 31.9%; Score 368; DB 4; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

153 CGCGACATCTCCCGGACATCCCGGATCATCAACGGGGGTCTACTCGGTATGTTGCT 212
DB 301 CCGCTTCCGCGGCTTGGATCAAGGTCAACATCGGGGCTCATCTTGGCTGTGCAAT 360
QY 213 CGTGGGCTTGGTGGCACTCGCTGTCTATGTTGCTGATCATCCGATCAACAAGATGA 272
DB 361 CCGGGGGCTCTGGGAACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 273 GACAGCAACCAATTATATATTTAATCTGCTTGGAGATGCTTTAGTTACTACAA 332
DB 421 GACAGCAACCAATTATATATTTAATCTGCTTGGAGATGCTTTAGTTACTACAA 480
QY 333 CATGCCCTTTCAGAGTACGCTCTACTTGTATGAATCTGCGCTTTGGGGATGCTGTG 392
DB 481 ACTGCCCTTTCAGAGGCAAGACATCTCTACTGCGCTTGGCCATTTGGAAAGCACTCTG 540
QY 453 GATGAGCGGACGCGCTCATTTGCGGTGGCAACCCCGTGAAGGCTTTGATTCGGAC 512
DB 601 CATGAGCGTGAACCGCTATGTTGCTATCTGCAACCTTATCCGCTGCTGATTTGGAC 660
QY 513 ACCCTTGAAGGCAAGATCATATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
DB 661 ATCCAGAAAGCCAGGCTGTTATGTTGCGCATATGCGCTTGGCTTCAAGTGTGAGT 720
QY 573 CTCTGCAATATGCTCTTGGAGGCAACAAAGTCAAGGAAAGCTGATGATGAGTGTCTC 632
DB 721 TCCTGTGCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
QY 633 CTGCAATTCACAGTATGA CTACTCGGATGGGACCTCTTCAATGAAGATGCTGTGCT 692
DB 775 GGTGAGATTCCTGCGGCTCAGAGCTATTTGGG---CCCTGATTCGCGCATCTGCAATCT 831
QY 693 CATCTTTCCTTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 752

D8
D7
D6
D5
D4
D3
D2
D1

832 CTTTTCCTTCATCATCCCTGTCGTATCACTCTGTGCTACAGACCCTCATGATTGG 891

753 GCGTCTCAAGAGCCGTCGCGGCTCCTTTCTGGCTCCCGAAGAAGATCGCAACTGCCGTA 812

892 ACGACTTGTCGTGTGCCTGCTGCTTTCAAGGCTCCCGGGAAGAACCGAAACTGCGCGC 951

813 GATCACCAAGCTGCTCTGTGTGTGTGTGAGTAGTCTTCGCTCTGCTGAACTCCATTCGA 872

952 TATCACTCGACTGGT 1011

873 CATATTCACTGT 932

1012 GGTGTTTTTCCCGGTTCAAAGACGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1071

933 CTATTTACTCTGTGCATCGCCTTAAAGCTATAACAACAGTAGCCTGAATCCCATTTCTTACGC 992

1072 CCTCGGCTTTGTGCACAGCCCTGTGGGCTATGTCAACAGTTGTCTCAATCCCATTTCTTATGC 1131

993 CTTTCTTGATGAATACTTCAAGCGGTGTTTCCGGGACTTTCGCTTTCACACTGAAGAATGAG 1052

1132 TTCTCGATAGAACTTCAAGGCGCTTGTTTAGAAAGTTCTGTGTGCTTTCATCCCTGCA 1191

1053 GATGAGCGGCGAGAGCACTAGCAGAGTCCGAATATCAAGTTAGATCTCTG 1102

1192 CCGGAGATGTGAGGTTTCTGATCTGTGTCCGAGCATGTTGCCAAGATGTTTG 1241

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RESULT 64
US-09-743-871B-14
; Sequence 14, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUSE
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743, 871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093, 002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 14
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-743-871B-14

Query Match      31.9%; Score 367.8; DB 4; Length 1134;
Best Local Similarity 62.1%; Pred. No. 1.3e-80;
Matches 617; Conservative 0; Mismatches 367; Indels 9; Gaps 2;

Qy      105 GCCGACAGCAA GCGGACGCGCGCTCGGAGAGACGGCAGCTGGAGCCCGGCACATCTC 164
Db      81 GTCCTCTTGAGCCCCCAACACAGCTGCTGCCCCCGCATCTGCTGCAATGCGAGCCA 140
Qy      165 CCCGGCATCCCGGTATCATACGCGCGGTACTCTCGTAGTGTCTGCTGCGCTTGGT 224
Db      141 CGGGCGCTTCTCGGCCCTCGGGGCTCAAGGTACACCATGTGGGGCTTACCTGGCGGTG 200
Qy      225 GGGCACTCGCTGGTCATGTTCTGTGATCATCCGATCACAAAGATGAAGACGACACCA 284
Db      201 TGTGGAGAGGCTCTGGGGAACCTGCTGTATGACACCAAAATGAAGACAGCACCA 260
Qy      285 CATTACATATTTAACCTGGCTTGGCAGATGCTTTAGTTACTTCAACACCATGCGCTTCA 344
Db      261 TATTACATCTTTAACCTGGCCCTGGCCGACACATCTGTCCTGCTGACGCTGCCCTTCCA 320
Qy      345 GAGTACGCTTACTTGTATGAATTCCTGGCCTTTTGGGAGATGCTGTGCAAGATAGTAT 404

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Db	321	GGGACGGACKATCCCTCTGGGGCTTTGGCCGTTTGGGAATGCGCTGTGCAAGACATCAT	380
Qy	405	TTCCATTGATTATTAACAACATGTTCCACGACATCTTCACTTTGACCATGATGAGCGTGA	464
Db	381	TGGCATTTAGCTACTACAACTATGTTCAACGAGCACTTTCACCTTCACTGCGCATGAGTGTGA	440
Qy	465	CCGCTACATTGCGGTGTGCGACCCCGTGAAGCTTTGGACTTTCGCGACACCTTTGAAGC	524
Db	441	TGCGTATGTATACCATCTGCGACCCCATCCGTGCTTCGACGTCGCCACGCTCCAGCAAAAC	500
Qy	525	AAAGATCATCAATATCTGATCTGGCTGTGTCGTCATCTGTGTGGATCTCGCAATAGT	584
Db	501	CGAGGCTGTCAATGTGGCCATTTGGAGCCCTTGCCCTCTGTGTGCGTGTTCCTGTTCAT	560
Qy	585	CCTTGAAGGACCAAAAGTCAGGGAAGAAGTCGATGATCAATTGAGTCTCTTGCAGTTGCC	644
Db	561	CATGGGCTCGGACACAGTGTGAAGATGAAG-----ATCGAGTCCCTGTGTGGAAATGCC	614
Qy	645	AGATGATGACTACTCTGTGTGGGACCTTCTTCAATGAAGATCTGCGTCTTCATTTTGGCCTT	704
Db	615	TACCCCTCAGGATTAC--TGGGGCCCGGTGTTTGCATCTGCAATCTTCTCTCTCTT	671
Qy	705	CGTATATCCCTGTCCTCATCATCATGTCGTGTACACCCGATGATCCGCGCTCAAGAG	764
Db	672	CATGCTCCCGGTGCTCGTCAATCTCTGTGTACAGCTCATGATCCGAGCGGCTCGTGG	731
Qy	765	CGTCCGAGCTCTTTCGTGAGCTCCGAGAGAAAGATGCAACCTGCTGAAGATACACAGACT	824
Db	732	AGTCCGCTGCTCTCGGGCTCCCGAGAAAGAACCGAACTCGGGCGCATATCCTGGCT	791
Qy	825	GGTCCGTGTGTGTGTGGAGTCTTTCGTGCTGTGCTGACCTCCCATTTCAATATTCATCTT	884
Db	792	GGT	851
Qy	885	GGTGAAGGCTTTGGGGAGCACTCCCAAGACACAGCTGCTCTTCACAGTATTTACTCTG	944
Db	852	GGCCCAAGGGCTGGGGGTTTCAAGCCGAGAGGAGATCTGCGGTGCAATTTGCGCTTCG	911
Qy	945	CATGAGCTTAAAGCTATATACCAACAGTAGGCTGAATCCATTTCTTACGCGCTTTGTATGA	1004
Db	912	CAGGCGCTTGGGGCTACGTCMAACAGTGTCTCAACCCCATCTCTACGCTTCTTGGATGA	971
Qy	1005	AAACTTCAAGGGGTGTTCCTCGGAGCTTTCGTCTTTCACACTGAAGATGAGATGAGAGCGCA	1064
Db	972	GAACTTAAAGGCTGTCTTCGCGCAAGTTCTGTGTGTGTCATCTGCGCTGCGCGGAGCGTGA	1033
Qy	1065	GAGCACTTAGCAAGATCCGAATATACATTTACAGA	1097
Db	1032	GGTGTGTGATCCGCGTGGCGACATTTGCCAAGAA	1064

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1      RESULT 65
2      US-08-147-592A-5
3      ; Sequence 5, Application US/08147592A
4      ; Patent No. 6096513
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Bell, Graeme I
7      ; APPLICANT: Reisine, Terry
8      ; APPLICANT: Yasuda, Kazuki
9      ; TITLE OF INVENTION: Opioid Receptor Genes,
10     ; TITLE OF INVENTION: Compositions and Methods
11     ; NUMBER OF SEQUENCES: 43
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Arnold, White & Durkee
14     ; STREET: P.O. Box 4433
15     ; CITY: Houston
16     ; STATE: Texas
17     ; COUNTRY: United States of America
18     ; ZIP: 77210
19     ; COMPUTER READABLE FORM:
20     ; MEDIUM TYPE: Floppy disk
21     ; COMPUTER: IBM PC compatible
22     ; OPERATING SYSTEM: PC-DOS/MS-DOS
23     ;

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 161..1261
US-08-147-592A-5

Query Match 31.9%; Score 367.8; DB 3; Length 1330;
Best Local Similarity 63.4%; Pred. No. 1.4e-80;
Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
154 GCGCATCTCCCGCGCCATCCCGGTATCATCAGCGCGGTCTACTCCGTAGTGTCTC 213
281 GCTTCTCGCCCTTGACTCAAGTCAACATCGGGGCTCTACTTGGCTGTGTGATC 340
214 GTGGCTTGTTGGGCACTCGTGTCTCATGTTCTGATCATCTCCATACAAAGATGAG 273
341 GGGGGGCTCTGGGGAACCTGCTCTCATGATGATCTCTCAAGCACCAAGATGAG 400
274 ACAGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 333
401 ACTGTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 460
334 ATGCCCTTCAAGATGAGTCTACTTGTATGAAATCTGAGCTTTTGGGATGTGCTGTC 393
461 CTGCCCTTCAAGGAGACAGATCTTCTGTGGCTTCTGGCATTTGGGAATGCATGTGC 520
394 AAGATGAAATTTTCATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 453
521 AAGACGTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
454 ATGAGCGTGAGCCGTATATGCGTGTGCAACCCCGTGAAGGCTTTGAGCTTCGACA 513
581 ATGAGTGAGACCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 640
514 CCCTTGAAGGAGGATCATCAATATCTGATGAGTGGCTGTGCTCATCTGTTGGCATC 573
641 TCCAGTAAAGCCCAAGCCGTTATGTGCTTATGAGGCGCTGTGCTTGGTGTGTGTT 700
701 CCTGTGTCATCATGAGGCTCAGACAAAGT-----GAGAGTGAAGAGATGAGGCTG 754
574 TCTGCAATATGCTCTTGAAGGACCAAGTCAAGGAAAGCTGATGATGATGATGATG 633
634 TTGAGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
755 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 811
694 ATCTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 753

812 CTTTCTTCTATCATCCGCTTGTATCATCTCTGTCTACAGCTTATGATGATGATG 871
754 GCTCTCAAGAGCGTCCGCTCTCTTGTGCTCTCCAGAGAAAGATCCGAACCTGTAG 813
872 CGACTTGTGTGTCCGCTCTCTTCAAGGCTCCGAGAGAAAGACCGGAACCTGTAG 931
814 ATCACAGACTGTCTGT 873
932 ATCACAGCTGT 991
874 ATATTCATCTGT 933
992 GTCTTGT 1051
934 TATTACTTGT 993
1052 CTGGCTTGT 1111
994 TTTCTGT 1053
1112 TTTCTGT 1171
1054 ATGAGCGGAT 1098
1172 CGGAGATGAT 1216

RESULT 66
US-08-292-694A-5
Sequence 5, Application US/08292694A
Patent No. 6319686
GENERAL INFORMATION:
APPLICANT: BELL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUDA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,694A
FILING DATE: August 19, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/147,592
FILING DATE: 5 No. 6319686ember 1993
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US94/05747
FILING DATE: 20 May 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARK B. WILSON
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WTM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1330 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 MOLECULE TYPE: cDNA
 NAME/KEY: CDS
 LOCATION: 161..1261
 US-08-292-694A-5

Query Match 31.9%; Score 367.8; DB 4; Length 1330;
 Best Local Similarity 63.4%; Pred. No. 1.4e-80;
 Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

154 GGGCAATCTCCCGCCATCCCGGTCAATCAAGCGGCTACTCCGTAGTGTCTG 213
 281 GCGTTCCTGCGCCCTTGAGACTCAAGGTCAACATCGGGCTTACTTGGCTGTGATC 340
 214 GTGGCTTGTTGGGCACTCGGTGATGTCATGTCATCATCCATACAAAGATGAAG 273
 341 GGGGGGCTCTGGGAACTGCTCGTATGATGATCATCTCAGGCAACCAAGATGAAG 400
 274 ACAGCAACCAATTATTAATTTAACTGCTTTGGCAGATGCTTAACTTAACTAACACC 333
 401 ACTGCTACCAACATTTATTAATTTATCTGGCACTGGCATACCTCGTCTTGGCTGACA 460
 334 ATGCCCTTCAAGATACGGTCACTTGAATGATGAAATGCTGGCTTTGGGGATGCTGTC 393
 461 CTGCGCTTCCAGGGCAACAGATCTCTTCTGGGCTTCTGGCAATTTGGGATCACTGTGC 520
 394 AAGATAGTAATTTCAATGATTAATTAACAATGTTTCAACAGGATCTTCACTTGAACATG 453
 521 AAGACGGTCATGTCATGATCACTAACAACATGTTTACAGACATTTGACTGTGC 580
 454 ATGACGGTGAACCGCTCACTTCCGTGTCACCCCGTGAAGCTTTGACTTCCGACA 513
 581 ATGATGTAGAACCGTTATGATCTATCTGCCACCTTATCCGCTTGTATGTTGGACA 640
 514 CCTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTGTCATCTGTGGACATC 573
 641 TCCAGTAAACCCAGCCCTTATATGTCATATAGGCCCTTGGCTTGGTGTGTG 700
 574 TCTGCAATAGTCTTGAAGGCAACAAAGTCAAGGAAAGCTGATGTCAATTAAGTCTCC 633
 701 CCTGTGTCATATGAGGCTCAGCACAAGT-----GAGGATGAAAGATGAGTGTGC 754
 634 TTGCAATTCCAGATGATGACTACTCTGTGGTGAACCTTCTCATGAAGATCTGCGTTTC 693
 755 GTGGAGATCCCGCCCTCAGAGA---CTATTGGGGCCCTGTATTGGCATCTGCATCTTC 811
 694 ATCTTGGCTTGTATCCCTGCTCCATCATCTGCTGTACTAACCCTGATATCTG 753
 812 CTTTCTCTTATATCTCCGCTTCTGATCATCTCTGTCTAAGCTTCAATGATGGA 871
 754 GGTCTCAAGAGCGTCCGCTCTTCTGAGCTCCGAGAGAAAGATCGCAACTCGGTAGG 813
 872 CGACTTGTGATGTCCGGCTGCTTTCAGGCTCCGAGAGAAAGACCGAAGCTGGAGACG 931
 814 ATCAACAAGCTGTGCTGT 873
 932 ATCAACAAGCTGT 991
 874 ATATTCATCTGT 933
 992 GTCTTTGTCTGT 1051
 934 TATTACTTGT 993
 1052 CTGGCTTCTGT 1111

QY 994 TTTCTGATGAATACTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAG 1053
 DB 1112 TTTCTGATGAATACTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAG 1171
 QY 1054 ATGAGCGGCAAGCACTAGCAGAGTCCGAAATTAAGTTCAAGAT 1098
 DB 1172 CCGGAGATGCAAGTTTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1216

RESULT 67
 US-08-986-209A-1
 Sequence 1, Application US/08986209A
 Patent No. 6660496
 GENERAL INFORMATION:
 APPLICANT: Sloan-Kettering Institute for Cancer Research
 APPLICANT: Pasternak, Gavril W
 APPLICANT: Pan, Ying-Xian
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTOR
 FILE REFERENCE: 830002-2004
 CURRENT APPLICATION NUMBER: US/08/986,209A
 CURRENT FILING DATE: 1997-12-05
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 2600
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (299)..(1402)
 OTHER INFORMATION:
 US-08-986-209A-1

Query Match 31.9%; Score 367.8; DB 4; Length 2600;
 Best Local Similarity 63.4%; Pred. No. 1.8e-80;
 Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

154 GGGCAATCTCCCGCCATCCCGGTCAATCAAGCGGCTACTCCGTAGTGTCTG 213
 419 GCGTTCCTGCGCCCTTGAGACTCAAGGTCAACATCGGGCTTACTTGGCTGTGATC 478
 214 GTGGCTTGTTGGGCACTCGGTGATGTCATGTCATCATCCATACAAAGATGAAG 273
 479 GGGGGGCTCTGGGAACTGCTCGTATGATGATCATCTCAGGCAACCAAGATGAAG 538
 274 ACAGCAACCAATTATTAATTTAACTGCTTTGGCAGATGCTTAACTTAACTAACACC 333
 539 ACTGCTACCAACATTTATTAATTTATCTGGCACTGGCATACCTGCTGTGCTGACA 598
 334 ATGCCCTTCAAGATACGGTCACTTGAATGATGAAATGCTGGCTTTTGGGATGCTGTGC 393
 599 CTGCGCTTCCAGGGCAACAGATCTCTTCTGGGCTTCTGGCAATTTGGGATGACATGTGC 658
 394 AAGATAGTAATTTCAATGATTAATTAACAATGTTTCAACAGATCTTCACTTGAACATG 453
 659 AAGACGGTCATGTCATGATCACTAACAAGTGTTCACAGACATTTCACTTGACTGCC 718
 454 ATGACGGTGAACCGCTCAATGCGGTGTCACCCCGTGAAGGCTTTGAGACTTCCGACA 513
 719 ATGATGTAGAACCGTTATGATGCTATCTGCCACCTTATCCGCTTGTGATGTTGGACA 778
 514 CCTTGAAGGCAAGATCATCAATATTAATGATCTGTGCTGTGTGTGTGTGTGTGTGTGT 573
 779 TCCAGTAAACCCAGGCGCTTAAATGTGTCATATGAGCCCTGAGCTTGTGTGTGTGTGT 838
 574 TCTGCAATAGTCTTGAAGGCAACAAAGTCAAGGAAAGCTGATGTCAATTAAGTCTTC 633
 839 CCTGTGTCATCACTGAGGCTCAGCACAAGT-----GAGGATGAAAGATGAGTGTGCTG 892
 634 TTGCAATTCCAGATGATGACTACTCTGTGGTGAACCTTCTCATGAAGATCTGCGTTTC 693

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Db      893 GTGAGATCCCGCCCTCAGGA---CTATTGGGGCCCTGTAATTGGCCATCTGCATCTTC 949
Qy      694 ATCTTGCTTGTGTATCCCTGCTCATCATCATGTCTGCTACACCTGTATGATCTG 753
Db      950 CTTTTCCTTATCATCCCGGCTTCATCATCTGCTGCTACAGCCTCATGATTGCA 1009
Qy      754 CCGTCAAGAGCGTCGGGCTCCCTTTGCTCCCGAGAGAAAGATGGCAACCGGCTAGG 813
Db      1010 CCACTTCGGGTGTGCGGCTGCTTTACAGCTCCCGAGAGAGACCGGAACCTTGAGACC 1069
Qy      814 ATACCAAGCTGCTGCTGTGTGTGTGAGAGTCTTCGTGCTGCTGAGACTCCCATTCAC 873
Db      1070 ATCAACAGCGCTGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1129
Qy      874 ATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
Db      1130 GTCTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
Qy      934 TATTACTTGTGATCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
Db      1190 CTGGCTTGTGACAGCCCTGAGCTATGTCAACAGTGTGTGTGTGTGTGTGTGTGTGT 1249
Qy      994 TTTCTGTATGAATACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
Db      1250 TTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1309
Qy      1054 ATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1098
Db      1310 CGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1354

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RESULT 68
US-09-743-871B-13
; Sequence 13, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUS
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743,871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093,002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 13
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-743-871B-13

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Query Match      30.9%; Score 357; DB 4; Length 1177;
Best Local Similarity 63.3%; Pred. No. 5.8e-78;
Matches 616; Conservative 0; Mismatches 320; Indels 37; Gaps 3;

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Qy      153 GCGGCAATCTCCCGGCGCATCCGCGTATCATACCGCGGCTTACTCCGTAAGTTCGT 212
Db      144 GCGCTTCTGCGCCCTCGGGCTCAAGGTACATCGTGGGCTCTTACCTGCGCGTGTGT 203
Qy      213 CGTGGGCTTGTGTGCACTGCTGTGATGTTGCTGTATCATCCGAT-----259
Db      204 CGAGGGGCTCTGGGGAAGTCCCTTGTATGTAGTATCTCTCAGTGAAGGCTGGGCCCA 263
Qy      260 -----ACCAAGATGAAGACAGACCAACCAATTATTAATTAACCTGG 304
Db      264 AGTTCCTGTCTGACACCAAAATGAAGACAGCACCAATATTATTAATTAACCTGG 323
Qy      305 CTTTGGAGATGCTTTTGTATCTACAAACCATGCGCTTTCAAGATGAGTGTATGATGA 364
Db      324 CCTGGCGGACACTGTGTCTGTCTGACGTGCGCTTTCAGGGACGAGACATCTCTCTGG 383

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Qy      365 ATCTCGCCCTTTGGGAGATGTGCTGTGCAAGATGTAATTTCCATTGATTACTACAA 424
Db      384 GCTTCGCGCGTTTGGGAATCGCTGTGCAAGAGATGATGATGATGATGATGATGATGAT 443
Qy      425 TGTTCACAGCATCTTCACTTGAACATGATGAGCGGAGACCGCTACATTCGCGTGGCC 484
Db      444 TGTTCACAGCATCTTCACTTGAACATGATGAGCGGAGATGATGATGATGATGATGATGAT 503
Qy      485 ACCCGTGAAGCTTTGACCTTTCGACACCCCTTGAAGGCAAGATCATCAATATTCGCA 544
Db      504 ACCCATCGAGCCCTGACGCTCCGACAGTGCAGCAAAAGCCAGAGCTGTCAATGGCCA 563
Qy      545 TCTGCTGCTGTGCTGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 604
Db      564 TCTGGCCCTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 622
Qy      605 GGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
Db      623 -----GAGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
Qy      665 GGAACCTCTTGATGAAGATCTGAGCTTTCATCTTTGCTGTGTGTGTGTGTGTGTGTGTGT 724
Db      675 GGGGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 734
Qy      725 TCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 784
Db      735 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 794
Qy      785 CCCGAGAGAAAGATGAGACCTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 844
Db      795 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy      845 TCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 904
Db      855 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 914
Qy      905 CCGTCCAGAGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 964
Db      915 AGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 974
Qy      965 ACAATGACCTGAATCCATCTCTACCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024
Db      975 ACAGCTGCTCAACCCCATCTGTAGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
Qy      1025 GGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1084
Db      1035 GCAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1094
Qy      1085 ATACAGTTCAAGA 1097
Db      1095 GCATGTCGAAGA 1107

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RESULT 69
US-08-147-949A-1
; Sequence 1, Application US/08147949A
; Patent No. 5747279
; GENERAL INFORMATION:
; APPLICANT: Pasteur, Gavril W.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:

```

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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,949A
FILING DATE: 05-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44782/JPM/JRM
TELEPHONE/COMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 299..1401
OTHER INFORMATION:
US-08-147-949A-1

```

Query Match 29.9%; Score 344.8; DB 1; Length 2600;

Best Local Similarity 63.2%; Pred. No. 7,6e-75;

Matches 598; Conservative 0; Mismatches 337; Indels 11; Gaps 4;

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154 GCGCATCTCCCGCCGATCCGGTCTCATCATCAGCGCGGTCTACTCCGTAAGTTCTGC 213
419 GCCTTCCTGCGCCCTTGAGCTCAAGGTCAACGTCATCGGGCTTACTTGGCTGTGATC 478
214 GTGGCTTGTGGGCACTCGTGTCTATGTTCTGATATCCGATACCAAGATGAAG 273
479 GGGGGGCTCTGGGAACTCGCTCATGATGTCATCTCAGGACACCAAGATGAAG 538
274 ACAGCAACCAATTTACATATTTTAACTGCTTGGAGATGCTTGTAGTACTCAACC 333
539 ACTGCTACCAATTTACATATTTTAACTGCTTGGAGATGCTTGTAGTACTCAACC 598
334 ATGCCCTTTCAGAGTACGCTTCTTCTGATGATGATGATGATGATGATGATGATG 393
599 CTGCCCTTTCAGAGTACGCTTCTTCTGATGATGATGATGATGATGATGATGATG 658
394 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 453
659 AAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
454 ATGAGCTGAGACCGCTACATTTGCGGTGCGACCCCGTGAAGCTTTGAGCTTCCGACA 513
719 ATGAGCTGAGACCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 778
514 CCCTTGAAGGCAAGATCATCAATATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 573
779 TCCAGTAAAGCCCAAGCGCTTAAATGAGCCATATG- GCTTGGCTTGGTGTGTGT 837
574 TCTGCAATAGTCTTGGAGGCAACAAAGTCAGGGAAGAGTGTGATGATGATGATG 633
838 CTTGTTGCTATCATGAGGCTCAGACAAAGT-----GAGAGATGAAGATCAGAGCTCG 891
634 TTGAGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
892 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 948
694 ATCTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 752
949 CTTTTCCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1008

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QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTCCCGAAGAAAGATCGCACTGCTAG 812
DB 1009 AGCACTTGTGTGTGTCCTGCTCTCTTCAAGCTCCGAGAGAGAGACCGGACTGGAG 1068
QY 813 GATCAACGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 1069 CATCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1128
QY 873 CATATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1129 GCTCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1188
QY 933 CATATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1189 TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1248
QY 993 CTTTCTGTATGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1249 TTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1308
QY 1053 GATGAGCGGCGAGAGCACTAGCAAGTCCGAAATACAGTTCAAGAT 1098
DB 1309 CCGGAGATGAGAGGTTTCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1354

```

RESULT 70

US-09-743-871B-11

; Sequence 11, Application US/09743871B

; Patent No. 6627734

; GENERAL INFORMATION:

; APPLICANT: Memorial Sloan-Kettering Cancer Center

; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUS

; FILE REFERENCE: 830002-2001.1

; CURRENT APPLICATION NUMBER: US/09/743,871B

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: PCT/US99/15977

; PRIOR FILING DATE: 1997-07-15

; PRIOR APPLICATION NUMBER: 60/093,002

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patent In version 3.0

; SEQ ID NO: 11

; LENGTH: 1223

; TYPE: DNA

; ORGANISM: mus musculus

US-09-743-871B-11

Query Match 29.1%; Score 336.2; DB 4; Length 1223;

Best Local Similarity 63.9%; Pred. No. 7,2e-73;

Matches 544; Conservative 0; Mismatches 298; Indels 9; Gaps 2;

```

QY 252 CATCCGATACCAAGATGAGAGAGCAACCAATTTATATTTAACTGGCTTGGC 311
DB 281 CAGCAGGACCAAGATGAGAGAGCAACCAATTTATATTTAACTGGCCTGGC 340
QY 312 AGATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 371
DB 341 TGAATCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 400
QY 372 GCTTTTGGGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 431
DB 401 GCAATTTGGGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 460
QY 432 CAGCATCTTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
DB 461 CAGCATCTTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 520
QY 492 GAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
DB 521 CCGTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 580

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TELEX: 90-4030 MRSNFOERSMSH
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 830 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-405-271A-13

Query Match 27.7%; Score 319.6; DB 4; Length 830;
 Best Local Similarity 60.8%; Pred. No. 7.1e-69;
 Matches 502; Conservative 0; Mismatches 312; Indels 11; Gaps 4;

```

QY 257 GATACACAAGATGAGAGACAGACCAACATTATTAACCGGCTTGGGAGATG 316
DB 16 GATACACCAAGATGAGAGCTGCCACCAACATCTCACTTTCACTTGGCTCT-GCAGATG 74
QY 317 CTTTAGTACTCAACACCATGCCCTTCAAGTAGCGTCTACTTGAATTCCTGGCCTT 376
DB 75 CCTTAGCCACGATACCTGCCCTTCAAGTAGTGAATTAACCTAATGGGAACATGGCCAT 134
QY 377 TTGGGAGATGCTGTGCAAGATAGTAATTTCAATTGATTACTCAACATGTTCCACGCA 436
DB 135 TTGGAACCATCTTTGCAAGATAGTATCTCCATGATTACTATTAACATGTTCCACGCA 194
QY 437 TCTTCACTTGACATGATGAGCGTGAACCGCTACATGGCGGTGGCCACCCCGTGAAG 496
DB 195 TATTACCTCTGCAACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 254
QY 497 CTTTGAAGTCTGCGACACCCCTTGAAGGCAAGATCATATATCTGCACTGTGCTGT 556
DB 255 CTTTGAAGTCTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
QY 557 CGTCACTGTGAGCATCTCTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGACGTG 616
DB 309 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 368
QY 617 ATGTGATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
DB 369 GTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
QY 677 TGAAGATGCTGCTCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
DB 426 TGAAGATGCTGCTCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
QY 737 ACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
DB 486 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
QY 797 ATTCGAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 856
DB 546 ACAGGAATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
QY 857 GCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 916
DB 606 GCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
QY 917 CAGTGTCTCTCCAGTATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 976
DB 666 CGTTCAGACTGTTCTTGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 725
QY 977 ATCCGATCTCTAGGCTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1036
DB 726 ACCGAGTCTTATCATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
QY 1037 TTCCACTGAAGATGAGATGAGCGGCGAGAGCACTAGCAGAGTCC 1081
DB 785 TCCGAACCTCTTCCAACTGAGCAAAACTCCACTGCAATTC 829

```

RESULT 76
 US-08-387-707-12
 Sequence 12, Application US/08387707

```

; Patent No. 626563
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,707
; FILING DATE: 10-SEP-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-387-707-12

```

Query Match 21.1%; Score 243; DB 3; Length 2447;
 Best Local Similarity 100.0%; Pred. No. 5.7e-50;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 368 CTTGCGCTTTTGGGAGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 427
DB 1 CTTGCGCTTTTGGGAGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 428 TCACGACATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTGCGGTGCGACC 487
DB 61 TCACGACATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTGCGGTGCGACC 120
QY 488 CCGTGAAGCTTTGATCTTCCGACACACCTTGAAGGCAAAATCATCATATCTGCATCT 547
DB 121 CCGTGAAGCTTTGATCTTCCGACACACCTTGAAGGCAAAATCATCATATCTGCATCT 180
QY 548 GAGTCTGTCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAAGTCAGGG 607
DB 181 GAGTCTGTCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAAGTCAGGG 240
QY 608 AAG 610
DB 241 AAG 243

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RESULT 77
 US-08-405-271A-12
 Sequence 12, Application US/08405271A
 Patent No. 6432652
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 APPLICANT: KEITH, DUANE E.
 TITLE OF INVENTION: OPIOID RECEPTOR GENES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATIE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFORMSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-405-271A-12

Query Match 21.1%; Score 243; DB 4; Length 2447;
Best Local Similarity 100.0%; Pred. No. 5.7e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 CTTGGCCCTTTGGGAGATGTGCTGTGCAAGATAGTATTTCCATTGATTAACAACATGT 427
DB 1 CTTGGCCCTTTGGGAGATGTGCTGTGCAAGATAGTATTTCCATTGATTAACAACATGT 60
QY 428 TCACGAGATCTTCACTTACCATGATGAGCGGTGACCGGCTACATTCGCGTGGCCACC 487
DB 61 TCACGAGATCTTCACTTACCATGATGAGCGGTGACCGGCTACATTCGCGTGGCCACC 120
QY 488 CCGTGAAGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGCATCT 547
DB 121 CCGTGAAGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGCATCT 180
QY 548 GCGCTGTGCTGATCTGTGAGCATCTGCAATAGTCTTGGAGGACCAAGTCAAGG 607
DB 181 GCGCTGTGCTGATCTGTGAGCATCTGCAATAGTCTTGGAGGACCAAGTCAAGG 240
QY 608 AAG 610
DB 241 AAG 243

RESULT 78
US-09-016-434-1446
Sequence 1446, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF INVENTIONS: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1446:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g693907
US-09-016-434-1446

Query Match 21.0%; Score 242.6; DB 4; Length 1317;
Best Local Similarity 55.0%; Pred. No. 5.6e-50;
Matches 523; Conservative 0; Mismatches 419; Indels 9; Gaps 2;

QY 96 CTGGGCGGAGCCCGACGACGACGACGCGCGCTCGAGAGAGCGGACGCGCCGC 155
DB 110 CTGGGCGGAGCCCGACGACGACGACGCGCGCTCGAGAGAGCGGACGCGCCGC 169
QY 156 GCACATCTCCCGGCGCATCCCGGTATCATCAGCGCGGTATCTCCGTATGTTCTGCT 215
DB 170 GGAAGCGCGGCGCGCGGCGCATGCTGCTATCAGTGCATCTTACGCGCTGCTGCTGCT 229
QY 216 GGGCTGTGGGGAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 275
DB 230 GGGCTGTGGGGAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 289
QY 276 AGCAACCAATTTAATATTTAATCTGCTTGGAGATGCTTGAATTAATCAACCAT 335
DB 290 GGGTACCAATTTAATATTTAATCTGCTTGGAGATGCTTGAATTAATCAACCAT 349
QY 336 GCCCTTCAAGATGAGGTCTACTTGAATGATGATGATGATGATGATGATGATGATGAT 395
DB 350 GCCCTTCAAGATGAGGTCTACTTGAATGATGATGATGATGATGATGATGATGATGAT 409
QY 396 GATAGTAATTTCCATTGATTAATTAATCAACATGTTCAACAGATCTTCACTTGAAT 455
DB 410 GCGGTGTGCTGAGGTGAGGCGCTCAACATGTTCAACAGATGTTGTTGTTCAACGCTGCT 469
QY 456 GAGCGTGAACCGTCAATTTGCGGTGCGACCCCGTGAAGGCTTGGACTTCCGACACC 515
DB 470 GAGCGTGAACCGTCAATTTGCGGTGCGACCCCGTGAAGGCTTGGACTTCCGACACC 529
QY 516 CTTGAAGGCAAGATCATCAATATTTGATGATGATGATGATGATGATGATGATGATGAT 575
DB 530 CAGCGTGAACCGTCAATTTGCGGTGCGACCCCGTGAAGGCTTGGACTTCCGACACC 589
QY 576 TGCATATGCTTGTGAGGACCAAGTCAAGGAGAGCGTGAATGATGATGATGATGAT 635
DB 590 CATGCGATCTTGTGAGGACCAAGTCAAGGAGAGCGTGAATGATGATGATGATGAT 649
QY 636 GCGTTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
DB 650 GCGTTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 700

STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 100..1272
 US-08-417-103-1

Query Match 19.9%; Score 229.6; DB 1; Length 1634;
 Best Local Similarity 55.1%; Pred. No. 9.2e-47;
 Matches 523; Conservative 0; Mismatches 409; Indels 18; Gaps 3;

Qy 75 CAGCAGCCCTGGTTCCTCCGCTGGGCGCCGAGCCCGACAGCAAGCGAGCGCGCTCGGA 134
 Db 171 CGGCGGCGAGGAGGCGCGCGCGCGCTGCGAGCGGAGAGAGAGCGAGCGGCGGAA 230
 Qy 135 GAGCGCGAGCTGAGAGCGCGCGCACATCTCCCGGCGATCCGGTCTATCATCAGCGCGT 194
 Db 231 TGCGTCCAGAGACGGGACCTTGAGGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 290
 Qy 195 CTACTCCGAGTGTCTGCTGGGCTGGTGGGCAATCCGCTGGTCTATGATCAT 254
 Db 291 CTACTCCGAGTGTCTGCTGGGCTGGTGGGCAATCTATGCTATCTATGATCATCT 350
 Qy 255 CCGATACACAAAGATGAGAGAGCAACCAATTTACATATTTAACTGGCTTTGGCAGA 314
 Db 351 GCGCTATGCCAAGATGAGAGAGCGGCGCACATCTACATCTTAAATCTGGCATTTGCTGA 410
 Qy 315 TGCTTAGTACTACAAACCATGCGCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCC 374
 Db 411 TGAGCTGCTCATGCTCAGCGTCCCTTCTAGTACCTCAGCTGTTGGCGCACATGCGC 470
 Qy 375 TTTTGGGATGTGCTGTGCAAGATAGTATTTCCATGTTACTTACACATGTTCCAGCG 434
 Db 471 CTTCGCTGCGCTCTGCTGCGGCTGCTGCTCAGCGTGAAGCGGCTCAACATGTTACAG 530
 Qy 435 CATCTTCACTTGACATGATGAGCGTGAGCGCTACATTTGGCGTGGCCACCCGTGA 494
 Db 531 CATCTACTGTCTGATGCTGCTGAGCTGAGCGGCTACGCGGCTGAGCGGCTGATCCATCA 590
 Qy 495 GCGCTTTGACCTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGT 554
 Db 591 GCGCGCGGCTACCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 650
 Qy 555 GTTCCTATCTGTGGCATCTCTGCAATAGTCTTGGAGGCGACCAAGTGAAGGAAAGCT 614
 Db 651 ATCGCTGCTGCTGATCTGCGCCATGCTGCTCTTCTCTGCGACCGGCGGCGGCGGCGG 710
 Qy 615 CGATGTCATGTAGTGTCTCTGAGTCTCCAGATGATGATGATGATGATGATGATGATGAT 674
 Db 711 CAGCG---TGCTTGAACATGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 767
 Qy 675 CATGAGATCTGCGCTTCTCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
 Db 768 CGT---GTTGTACACATTTCTCATGGGCTTCTGCTGCGCGGCGGCGGCGGCGGCGGCT 824
 Qy 735 CTACACCTGATGATCTGCGCTCAAGAGCTCCGCGCTCTTTTCTGCTCCCGAGAGAA 794
 Db 825 CTACCTGCTCATCATTTGCTMAAGATGCGATGCTGCGGCGGCGGCGGCGGCGGCGGCGG 884
 Qy 795 AGATGCAACCTGCGGCTGAGATACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
 Db 885 CAGGCGCTGCGAGCGGAGATACCTTAAATGATGATGATGATGATGATGATGATGATGAT 944
 Qy 855 CTGCTGAGCTCCCATTTACATATTTCACTGCTGAGGCTCTGGGAGAGCACTCCACAG 914
 Db 945 CTGCTGAGAGCTTTCTATGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 Qy 915 CACAGCTGCTCTCTGAGCTATTTACTTCTGCAATGCGCTTAAAGCTATACCAAGTAGCT 974
 Db 1005 CACGCTGAGCTC-----AGCTGCGCTCATCTCCGCGCTATGCGCAAGCTGCGC 1052
 Qy 975 GAATCCCATTTCTACGCTTTCTTGATGAAGAACTCAAGCGGCTGTTCC 1024

Db 1053 CAACCCATCTCTATGCTTCTCTCAGACAACTTCAAGCGCTCTTCC 1102

RESULT 82
 US-09-016-434-1302
 / Sequence 1302, Application US/09016434
 / Patent No. 6500938
 / GENERAL INFORMATION:
 / APPLICANT: Janice Au-Young
 / APPLICANT: Jeffrey J. Seilhamer
 / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 / TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 / NUMBER OF SEQUENCES: 1490
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 / STREET: 3174 PORTER DRIVE
 / CITY: PALO ALTO
 / STATE: CALIFORNIA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 / CURRENT APPLICATION DATA:
 / FILING DATE: US/09/016.434
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Zeller, Karen J.
 / REGISTRATION NUMBER: 37,071
 / REFERENCE/DOCKET NUMBER: PA-0002 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (650) 855-0555
 / TELEFAX: (650) 845-4166
 / INFORMATION FOR SEQ ID NO: 1302:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1634 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: GENBANK
 / CLONE: 9307433
 / US-09-016-434-1302

Query Match 19.9%; Score 229.6; DB 4; Length 1634;
 Best Local Similarity 55.1%; Pred. No. 9.2e-47;
 Matches 523; Conservative 0; Mismatches 409; Indels 18; Gaps 3;

Qy 75 CAGCAGCCCTGGTTCCTCCGCTGGGCGCCGAGCCCGACAGCAAGCGAGCGCGCTCGGA 134
 Db 171 CGGCGGCGAGGAGGCGCGCGGCGCGGCTGCGAGCGGAGAGAGCGGCGGCGGAA 230
 Qy 135 GAGCGCGAGCTGAGAGCGCGCGCACATCTCCCGGCGATCCGGTCTATCATCAGCGCGGT 194
 Db 231 TGCGTCCAGAGACGGGACCTTGAGCGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCT 290
 Qy 195 CTACTCCGAGTGTCTGCTGGGCTGGTGGGCAATCGCTGCTATGATCATGATCAT 254
 Db 291 CTACTCCGAGTGTCTGCTGGGCTGGTGGGCAATCTATGCTATGCTATGATCATCT 350
 Qy 255 CCGATACACAAAGATGAGAGAGCAACCAATTTACATATTTAACTGGCTTTGGCAGA 314
 Db 351 GCGCTATGCCAAGATGAGAGAGCGGCGCACATCTACATCTTAAATCTGGCATTTGCTGA 410
 Qy 315 TGCTTAGTACTACAAACCATGCGCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCC 374

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Db 411 TGAGCTGCTCAGTCTCAGGCTGCCCTTCTCTAGTCACTCCAGCTGTTGGCCAGCTGGCC 470
Qy 375 TTTTGGGAGATGTCCTGTGCAAGATAGTATTTTCCATTGATTCTCAACATTTTACCCAG 434
Db 471 CTTGCGTGGCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
Qy 435 CATCTTCACTTCACTGATGATGAGGCTGAGCCGCTACATTTGCGTGTGCTGCTGCTGCTGCTG 494
Db 531 CATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
Qy 495 GGCCTTTGACCTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGATCTGCTGCTGCT 554
Db 591 GCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
Qy 555 GTTCCTCATCTGTTGGCATCTCTGCAATAGTCTTTGAGAGCCAAAGTCAAGGAAGAGCT 614
Db 651 ATCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
Qy 615 CGATGCTCATTTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
Db 711 CACGG---TGGCTTGCACATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
Qy 675 CATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
Db 768 CGT---GTTGTACATTTCTCATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
Qy 735 CTACACCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
Db 825 CTACGTGCTCATGATTTGCTGAAGATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884
Qy 795 AGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Db 885 CAAAGGCTTCGAGGCGCAAGATCACTTAATGATGATGATGATGATGATGATGATGATGATGAT 944
Qy 855 CTGCTGATCTCCATTCATATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 914
Db 945 CTGCTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
Qy 915 CACGCTGCTCTCTCCAGCTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 974
Db 1005 CACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
Qy 975 GAATCCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
Db 1053 CAACCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1102

```

RESULT 83
US-07-816-283-3
Sequence 3, Application US/07816283
Patent No. 5436155

GENERAL INFORMATION:

APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Saino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-816-283-3

Query Match 19.6%; Score 226.6; DB 1; Length 1265;
Best Local Similarity 54.8%; Pred. No. 4,56-46;
Matches 523; Conservative 0; Mismatches 414; Indels 18; Gaps 3;

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Qy 78 CAGGCGCTGCTTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 137
Db 162 CTGACGAGGCGGCTCGGCGCTCGGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221
Qy 138 CGCGCAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 197
Db 222 TTCCCAAGATGAGACCTTAAGCGAGGAGCAGAGGATAGCGCATCTTCATCTTTCATCTA 281
Qy 198 CTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257
Db 282 CTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 341
Qy 258 ATACCAAGATGAGAGCAGCAACCAATTATCATATTTAATCTGCTTGGAGATGC 317
Db 342 CTACGCAAGATGAGAGCAGCAACCAATTATCATATTTAATCTGCTTGGATGA 401
Qy 318 TTTAGTTACTACCAACATATGCTTTCAGAGTACGCTACTTGTATGATTCCTGCTT 377
Db 402 GCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
Qy 378 TGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 437
Db 462 CCGCGCGCTACTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 521
Qy 438 CTTCACCTGACATGATGAGCGGAGCGGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
Db 522 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 581
Qy 498 TTTGACTTCGCAACCCCTTGAAGGCAAGATCATATTCATCTGCTGCTGCTGCTGCTGCTG 557
Db 582 AGCGCGCTACCGTGGCGCACTGCGCAAGTATGTAACCTGGCGCTGCGGCTGCTGCTGCTG 641
Qy 558 GTCACTGTTGGCATCTCTGCAATATGCTTGAAGGACCAAGATCAGGAGAGCGTGA 617
Db 642 ATTACTGCTATCTTGGCCATTCGCTGCTTCTGACGCGCGCAAGCCAGCAAGCATATGGCAC 701
Qy 618 TGTATTTAGAGGCTCTTGAAGTCCAGATGATGATCTACCTCGTGGGAGCTCTTCAT 677
Db 702 GG---TAGCTGCAACATGCTCATGCGCGAGCGCGCGCGCGCGCGCGCGCGCTGCTGCTG 758
Qy 678 GAAGATCTGCTCTTCACTTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 737
Db 759 ---CTATACCATTTCTCATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
Qy 738 CACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
Db 816 TGTGCTCATATTCGCAAGATGCGCATGCTGCGCTTAAGCGCTGCTGCGAGCGCGCAA 875
Qy 798 TCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
Db 876 GCGCTCAGAGCGCAAGTATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 935
Qy 858 CTGACTCCCATTCATATTCATCTGCTGAGGCTCTGCGGAGGACCTTCCACAGCAC 917

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Db 936 CTGATGCTCTTCTAGTGTACAGCTGTGCAAGTGTTCGCCGAGCAAGACGCCAC 995
QY 918 AGCTGCTCTCTACAGCTATTAATCTTGATGCTGCTTAAAGCTATACCAAGTACCTGA 977
Db 996 CGTGAGCC-----AGTTGCTGTCTATCTCGGGCTATGCGCAAGCTGTGCCA 1043
QY 978 TCCCATTTCTACGCGCTTTCTGATGAAATACTTCAAGCGGTGTTCCGGGACTTC 1032
Db 1044 CCCCATCTTACGCGCTTCTCTGCGACACTTCAAGCGCTTTTCAGCGCATC 1098

RESULT 84
US-08-417-103-3
Sequence 3, Application US/08417103
Patent No. 5723299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yulchiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1260
US-08-417-103-3

Query Match 19.6%; Score 226.6; DB 1; Length 1265;
Best Local Similarity 54.8%; Pred. No. 4.5e-46;
Matches 523; Conservative 0; Mismatches 414; Indels 18; Gaps 3;

QY 78 CAGCCCTGTGTTTCCCGCTGGGCGAGCCGACAGCAAGCGACGCGCGCTCGAGGA 137
Db 162 CTGCAAGAGGGGTCCGGGTCCGGCGCTGCGGACGAGGAAGACCTGCGAAGCGC 221
QY 138 CGCGAGCTGAGCGCGCGGACATCTCCCGGCGCATCCCGGTCATCAGCGCGGTCTA 197
Db 222 TTCCCAAGATGGACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 281
QY 198 CTCGCTAGTGTTCGTGCTGGGCTTGGTGCGCAACTGCTGTCTCATGTTCTGATCATCG 257
Db 282 CTCCTGTGTATCTGTGTGGACTGTGTGGAACTCTATGCTATGATCTCTGG 341

QY 258 ATACAAAGATGAAGACAGCAACCAATTATATTTAACTGTGCTTTGGCAGATGC 317
Db 342 CTACCCAAAGATGAAGACCGCTACCAACATCTACATTTCTAACTGGCTATGCTGATGA 401
QY 318 TTTAGTTTCTACAAACATGCGCTTTCAAGATACGGTCTACTTGATGAAATTCCTGCGCTTT 377
Db 402 GCTGCTCATGCTCAGCGGTGCCCTTTCTGTGTACTTCCAGCGTGTGGCCCACTGGCGCTT 461
QY 378 TGGGATGTGCTGTGCAAGATAGTAATTTCCATTATTACTACAACTGTTTCAACAGCAT 437
Db 462 CGCGCGCTACTTTGCGCCCTGTGTCTCAGCGTGTGATCGGTCAACATGTTTCAACAGCAT 521
QY 438 CTTCACCTTGAACATGATGAGGCTGACCGGTACTATGCGGTGTCACCGCGTGAAGGC 497
Db 522 CTACTGTCTGACTGTGCTTAAAGTGTGACCGCTATGCTGTGTGTCACCGCATCAAGGC 581
QY 498 TTTGACTTTCGCAACCGCTTGAAGCAAGATCATATATCTGCATCTGCTGTCTC 557
Db 582 AGCGGCTACGCTGGGCCCACTGTGGCCAAAGTATGAACCTGGGCGTGTGGCTCTGTTC 641
QY 558 GTCATCTGTGGCATCTCTGCATATGCTCTTGAAGGCACAAAGTCAGGAAAGCTGCA 617
Db 642 ATTACTGTGTATCTTGGCCATGCTGTCTTCTCAAGCAGCAGCCAGCAGCATGCGAC 701
QY 618 TGTATAGATGCTCTGCTGAGTTCCCAAGATGATGATCTCTGCTGAGACCTCTGAT 677
Db 702 GG--TAGCTTGAACATGCTCATATGCCAGCGCCGCCAGCGCTGTGTGGCTTGTGT 758
QY 678 GAAGATCTGCGTCTTCTATCTTGTGCTGTGATCCCTGTCTCATCATCATCTGTGCTA 737
Db 759 ---CTTATACATTTCTTCAATGAGGCTTCTGTGCTGTCTGTGGGCGCATTTGCTGTGTTA 815
QY 738 CACCTGATGATCTGCGCTCTCAAGAGCGTCCGCTCTTCTGTGCTCCCGAAGAAAGA 797
Db 816 TGTGCTCATATGTCGAAGATGCGCATGTGCGCTTCAAGCGTGTGCGACAGCGCA 875
QY 798 TCGCAACCTGCTGAGATCACAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 857
Db 876 GCGCTCAAGAGCAAGATCATCTATATGTATGTATGTATGTATGTATGTATGTATGT 935
QY 858 CTGACCTCCATTCATATTCATCTCTGTGTGAGGCTCTGAGGACACCTCCCAAGCAC 917
Db 936 CTGATGCTCTTCTTACAGTGTATGCTGTGCACTGTTCGCCGAGCAAGAGAGCGCAC 995
QY 918 AGCTGCTCTTCCAGCTATTAATCTGTGATGCTTAAAGCTATACCAACGTAAGCTGAA 977
Db 996 CGTGAGCC-----AGTTGCTGTCTATCTCGGGCTATGCGCAACAGCTGTGCCA 1043

QY 978 TCCCATTTCTACGCGCTTTCTTGAAGAAATACTTCAAGGGGTGTTCCGGGACTTC 1032
Db 1044 CCCCATCTTACGCGCTTCTGTGCGACACTTCAAGCGCTTTTCAGCGCATC 1098

RESULT 85
US-07-816-283-7
Sequence 7, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yulchiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 1991.12.31
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-7

```

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Query Match      19.2%; Score 221.2; DB 1; Length 1244;
Best Local Similarity 53.2%; Pred. No. 9.4e-45;
Matches 494; Conservative 0; Mismatches 428; Indels 6; Gaps 1;

QY 158 ACATCTCCCGGCGCATCCCGGTATCATCAAGCGGCTCTACTCCGTAGTTCGTGCGG 217
DB 133 ACTACGACATGACAAAGCAAGCGCGCTTCACTTACTCTACTCTCTGCTGTGTCG 192
QY 218 GCTTGAGGCAACCTCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 277
DB 193 GCGTGTGGGCAACCGCTGGTATTTATGTCATCTCTCGCTATCCCAAGATGAAGCA 252
QY 278 CAACCAACATTTACATTTTAACTGCTTTGCGAGATGCTTTAGTTACTCAACACATGC 337
DB 253 TCACCAACATGATGATCTTAACTGCGCATGAGATGAAGTCTTCAAGAGGCTTC 312
QY 338 CTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 397
DB 313 CTTCTTGGCCATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 372
QY 398 TAGTATTTCAATTTACTTACTTAACTGATGATGATGATGATGATGATGATGATGATG 457
DB 373 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
QY 458 GCGTGAACCGGTACATGTCGCTGTCACACCCCGTGAAGGCTTTGGACTTCCGCAACCT 517
DB 433 GCATGACCGGTACCTGCGCGGTGTCACCCCATTAAGTCAAGCAATGAGAGGCGACCC 492
QY 518 TGAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 577
DB 493 GAGACGCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
QY 578 CAATGATCCTTGAAGGCAACAAAGTCAGAGGAAGTCAATGATGATGATGATGATGATG 637
DB 547 TGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
QY 638 AGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 697
DB 607 TCAACTGCGCAAGGCGAATCCGGGGGCTGTACAGAGTTTCAATTAACGCTTCATCC 666
QY 698 TTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 757
DB 667 TGGGGTTCCTGTATCCCTTACCATCATTTGCTGTCTACTCTGTTCATCATCAACAAG 726
QY 758 TCAAGAGGTCGCGGCTCTTTCTGGCTCCGAGAAAGATGCAACCTGGGTAGATCA 817
DB 727 TGAAGTCTCTGGAATCCGAGTGGATCATCAAGAGAAAGTCAAGAAAGGTTGA 786
QY 818 CCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 877
DB 787 CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846

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QY 878 TCATCTGTGTGAGAGCTTGTGGGAGACCTTCCACAGACAGTGTCTCTCCAGCTATT 937
DB 847 TCAAGCTCTCTTCCGTGTGTGTGGCATGATCCACCCAGCCCTGAAGGCAATGTTG 906
QY 938 ACTTCTGATGCGCTTGAAGGCTATACCAACAGTAGTCAATCCATTTCTTACGCTTTTC 997
DB 907 ACTTGTGTGTATCTTCACTATGCAACAGCTGTGGCAACCCCATCTGTAGGCTTTCT 966
QY 998 TTGATGAAGTCTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCACTGAAGTGAATG 1057
DB 967 TGTCTCAACTTCAAGAGAGCTTCCAGATGTTCTTGTCTGTGATCAAGGTGATGTGTA 1026
QY 1058 AGCGCAGACGACCTAGCAGAGTCCGAAA 1085
DB 1027 CGAGGATGGGAGAGAGGCGACAGTAA 1054

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RESULT 86

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US-08-417-103-7
; Sequence 7, Application US/084117103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 24..1130
; US-08-417-103-7

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Query Match      19.2%; Score 221.2; DB 1; Length 1244;
Best Local Similarity 53.2%; Pred. No. 9.4e-45;
Matches 494; Conservative 0; Mismatches 428; Indels 6; Gaps 1;

QY 158 ACATCTCCCGGCGCATCCCGGTATCATCAAGCGGCTCTACTCCGTAGTTCGTGCGG 217
DB 133 ACTACGACATGACAAAGCAAGCGCGCTTCACTTACTCTACTCTCTGCTGTGTCG 192

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TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-816-283-5

Query Match 18.6%; Score 214.8; DB 1; Length 1351;
Best Local Similarity 54.0%; Pred. No. 3.5e-43;
Matches 485; Conservative 0; Mismatches 407; Indels 6; Gaps 2;

155 CGCAGATCTCCCGGCGCATCCGGGTATCATCAGCGGGTCTAATCCGAGTGGTGTG 214
189 CGTACTATGACCTGACCAAGCAATGACGTCTCATCTCATATTTTGGTCTGCATCA 248
215 TGGGCTTGGTGGGCAACCTGCTGTGATGTTGATCTATCCGATACAAAGATGAAGA 274
249 TTGGGTTGTGTGGCAACACACTTGTCTATTTATGTCTCTCGCTATGCGAAGATGAAGA 308
275 CAGCAACCAACATTTACATATTTAACTTGGCTTTGGCAGATCTTTAGTTACTACAAACA 334
309 CCATCACCACAACTTTACATCTCAACCTGGCATGCGAATAGAGCTTCATGCTGGGTC 368
335 TGCCCTTTGAGAGTACGCTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGTGCA 394
369 TGCCCTTTGCTGTGTGAGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
395 AGATAGTAATTTCCATGATTACTACAAATGTTACCGACATCTTACCTTGACATGA 454
429 GGGTGTCTATGATCTGTGATGAGATCAATCAAGTCAACGACATCTTCTGCTGACATGA 488
455 TGAGCGTGAGCCGCTACATTTGCGTGTGCGACCCGCTGAAGGCTTTGACCTTCCGACAC 514
489 TGAGCATGACCGATTAACCTGGCTGTGTGTCCACCCCATCAAGTCCGCAAGTGAAGAGAC 548
515 CTTTGAAGGCAAGATCATCATATCTGATCTGGCTGTGCTGTGCTGTGCTGTGCTGTG 574
549 CCGGAGCGCCAAATGATCAACATGCGCTGTGTGGGAGT---CTCTGCTGCTGCTATCT 605
575 CTGCAATAGTCTTGGAGGCAACAAAGTGAAGGAAGAGTGAATGATGATGATGCTCT 634
606 TGCCCATCATGATTAATATGCTGGGCTCCGAGCAACAGTGGGAGAGAACACCTGACCA 665
635 TGCACTTCCAGATGATGATGATCTCTGCTGGAGACCTCTTCAATGAAGTCTGCTCTTCA 694
666 TCACTGGCGCAAGTGAATCTGGGGCTGTGTACAGAGGTTTATCA---TCTACACTTTCA 722
695 TCTTTCCTTGTGATTCCTGTCTCTCATCATGCTGTGTGTACACCCCTGATGATCTGTC 754
723 TTTCTGGGGTCTTGTGTACCCCTCACCATCATCTGTCTTGTGTGTACCTGTTCAATATCATCA 782
755 GTCCTAAGAGCTCCGGCTCTTTCTGGGTCCCGAGAGAAAGATGAGCAACCTGCGTAAGA 814
783 AGGTAAAGCTCTTGAAATCCAGAGGGGCTCTTAAAGGAAGAAAGTCTGAAGAAAG 842
815 TCACAGAGATGCTGCTGTGTGTGTGTGAGTCTTGTGCTGTGTGTGAGTCTCCATTTACA 874
843 TCACCGAATGCTGT 902
875 TATTTATCTGT 934
903 TATTTACAGCTTTCTTCCGTCTCCATGCGCATGAGCCCAACCCCACTTAAAGCAATGT 962
935 ATTACTTGCATGCGCTTAAGGCTTAACCAAGTGAAGTGAATCCATCTCTAAGGCT 994
963 TTGACTTTGT 1022
995 TTTCTTGAAGAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
1023 TCTTGTGTGACAACTTCAAGAGAGCTTCAAGATGTCTCTGCTGTGTGTGTGTGTGTGT 1080

RESULT 90
US-08-417-103-5
Sequence 5, Application US/08417103
Patent No. 573229
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 83..1189
US-08-417-103-5

Query Match 18.6%; Score 214.8; DB 1; Length 1351;
Best Local Similarity 54.0%; Pred. No. 3.5e-43;
Matches 485; Conservative 0; Mismatches 407; Indels 6; Gaps 2;

155 CGCAGATCTCCCGGCGCATCCGGGTATCATCAGCGGGTCTAATCCGAGTGGTGTG 214
189 CGTACTATGACCTGACCAAGCAATGACGTCTCATCTCATATTTTGGTCTGCATCA 248
215 TGGGCTTGGTGGGCAACCTGCTGTGATGTTGATCTATCCGATACAAAGATGAAGA 274
249 TTGGGTTGTGTGGCAACACACTTGTCTATTTATGTCTCTCGCTATGCGAAGATGAAGA 308
275 CAGCAACCAACATTTACATATTTAACTTGGCTTTGGCAGATCTTTAGTTACTACAAACA 334
309 CCATCACCACAACTTTACATCTCAACCTGGCATGCGAATAGAGCTTCATGCTGGGTC 368
335 TGCCCTTTGAGAGTACGCTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGTGCA 394
369 TGCCCTTTGCTGTGTGAGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
395 AGATAGTAATTTCCATGATTACTACAAATGTTACCGACATCTTACCTTGACATGA 454
429 GGGTGTCTATGATCTGTGATGAGATCAATCAAGTCAACGACATCTTCTGCTGACATGA 488

Db 963 TTGACTTGTGTGCTTCAACCTATGCTAAGAGCAACCTATCTATATGCTT 1022
 Qy 995 TTCTTGAGAAACTTCAAGCGGTCTTCCGGACCTTCTGCTTTCACCTGAAGATGAG 1052
 Db 1023 TCTGTCTGACAACTTCAAGAGCTTCCAGAAATGCTCTGCTGTGCTCAAGGTGAG 1080

RESULT 92

US-09-170-496D-15
 ; Sequence 15, Application US/09170496D
 ; Patent No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AREN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-170-496D-15

Query Match 18.2%; Score 210.4; DB 4; Length 1002;
 Best Local Similarity 55.2%; Pred. No. 3.8e-42;
 Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

Qy 166 CCGGCATCCCGGTATCATCAAGCGGTCTACTCCGATGTTGCTGGGCTTGTG 225
 Db 124 CCGTTCCTTATGCTCTCTGCCCCCGTGTACTCCGGGATCTGTGCTGGGCTGACT 183
 Qy 226 GGCACGCTGCTGATGTTGTGATCATCCGATACAAAGATGAAGACGACCAAC 285
 Db 184 GGCACACGCGCGTATCTGTATCTTAAGGGCGCCCAAGATGAAGACGCTGACCAAC 243
 Qy 286 ATTACATATTTAACTGCTTGGCAGATGCTTAGTACTACAAACATGCGCTTGTG 345
 Db 244 GTGTTCATCTGAACCTGCGCGTCCGACGCGCTCTTACGCTGTACTGCGCTCAAC 303
 Qy 346 AGTACGCTTACTGATGAATCTCTGCGCTTTGGGGATGCTGTGCAAGATGAAT 405
 Db 304 ATCCGGGAGCACTGCTCAGATGAGCCCTTCGGGGAGCTGCTTGCAGAGCTGTGCTG 363
 Qy 406 TCCATGATTTACTAACAATGTTCAACGATCTTCACTTGAACATGATGAGCTGAGC 465
 Db 364 GCCGTCGACACTAACAATCTTCTTCAGCACTTACTTACCGTATGAGCGTGTGAC 423
 Qy 466 CGCTACATTTGCGTGTGCGACCCCGTGAAGG-----TTTGAAGCTTCGACACCTT 519
 Db 424 CGATTCCTGTGTGCTGTGCGACCGTGTGAGTCTCCGCCACATGCGCTTGGCGACCT 483
 Qy 520 AAGCAAAATATCATATCTGATCTGCTGCTGTGCTATCTGTTGGCATCTTGTGCA 579
 Db 484 GGGGCGAAGTGTGCGAGCTGTGTGTGCTGGCGTCAAGGCTCTGTGCTTGCCTTC 543
 Qy 580 ATAGTCTTGAAGGACCAAAAGTCAAGGAAGACGTGATGATGATGATGATGATGAT 639
 Db 544 TTCTCTTTCGTGGGTGCTA---CAGCAAGAGCTGTGAGGTCCAAAGCTGTGGGCTGAGC 600
 Qy 640 TTCCAGATGATGATCTCTCTGTGGAGACCTTTCATGAAGATCTGGGCTTTCATCTT 699
 Db 601 TTCCGCTGCGGAGCGGCTGTGTGCAAGGCGACCGT---GTCTACATTTGTGTCTG 657
 Qy 700 GCTTGTGATCTCTGTCTCTATCATGCTGTGCTACACCTGATGATCTGTGCTGCT 759
 Db 658 GGCCTTGTGCTGCGCGTGTGCACTGTGTGTCTTACACAGACCTCTGTGGGCGCTG 717

Qy 760 AAGAGCTCCGCGCTCTTCTGCTCCCGAGAAAGATCCGACCTGATGATCAAC 819
 Db 718 CGGCGCGTGGCTCTCGGACCAAGGCTTACGCAAGGCGGAGGATGAC 777
 Qy 820 AGACTGTCTGT 879
 Db 778 GTCTGT 837
 Qy 880 ATCTGT 939
 Db 838 TCTGT 897
 Qy 940 TTCTGATGCTGT 999
 Db 898 GTATCATCAGGCTTACGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
 Qy 1000 GATGAAACTTCAAGCGGTGTTCCG 1025
 Db 958 GATGCAACTTCCGAAAGACTTCCG 983

RESULT 93

US-08-148-215A-3
 ; Sequence 3, Application US/08148215A
 ; Patent No. 5591602
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Dowd, Brian F.
 ; TITLE OF INVENTION: Opioid Receptor: Compositions and Methods
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: 321 No. 5591602th Clark Street, Suite 800
 ; CITY: Chicago
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60610
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/148,215A
 ; FILING DATE: 05-NOV-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5591602thrup, Thomas E.
 ; REGISTRATION NUMBER: 33,268
 ; REFERENCE/DOCKET NUMBER: OPIA003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-744-0090
 ; TELEFAX: 312-755-4489
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1518 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 349..1347
 ; US-08-148-215A-3

Query Match 18.2%; Score 210.4; DB 1; Length 1518;
 Best Local Similarity 55.2%; Pred. No. 4.4e-42;
 Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

Qy 166 CCGGCATCCCGGTATCATCAAGCGGTCTACTCCGATGTTGCTGGGCTTGTG 225
 Db 472 CCGTTCCTTATGCTCTCTGCCCCCGTGTACTCCGGATCTGTGTGGGCTGACT 531
 Qy 226 GGCACGCTGCTGATGTTGTGATCATCCGATACAAAGATGAAGACGACCAAC 285

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Db      532 GGCACACGCGCGTATCTTGTATCTTAAGGGGCGCCCAAGATGAACGGTGACCAAC 591
Qy      286 ATTACATATTATTAACCTGGCTTTGGCAGATGCTTTAGTACTACAACCATGCGCTTTGAG 345
Db      592 GTGTTCATCTGAACCTTGCGCGTGGCGACGGGGCTTTCACGGTGTACTGGCGCTGCAAC 651
Qy      346 AGTACGGTCTACTGATGAATTTCCGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Db      652 ATCGGGAGGACACCTGCTCAGATCGGCTTTCGGGGAGCTGCTTGAAGGTGGTGTG 711
Qy      406 TCCATTGATTAATAACAATGTTTACACAGCATCTTTCACCTTGAACCATGATGAGCGTGGAC 465
Db      712 GCCCGACACATCAACATCTTCTCCAGCATCTTCTCAGCGGTATAGCGGTGAC 771
Qy      466 CGTACATTTGCGGTGTGCGACCCCGTGAAGC-----TTTGAATTCCGACACCCCTTG 519
Db      772 CGATACCTGTGTGTCTGGCCACCGTGAAGTCCCGCACATGCTCCGTGGCGGACCTAACCG 831
Qy      520 AAGCAAGATCATATATCTGCATCTGGCTGTGTGTATCTGTGGCATCTGTGCA 579
Db      832 GGGGGAAGGTGCGCAGCTGTGTCTGTGGCGTCAAGGTCTGTGCTTCCCTTC 891
Qy      580 ATAGCTTTGAGGACCAAAAGTCAAGGAGAGCTGATGTCATTTAGTGTCTCTTGGAG 639
Db      892 TTCTCTTCTGCTGGGCTGA---CAGCAACAGCTGAGGTCCCAAGCTGTGGGCTGAGC 948
Qy      640 TTCCCAATGATGATCTACTCTGTGTGGAGCTTTTCAATGAAGATCTGGCTTTCATCTTT 699
Db      949 TTCCCGTGGCCGAGCGGGGTCTGTTCAAAGGCCACCGT---GTCTACACTTTGGTCTCG 1005
Qy      700 GCTTCGTGATCCCTGTCTCTATCATGCTGTGCTACACCTGTATGATCTGTGCTG 759
Db      1006 GACTTGAGTGTGCTGCTGTGACCACTGTGTGCTTCAACAGACCTCTGTGGAGGCTG 1065
Qy      760 AAGAGCTGCGGCTCTTCTGTGCTCCGAGAGAAATCGCAACCTGCGTGAATCAAC 819
Db      1066 CGGGCGGTGGGCTCGCTGTGAGACCAAGCTCAAGGAAGGCGAGGAGGTGAGC 1125
Qy      820 AGACTGTGCTGTGTGTGTGTGCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
Db      1126 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1185
Qy      880 ATCCGTGTGAGGCTCTGTGGGAGGACCTCCCAAGACAGCTGTCTCCAGCTATTAC 939
Db      1186 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1245
Qy      940 TTCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 999
Db      1246 GTCATCACAGCTCAAGTACGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1305
Qy      1000 GATGAACCTTCAAGCGGTGTTCCG 1025
Db      1306 GATGACAACTTCGGAGAACTTCCG 1331

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RESULT 94

US-09-016-434-1480
 / Sequence 1480, Application US/09016434
 / Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g953234
; US-09-016-434-1480

```

Query Match 18.2%; Score 210.4; DB 4; Length 1518;
 Best Local Similarity 55.2%; Pred. No. 4.4e-42;
 Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

```

Qy      166 CGGACATCCGCTCATCATCAAGCGGCTTACTCCGTAGTGTGTGTGTGTGTGTGTGT 225
Db      472 CGGTTCCTCTATGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 531
Qy      226 GGCACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 285
Db      532 GGCACACGCGCGTATCTTGTATCTTAAGGCGCCCAAGATGAACGGTGACCAAC 591
Qy      532 GTGTTCATCTGAACCTTGCGCGTGGCGACGGGGCTTTCACGGTGTACTGGCGCTGCAAC 651
Db      592 AGTACGGTCTACTGATGAATTTCCGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Qy      346 AGTACGGTCTACTGATGAATTTCCGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Db      652 ATCGGGAGGACACCTGCTCAGATCTGTGCGCTTTCGGGGAGCTGCTGTGCAACCTGGTGTG 711
Qy      406 TCCATTGATTAATAACAATGTTTACACAGCATCTTTCACCTTGAACCATGATGAGCGTGGAC 465
Db      712 GCCCGACACATCAACATCTTCTCCAGCATCTTCTCAGCGGTATAGCGGTGAC 771
Qy      466 CGTACATTTGCGGTGTGCGACCCCGTGAAGC-----TTTGAATTCCGACACCCCTTG 519
Db      772 CGATACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 831
Qy      520 AAGCAAGATCATATATCTGCATCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Db      832 GGGGGAAGGTGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
Qy      580 ATAGCTTTGAGGACCAAAAGTCAAGGAGAGCTGATGTCATTTAGTGTCTCTTGGAG 639
Db      892 TTCTCTTCTGCTGGGCTGA---CAGCAACAGCTGAGGTCCCAAGCTGTGGGCTGAGC 948
Qy      640 TTCCCAATGATGATCTACTCTGTGTGGAGCTTTTCAATGAAGATCTGGCTTTCATCTTT 699
Db      949 TTCCGTGTGGCGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1005
Qy      700 GCTTCGTGATCCCTGTCTCTATCATGCTGTGCTTCAACAGCTGTGATGATCTGTGTCTG 759

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TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 68..1051
 US-08-148-215A-1

Query Match 15.2%; Score 175.6; DB 1; Length 1054;
 Best Local Similarity 51.6%; Pred. No. 1.2e-33;
 Matches 450; Conservative 0; Mismatches 419; Indels 3; Gaps 2;

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QY 154 GCGCATATCTCCCGCCATCCCGGTATCATCAGCGCGGTCTACTCGTAGTGTCTG 213
DB 155 GCGCGCGTGGCGCGCGCGCGGTGCGGTGACAGATTGTACGCGGTATCTGCGCC 214
QY 214 GTGGGCTTGGTGGCACTCGGTGATGTTGTTGATCATCCGATACCAAGATGAAG 273
DB 215 GTGGGTCTGGCGGGCACTCCCGGTGTGATGTTGTTGCGGGCGCGCATGAAG 274
QY 274 ACAGCAACCAACATTATTAACCTGGCTTGGGAGATGTTAGTACTACCAAC 333
DB 275 ACCGTACCAACCTGTATCTCAACCTGGCATGCGAGAGCTTTACGCTGTG 334
QY 334 ATGCCCTTCAAGATAGCGGTCTACTTGAATTCCTGGCTTTGGGATGTGCTGTC 393
DB 335 CTGCCATCAACATGCGCGAATCTCGTGGCGGAGTGGCCCTTGGGGAGCTCATGTGC 394
QY 394 AAGATAGTAATTTCCATTGATTACTACCAATGTTACCAAGATCTTACCTTGACATG 453
DB 395 AAGCTCATGTGGCTATGACACAGTACCAACCTTCTCCAGCTCTACTTCTCACCGTC 454
QY 454 ATGAGCGTGGACCGGTATATGCGGTGGCCACCCCGTGAAGGCTTGGACTTCGGACA 513
DB 455 ATGACCGCGCGACCGTACTGTTGTGGTGGCCACTGCGGAC--TCGCGCGGGTGGCG 512
QY 514 CCCTTGAAGGCAAGATCATCAATATCTGCATCTGGTGTCTGCTCATCTGTTGGCATC 573
DB 513 GCGCGACTACAGCGCGCGCGCGGTGAGCTGCGG--TGTGGGGATGCTCACACTC 571
QY 574 TCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGCTGATGTCATTAGTGTCTC 633
DB 572 GTGCTAGTCTTTCGCAAGTCTTTCGCGCGGTAGACGACAGGCGCGCGCATGTGC 631
QY 634 TTGCAATTCAGATGATGATCTCTGTGTGGACCTTCTATGAAGTCTGCGCTTC 693
DB 632 GTGCTAGTCTTTCGCAAGCGCGGCGCTTGTGTGGCGCGAGCGCGCTTACACGCTC 691
QY 694 ATCTTGGCTTGTGATCCCTGCTCATCATCATCTGTCTGTACACCTGATGATCTG 753
DB 692 GTGCTGGGCTTGCATCCCGGTGTCACCATCTGTGTCTTATACCACTGCTGTGC 751
QY 754 GGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATCGCAACCTGCGTGA 813
DB 752 CGGCTGCAATGCGCATCGGCTGGAACGCAAGCGCGCTGAGCGCGCAAGAGCGG 811
QY 814 ATCAACCACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
DB 812 GTGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
QY 874 ATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
DB 872 CTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
QY 934 TATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
DB 932 TCTTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
QY 994 TTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1025
DB 992 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023

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RESULT 99

US-09-016-434-1479
 ; Sequence 1479, Application US/09016434
 ; Patent No. 6500938

GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA

ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
 FILING DATE: US/09/016,434

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 FILING DATE:
 APPLICATION NUMBER:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1479:

SEQUENCE CHARACTERISTICS:

LENGTH: 1596 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9953232

US-09-016-434-1479

Query Match 15.2%; Score 175.6; DB 4; Length 1596;
 Best Local Similarity 51.6%; Pred. No. 1.4e-33;
 Matches 450; Conservative 0; Mismatches 419; Indels 3; Gaps 2;

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QY 154 GCGCATATCTCCCGCCATCCCGGTATCATCAGCGCGGTCTACTCGTAGTGTCTG 213
DB 613 GCGCGCGTGGCGCGCGCGGTGCGGTGACAGATTGTACGCGGTATCTGCGCC 672
QY 214 GTGGGCTTGGTGGCACTCGGTGATGTTGTTGATCATCCGATACCAAGATGAAG 273
DB 673 GTGGGTCTGGCGGGCACTCCCGGTGTGATGTTGTTGCGGGCGCGCATGAAG 732
QY 274 ACAGCAACCAACATTATTAACCTGGCTTGGGAGATGTTAGTACTACCAAC 333
DB 733 ACCGTACCAACCTGTATCTCAACCTGGCATGCGAGAGCTTTACGCTGTG 792
QY 334 ATGCCCTTCAAGATAGCGGTCTACTTGAATTCCTGGCTTTGGGATGTGCTGTC 393
DB 793 CTGCCATCAACATGCGCGAATCTCGTGGCGGAGTGGCCCTTGGGGAGCTCATGTGC 852
QY 394 AAGATAGTAATTTCCATTGATTACTACCAATGTTACCAAGATCTTACCTTGACATG 453
DB 853 AAGCTCATGTGGCTATGACACAGTACCAACCTTCTCCAGCTCTACTTCTCACCGTC 912
QY 454 ATGACGTGGACCGGTATGATGCGGTGGCCACCCCGTGAAGGCTTGGACTTCGCACA 513

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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 528 Seconds
(without alignments)
9284.887 Million cell updates/sec

Title: US-09-904-584-1
Perfect score: 1154
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
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6: geneseqn2003s:*
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8: geneseqn2005s:*
9: geneseqn2006s:*
10: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1146	99.3	1182	7	ABZ42678 Human opi
3	1146	99.3	1182	9	AAD58490 Human kap
4	1146	99.3	1182	9	AD884861 Farnesyl
5	1143	99.0	1143	2	AAT90998 Human kap
6	1142	99.0	1142	2	AAT12550 Human kap
7	1137.8	98.6	1284	3	AAT90999 Human kap
8	1137.8	98.1	1143	5	AB198011 Non-endog
9	1001	86.7	1275	2	AAT92601 Human kap
10	910.8	78.9	1408	2	AAV49254 Mouse kap
11	910.8	78.9	1410	2	AAV75926 Mouse kap
12	910.8	78.9	2481	2	AAQ86725 Mammalian
13	869.6	75.4	1000	2	AAQ75931 Human kap
14	448	38.8	2135	5	AAAF85416 Nucleotid
15	446.4	38.7	1618	2	AAQ89222 Rat mu op
16	446.4	38.7	1618	2	AAQ89223 Transcrip
17	446.4	38.7	1618	2	AAQ89223 Transcrip
18	443.4	38.4	2070	2	AAQ79199 Rat mu su
19	436.4	37.8	2162	2	AAV61994 Human mu-
20	434.8	37.7	1239	6	ABBS54814 CDNA enco
21	434.8	37.7	1245	6	ABBS54813 CDNA enco
22	434.8	37.7	1431	6	ABBS54812 CDNA enco
23	434.8	37.7	1610	2	AAQ89226 Human mu

24	434.8	37.7	1610	3	AAA59503 CDNA enco
25	434.8	37.7	2149	6	ABBS54815 CDNA enco
26	434.8	37.7	2160	2	AAQ93102 Human mu
27	434.8	37.7	2162	2	AAV61995 Human mu-
28	434.8	37.7	2162	2	AAV61986 Human mu-
29	434.8	37.7	2162	2	AAV61988 Human mu-
30	434.8	37.7	2162	2	AAV61984 Human mu-
31	434.8	37.7	2162	2	AAV61987 Human mu-
32	434.8	37.7	2162	2	AAV61980 Human mu-
33	434.8	37.7	2162	2	AAV61985 Human mu-
34	434.8	37.7	2162	2	AAV61989 Human mu-
35	434.8	37.7	2162	2	AAZ88470 Human mu
36	434.8	37.7	2162	6	ABK14953 Human mu
37	434.8	37.7	2162	7	ACAS6781 Human big
38	434.8	37.7	2162	7	ABZ42697 Human opi
39	434.8	37.7	2162	9	ADC21534 Human DNA
40	434.8	37.7	2279	7	AAV61992 Human mu-
41	434.8	37.5	1176	6	AAV61991 Human mu-
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43	433.2	37.5	2162	2	AAV61992 Human mu-
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46	433.4	37.5	1334	3	AAZ60728 CDNA enco
47	433.4	37.5	1346	3	AAZ60737 CDNA enco
48	433.4	37.5	1365	3	AAZ60736 CDNA enco
49	433.4	37.5	1423	3	AAZ60726 CDNA enco
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51	432.4	37.5	1729	3	AAZ60734 CDNA enco
52	431.6	37.4	1182	5	AB198013 Non-endog
53	431.6	37.4	1203	5	AB198012 Non-endog
54	430.8	37.3	2045	3	AAZ60735 CDNA enco
55	430.8	37.3	2229	2	AAV49252 Mouse mu
56	430.4	37.3	1149	6	ABX13057 Human MOR
57	429.2	37.2	1542	3	AAZ60729 CDNA enco
58	429.2	37.2	1981	5	AAAD1041 Murine de
59	429.2	37.2	1981	6	ABBS53445 DNA beque
60	427.6	37.1	1981	2	AAO56705 Partial s
61	422.6	36.6	1821	2	AAO56700 Sequence
62	422.6	36.6	1829	5	AAAD1035 Murine de
63	422.6	36.6	1829	6	ABBS53439 CDNA enco
64	422.6	36.6	2218	7	AAV49253 Mouse del
65	422.6	36.6	2219	7	ABV75085 Murine de
66	422.6	36.6	2272	2	AAO75927 Mouse del
67	415.6	36.0	1176	7	AAO50856 Human mod
68	411.4	35.6	2216	2	AAQ66656 Murine de
69	408.6	35.4	1773	7	ACA56807 Human sig
70	408.6	35.4	1773	7	ABT34217 Human del
71	408.6	35.4	1773	7	ABV75086 Human del
72	408.6	35.4	1773	7	ABZ42658 Human opi
73	407	35.3	1119	5	AB198009 Non-endog
74	402.2	34.9	1197	7	AAAD50857 Human mod
75	395	34.2	1829	7	ABX94262 Human ORP
76	393.4	34.1	1805	6	ABBS53446 CDNA enco
77	393.4	34.1	1829	7	ABX94264 Human ORP
78	393.4	34.1	1829	7	ABX94263 Human ORP
79	393.4	34.1	1973	7	ACA56793 Human sig
80	393.4	34.1	1973	9	ADC40517 DNA deriv
81	393.4	34.1	2534	7	ABX94045 CDNA enco
82	393.4	34.1	2534	7	ABZ42709 Human opi
83	391.8	34.0	1113	5	AB198010 Non-endog
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85	387.6	33.6	1238	3	AAZ60727 CDNA enco
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87	384	33.3	1670	6	ABBS54825 DNA enco
88	377.6	32.7	1243	7	ABX94042 Rat orpha
89	377.6	32.7	1387	7	ABX94039 Rat orpha
90	377.6	32.7	1567	2	AAO89233 Rat opiol
91	377.6	32.7	1567	2	AAA59510 CDNA enco
92	376	32.6	2706	2	AAQ92872 Rat opior
93	375.6	32.5	945	6	ABBS54811 CDNA enco
94	368	31.9	1452	2	AAAT90381 Rat metha
95	368	31.9	1452	2	AAAT89585 Rat orpha
96	368	31.9	1452	2	AAV56017 Rat metha

97	368	31.9	1452	3	AAZ91047	AAZ91047 Rat metha	c 170	188.2	16.3	348	4	AA124178	AA124178 Probe #14
98	368	31.9	1452	4	AAH26613	AAH26613 Rat anti-	c 171	188.2	16.3	348	4	ABA69297	ABA69297 Human foe
99	368	31.9	1452	5	AA515709	AA515709 Rat metha	c 172	188.2	16.3	348	4	AA149465	AA149465 Probe #18
100	367.8	31.9	1134	3	AAZ60659	AAZ60659 DNA encod	c 173	188.2	16.3	348	4	ABA51291	ABA51291 Human bre
101	367.8	31.9	1330	2	AAQ75928	AAQ75928 Mouse opi	c 174	188.2	16.3	348	4	ABA36326	ABA36326 Probe #14
102	366.2	31.7	2600	6	AA172372	AA172372 KOR3 gene	c 175	188.2	16.3	348	4	AAK43397	AAK43397 Human bon
103	357	30.9	1177	3	AAZ60658	AAZ60658 DNA encod	c 176	188.2	16.3	348	4	AAK17583	AAK17583 Human bra
104	347.2	30.1	1228	7	ABX94043	ABX94043 Rat orpha	c 177	188.2	16.3	348	4	ABSA3018	ABSA3018 Human liv
105	347.2	30.1	1372	7	ABX94040	ABX94040 Rat orpha	c 178	188.2	16.3	348	5	AB109740	AB109740 Probe #97
106	344.8	29.9	2600	2	AAQ90096	AAQ90096 Mouse Kap	c 179	188.2	16.3	348	6	ABSI17490	ABSI17490 Human gen
107	344.8	29.9	2600	2	ADD49196	ADD49196 Mouse Kap	c 180	186.4	16.2	1008	8	ACCT9883	ACCT9883 Bovine GP
108	336.2	29.1	1223	3	AAZ60656	AAZ60656 DNA encod	c 181	186.4	16.2	1008	8	ADBS2675	ADBS2675 Primary r
109	336.2	29.1	1283	3	AAZ60657	AAZ60657 DNA encod	c 182	184	15.9	1155	9	ABSA69714	ABSA69714 Novel mur
110	336.2	29.1	1421	7	ABX94038	ABX94038 Rat orpha	c 183	181.8	15.8	318	6	ABO22580	ABO22580 Oligonuc1
111	335.8	29.1	1566	7	ABX94037	ABX94037 Rat orpha	c 184	179.8	15.6	540	6	ABO22581	ABO22581 Oligonuc1
112	327.4	28.4	2634	3	AAZ60653	AAZ60653 DNA encod	c 185	179.8	15.6	540	6	ABO22581	ABO22581 Oligonuc1
113	327	28.3	1256	3	AAZ60654	AAZ60654 DNA encod	c 186	178.8	15.5	1000	6	ABK94683	ABK94683 G protein
114	321.8	27.9	829	2	AAQ56703	AAQ56703 Partial s	c 187	178.8	15.5	1000	7	AA151778	AA151778 Human G p
115	319.6	27.7	830	5	AAAD11039	AAAD11039 Human mu	c 188	178.8	15.5	1000	7	ABX92985	ABX92985 Screening
116	319.6	27.7	830	5	ABSS5343	ABSS5343 Human opi	c 189	178.8	15.5	1000	7	ABT33305	ABT33305 GPR7 11ga
117	291.2	25.2	2602	7	ABX94254	ABX94254 Human orp	c 190	178.8	15.5	1000	8	ACCT9856	ACCT9856 Human GPR
118	289.6	25.1	1947	7	ABX94261	ABX94261 Human orp	c 191	178.8	15.5	1000	9	ADCS1932	ADCS1932 Human GPR
119	268.6	23.3	3200	7	ABX94053	ABX94053 Rat orpha	c 192	177	15.3	987	6	ABK94565	ABK94565 G protein
120	268.8	22.3	8372	9	ABX94036	ABX94036 Rat orpha	c 193	177	15.3	987	7	ABT33314	ABT33314 GPR7 11ga
121	257.4	22.3	1843	9	ADC86876	ADC86876 Human GPC	c 194	177	15.3	987	8	ACCT9865	ACCT9865 Rat TGR26
122	243	21.1	2447	2	AAQ56702	AAQ56702 Partial s	c 195	177	15.3	987	8	ADCS1916	ADCS1916 Rat GPR8-
123	243	21.1	2447	5	AAAD11038	AAAD11038 Human Kap	c 196	176.8	15.3	993	7	ABT33331	ABT33331 GPR7 11ga
124	243	21.1	2447	6	ABSS3442	ABSS3442 Human opi	c 197	176.8	15.3	993	8	ACCT9882	ACCT9882 Bovine GP
125	242.6	21.0	1317	7	ACSA6848	ACSA6848 Human sig	c 198	175.6	15.2	987	3	AAA30587	AAA30587 Human G p
126	242.6	21.0	1427	6	AB168104	AB168104 Ovary can	c 199	175.6	15.2	987	6	ABK49959	ABK49959 Coding re
127	241	20.9	1167	7	AA139556	AA139556 CDNA encod	c 200	175.6	15.2	987	7	ABZ42743	ABZ42743 Human G p
128	241	20.9	1167	6	ABZ42764	ABZ42764 Human som	c 201	175.6	15.2	987	9	ABZ42530	ABZ42530 Human G p
129	241	20.9	9190	6	AA139555	AA139555 Genomic D	c 202	175.6	15.2	1054	2	AAQ83681	AAQ83681 Epsiln o
130	240.4	20.8	599	6	ABK34413	ABK34413 Human CDN	c 203	175.6	15.2	1054	2	AAQ83681	AAQ83681 Epsiln o
131	239.4	20.7	1167	5	AB198027	AB198027 Non-endor	c 204	175.6	15.2	1596	7	ACSA6881	ACSA6881 Human sig
132	235	20.4	329	9	ADD49504	ADD49504 Human lun	c 205	175.2	15.2	1595	6	ABK48100	ABK48100 DNA encod
133	229.6	19.9	1176	8	ADB67674	ADB67674 Human som	c 206	172.4	14.9	987	3	AAA30712	AAA30712 DNA encod
134	229.6	19.9	1176	8	ADB67674	ADB67674 Human som	c 207	172.4	14.9	987	3	AAQ43012	AAQ43012 DNA encod
135	229.6	19.9	1634	2	AAQ45553	AAQ45553 Human som	c 208	170.2	14.7	987	6	ADCS2688	ADCS2688 Human G p
136	229.6	19.9	1634	2	AAQ45553	AAQ45553 Human som	c 209	170.2	14.7	987	6	ABK94661	ABK94661 G protein
137	226.6	19.6	1265	2	AAQ45654	AAQ45654 Murine sig	c 210	170.2	14.7	1083	6	ABK94660	ABK94660 G protein
138	226.4	19.6	1176	5	AB198024	AB198024 Non-endor	c 211	170.2	14.7	1083	6	ADCS1926	ADCS1926 Mouse TGR
139	221.8	19.2	1904	6	AB199251	AB199251 Mouse isc	c 212	169	14.6	1095	7	ABZ42765	ABZ42765 Human som
140	221.8	19.2	1244	2	AAQ45656	AAQ45656 Murine isc	c 213	169	14.6	1245	8	ADB67669	ADB67669 Human som
141	219.4	19.0	2518	3	AAZ60655	AAZ60655 DNA encod	c 214	169	14.6	4881	5	AAAS92481	AAAS92481 DNA encod
142	216.4	18.8	1110	2	AAQ29155	AAQ29155 Pituitary	c 215	169	14.6	5133	5	AAAS92481	AAAS92481 DNA encod
143	215.2	18.6	1023	6	AB161580	AB161580 Human GPR	c 216	167.4	14.5	1095	5	AB198028	AB198028 Non-endor
144	215.2	18.6	1023	6	ABK94573	ABK94573 G protein	c 217	167.4	14.5	1285	9	ACSA6768	ACSA6768 Human sig
145	215.2	18.6	1023	6	ABX92900	ABX92900 Screening	c 218	167.4	14.5	1285	9	ADCS2031	ADCS2031 Human G p
146	215.2	18.6	1023	7	ABT33330	ABT33330 GPR7 11ga	c 219	162.2	14.1	1257	7	ABZ42763	ABZ42763 Human som
147	215.2	18.6	1023	8	ACCT9881	ACCT9881 Human GPR	c 220	162.2	14.1	1257	7	AAQ59598	AAQ59598 Human GPC
148	215.2	18.6	1023	8	ADCS1942	ADCS1942 Human GPR	c 221	162.2	14.1	1296	2	AAQ45657	AAQ45657 Human som
149	214.8	18.6	1110	7	ABZ42762	ABZ42762 Human som	c 222	162.2	14.1	1413	7	ACSA6723	ACSA6723 Human sig
150	214.8	18.6	1110	7	AAOT09250	AAOT09250 Human som	c 223	160.6	13.9	1257	5	AB198026	AB198026 Non-endor
151	214.8	18.6	1351	2	AAQ45655	AAQ45655 Human som	c 224	160.4	13.9	726	2	AAAT77788	AAAT77788 G-protein
152	214.8	18.6	1351	2	AAQ45655	AAQ45655 Human som	c 225	156.2	13.5	1796	2	AAQ45658	AAQ45658 Murine so
153	214.8	18.6	1510	9	ADC86824	ADC86824 Human GPC	c 226	156.2	13.5	1797	9	ABN85440	ABN85440 Murine SO
154	211.6	18.3	1110	5	AB198025	AB198025 Non-endor	c 227	156.2	13.5	1797	9	AAAS9961	AAAS9961 Mouse GPC
155	210.4	18.2	999	6	AB161598	AB161598 Human GPR	c 228	153.4	13.3	1384	7	ABT41859	ABT41859 Toxictly
156	210.4	18.2	999	6	ABX92918	ABX92918 Screening	c 229	147	12.7	540	6	ABO22578	ABO22578 Oligonuc1
157	210.4	18.2	999	9	ADCS1821	ADCS1821 Human GPR	c 230	147	12.7	540	6	ABO22579	ABO22579 Oligonuc1
158	210.4	18.2	1002	3	AAA30590	AAA30590 Human G p	c 231	143.4	12.4	442	4	AA114990	AA114990 Probe #49
159	210.4	18.2	1002	6	AB161563	AB161563 Human GPR	c 232	143.4	12.4	442	4	ABAS6723	ABAS6723 Human foe
160	210.4	18.2	1002	6	ABZ42744	ABZ42744 Human G p	c 233	143.4	12.4	442	4	AA136336	AA136336 Probe #50
161	210.4	18.2	1002	9	ADCS22534	ADCS22534 Human G p	c 234	143.4	12.4	442	4	ABA46180	ABA46180 Human bre
162	210.4	18.2	1002	9	ACFS7976	ACFS7976 Human GPR	c 235	143.4	12.4	442	4	ABBA6342	ABBA6342 Probe #48
163	210.4	18.2	1518	2	AAO83682	AAO83682 Epsiln o	c 236	143.4	12.4	442	4	AAK30381	AAK30381 Human bon
164	210.4	18.2	164	7	ACSA6682	ACSA6682 Human sig	c 237	143.4	12.4	442	4	AAK04853	AAK04853 Human bra
165	208	18.0	1898	6	ABN85443	ABN85443 Murine SO	c 238	143.4	12.4	442	4	ABBS30020	ABBS30020 Human liv
166	207.2	18.0	1002	3	AAH30713	AAH30713 DNA encod	c 239	143.4	12.4	442	5	AA104755	AA104755 Probe #47
167	207.2	18.0	1002	3	ADCS2690	ADCS2690 Human G p	c 240	143.4	12.4	442	6	ABSO4979	ABSO4979 Human gen
168	204.8	17.7	441	2	AAAS9781	AAAS9781 DNA encod	c 241	140.6	12.2	487	6	ABV99026	ABV99026 Human pan
169	195	16.9	887	7	ABX94044	ABX94044 Rat orpha	c 242	138.6	12.0	467	6	ABV95333	ABV95333 Human pan

243	134.8	11.7	2400	5	AA592478	DNA	encod	316	107.8	9.3	705	4	AA532617	AA632617	Human	gen
244	133.4	11.5	1602	5	AAH49418	D. melano		317	107.8	9.3	705	4	AA532616	AA632616	Human	gen
245	130.4	11.3	1332	4	AB123371	Drosophill		318	106.4	9.2	1690	2	AAV10327	AAV10327	Rat	GalR2
246	130.4	11.3	1332	4	AA557175	CDNA	enco	319	106.4	9.2	1714	2	AAV19790	AAV19790	Rat	galan
247	130.4	11.3	1332	4	ADC35503	Drosophill		320	105.2	9.1	1092	3	AAZ45405	AAZ45405	DNA	encod
248	130.4	11.3	3332	4	ABL23370	Drosophill		321	105.2	9.1	1092	4	AAE85450	AAE85450	Nucleotid	
249	130.4	11.3	3332	4	AA557174	DNA	encod	322	105.2	9.1	1349	5	AB197903	AB197903	Non- endog	
250	130.4	11.3	3332	4	ADC35902	Drosophill		323	105.2	9.1	1349	7	ACC70132	ACC70132	Nucleotid	
C 251	129.6	11.2	687	6	AB161581	GPR8-reia		324	104	9.0	822	2	AAO29156	AAO29156	Brain	com
C 252	129.6	11.2	687	6	ABK94574	G-protein		325	104	9.0	1098	4	AAE83681	AAE83681	Human	G-p
C 253	129.6	11.2	687	6	ABX92901	Screening		326	103.8	9.0	1194	4	AAAD07922	AAAD07922	Human	G-p
C 254	129.6	11.2	687	9	ADC51794	GPR8 ribo		327	103	8.9	2156	7	ABT42154	ABT42154	Toxicity	r
255	125.4	10.9	421	8	ACH46785	Human inf		328	103	8.9	2156	7	ADB53167	ADB53167	Primary	r
256	123.4	10.8	723	7	AAE77787	G-protein		329	102.2	8.9	1047	2	AAE29436	AAE29436	Human	G1
257	123.4	10.7	1309	7	ABE42788	Human gal		330	102.2	8.9	1050	5	AB197991	AB197991	Non- endog	
258	123.4	10.7	1365	2	AAE79976	Human gal		331	102.2	8.9	1053	7	ACA56825	ACA56825	Human	819
259	123.4	10.7	1365	2	ADAO9963	CDNA	enco	332	102.2	8.9	1053	9	ADBE31726	ADBE31726	Human	283
260	122.4	10.6	1164	6	ABK14062	Human gal		333	102.2	8.9	1544	2	AAE86839	AAE86839	CDNA	enco
261	122.4	10.6	1164	7	ABE81596	Human gal		334	102.2	8.9	3056	7	ABZ42667	ABZ42667	Human	g1
262	121.2	10.5	1080	2	AAE30385	Probe bas		335	102.2	8.9	3083	2	AAO97304	AAO97304	Galanin	r
263	120.8	10.5	1164	5	AB197992	Non- endog		336	102	8.8	1116	2	AAE31336	AAE31336	CC-chemok	
264	120.6	10.5	1116	7	ABT40233	Human T1G		337	102	8.8	1116	2	AAV07404	AAV07404	Human	C-C
265	119.6	10.4	1450	9	ADB58547	Toxicity-		338	102	8.8	1128	9	AAE62464	AAE62464	Human	MCH
266	119.6	10.4	1450	9	ADB58547	Toxicity-		339	102	8.8	6582	9	AAE62466	AAE62466	Human	MCH
267	119	10.3	1065	2	AAE86154	Human MIP		340	101.8	8.8	6595	9	AAE62470	AAE62470	Human	MCH
268	119	10.3	1495	2	AAO62695	C-C	chemo	341	101.8	8.8	6595	9	AAE62471	AAE62471	Human	MCH
269	119	10.3	1495	3	AAE35142	Human ade		342	101.2	8.8	1068	3	AAE35144	AAE35144	Human	ade
270	119	10.3	1495	3	AAE21264	Human low		343	101.2	8.8	1068	3	AAE21266	AAE21266	Human	low
271	119	10.3	1495	7	ABE96958	Human nuc		344	101.2	8.8	1068	5	AB197977	AB197977	Non- endog	
272	119	10.3	1495	7	ACA56592	Human 819		345	101.2	8.8	1068	6	AAE25222	AAE25222	Human	che
273	119	10.3	1516	9	ADC86210	Human GPC		346	101.2	8.8	1068	6	ABA94340	ABA94340	Human	CC
274	119	10.3	1900	7	ABE42722	Human che		347	101.2	8.8	1068	7	ABE29680	ABE29680	Human	nuc
275	119	10.3	2156	2	AAE90384	Human MIP		348	101.2	8.8	1071	2	AAE79996	AAE79996	Human	CKK
276	119	10.3	2156	3	AAE35136	Human ade		349	101.2	8.8	1071	2	ADC78872	ADC78872	Human	PRO
277	119	10.3	2156	3	AAE35140	Human ade		350	101.2	8.8	1193	9	AAE31335	AAE31335	CC-chemok	
278	119	10.3	2156	3	AAE21262	Human low		351	101.2	8.8	1193	2	AAV07403	AAV07403	Human	C-C
279	119	10.3	2156	7	AAE21258	Human low		352	101.2	8.8	1201	3	AAE35145	AAE35145	Human	ade
280	119	10.3	2156	7	ABE29695	Human nuc		353	101.2	8.8	1201	3	AAE21267	AAE21267	Human	low
281	119	10.3	2156	7	ABE29695	Human nuc		354	101.2	8.8	1201	6	ABE84282	ABE84282	Human	CDN
282	119	10.3	2156	7	ABE29695	Human nuc		355	101.2	8.8	1201	6	ABE29696	ABE29696	Human	nuc
283	119	10.3	2156	7	ABE29695	Human nuc		356	101.2	8.8	1201	7	ACA56487	ACA56487	Human	819
284	119	10.3	2214	6	ABE42634	Human C-C		357	101.2	8.8	1201	7	ABE42635	ABE42635	Human	C-C
285	119	10.3	2772	10	ADE77006	Human CDN		358	101.2	8.8	1689	2	AAE31334	AAE31334	CC-chemok	
286	119	10.3	6606	3	AAE35143	Human ade		359	101.2	8.8	1689	2	AAE58783	AAE58783	Human	C-C
287	119	10.3	6606	3	AAE21265	Human low		360	101.2	8.8	1689	2	AAV07402	AAV07402	Human	C-C
288	119	10.3	6606	7	ABE29695	Human nuc		361	101.2	8.8	1689	3	AAE35146	AAE35146	Human	ade
289	118.6	10.3	1219	7	AAV19791	Human gal		362	101.2	8.8	1689	3	AAE21268	AAE21268	Human	low
290	118	10.2	1080	6	ABO81123	Rat angio		363	101.2	8.8	1689	6	ABE40462	ABE40462	Human	C-C
291	116.8	10.1	28199	7	ADAO6858	Takiflugu		364	101.2	8.8	1689	7	ABE29696	ABE29696	Human	nuc
292	115.4	10.0	1609	4	AAE14575	Human CDN		365	101.2	8.8	1689	7	AAE13645	AAE13645	Human	CDN
293	115.4	10.0	1617	7	ACC49540	Tumour-as		366	101.2	8.8	1717	6	AAE25221	AAE25221	Human	che
294	115.2	10.0	1197	3	AAE39343	Human G-p		367	101.2	8.8	1717	6	AAE25245	AAE25245	Human	che
295	115.2	10.0	1197	3	AAE64352	CDNA	enco	368	101.2	8.8	1717	6	ABE67066	ABE67066	Thyroid	c
296	115.2	10.0	1197	4	AAAD07921	Human G-p		369	101.2	8.8	1915	2	AAE85162	AAE85162	Human	che
297	115.2	10.0	1197	4	AAH49533	Human GPC		370	101.2	8.8	1915	9	ADC03342	ADC03342	Human	CDN
298	115.2	10.0	1197	7	ABE95717	DNA	encod	371	101.2	8.8	3426	6	ABE04010	ABE04010	Human	ova
299	115.2	10.0	1197	7	ABE42844	Human G-p		372	101.2	8.8	3958	3	AAE35147	AAE35147	Human	ade
300	115.2	10.0	1197	8	ACA62277	Human G-p		373	101.2	8.8	3958	7	AAE21269	AAE21269	Human	low
C 301	115.2	9.9	585	6	ABQ31859	Oligonuc		374	101.2	8.8	3958	7	ABE29696	ABE29696	Human	nuc
302	113.8	9.9	585	6	ABQ31858	Oligonuc		375	101.2	8.8	5091	2	AAE93601	AAE93601	Human	eos
303	113.6	9.8	1197	6	AAO08840	Human G-p		376	101.2	8.8	5791	7	ABE26879	ABE26879	Nucleotid	
304	113.6	9.8	1197	6	ABO81125	Human G-p		377	101	8.8	1068	5	ABE19799	ABE19799	Non- endog	
305	112.6	9.8	2050	7	ABE10897	DNA	encod	378	100.4	8.7	1068	6	AAE51060	AAE51060	Human	CDN
306	111.6	9.7	1116	7	ABT40234	Mouise T1G		379	100.4	8.7	1426	3	AAE34773	AAE34773	Human	ade
307	111.4	9.7	1892	6	AAI72351	DEZ orpha		380	100.4	8.7	1426	3	AAE20895	AAE20895	Human	CCR
308	108.8	9.4	910	6	ABE54823	CDNA	enco	381	100.4	8.7	1426	7	ABE26589	ABE26589	Human	CCR
309	108	9.4	1116	6	ABK14070	Rat galan		382	100.4	8.7	1586	2	AAE44099	AAE44099	Human	G-p
310	108	9.4	1116	6	ABK14071	Rat galan		383	100.4	8.7	1586	2	AAE36733	AAE36733	Nucleotid	
311	108	9.4	1119	2	AAE25519	Rat galan		384	100.4	8.7	1586	6	ABE12430	ABE12430	CDNA	enco
312	108	9.4	1119	6	ABE01609	Rat galan		385	100.4	8.7	1586	6	ABE12431	ABE12431	CDNA	enco
313	108	9.4	1119	6	ABE08444	Galanin-1		386	100.4	8.7	1944	6	ABE51059	ABE51059	Human	DNA
314	108	9.4	1193	2	AAE79975	Rat galan		387	100.4	8.7	1944	2	AAE24386	AAE24386	Human	CC
315	108	9.4	1193	8	ADAO9973	CDNA	enco	388	100.4	8.7	1953	7	ACA56498	ACA56498	Human	819

389	100.4	8.7	2370	7	ABZ42640	Abz42640 Human C-C	462	97.2	8.4	2152	3	AAZ90522	Aaz90522 Human GPC
390	100.4	8.7	2372	7	ABZ68884	Abz68884 Nucleotid	C 463	97.2	8.4	2230	10	ADZ76960	Adz76960 Human CDN
391	100.4	8.7	2382	4	AAZ03022	AAZ03022 Human dia	464	97.2	8.4	2488	3	AAZ91191	Aaz91191 Human MCH
392	98.8	8.6	1068	2	AAZ28385	AAZ28385 Human MCP	465	97.2	8.4	3483	3	AAZ30875	Aaz30875 Human 11c
393	98.6	8.5	1095	3	AAZ45993	AAZ45993 CDNA enco	466	97.2	8.4	8483	6	AAZ57066	Aaz57066 Human mel
394	98.4	8.5	1080	9	AAZ62483	AAZ62483 Monkey MC	467	97	8.4	169	7	ABV75088	Abv75088 Delta-opi
395	98	8.5	1073	5	AAZ05847	AAZ05847 Fruit fly	468	97	8.4	585	6	ABQ31861	Abq31861 Oligonuc1
396	98	8.5	1073	5	AAZ05847	AAZ05847 Fruit fly	C 469	97	8.4	585	6	ABQ31860	Abq31860 Oligonuc1
397	97.8	8.5	1116	7	ABT40235	ABT40235 Rat TIG2	470	96.4	8.4	590	4	ABQ18607	Abq18607 Drosophi1
398	97.8	8.5	1451	5	AAZ05853	AAZ05853 Fruit fly	471	96.4	8.4	990	4	AAZ57149	Aaz57149 CDNA enco
399	97.8	8.5	1451	5	AAZ05853	AAZ05853 Fruit fly	472	96.4	8.4	990	4	AAZ57149	Aaz57149 CDNA enco
400	97.2	8.4	980	3	AAA30879	AAA30879 Human 11c	473	96.4	8.4	1074	4	ABL57473	AbL57473 Fruit fly
401	97.2	8.4	1062	4	AAA91187	AAA91187 Human MCH	474	96.4	8.4	1778	8	ABL05353	AbL05353 Drosophi1
402	97.2	8.4	1062	4	AAH13652	AAH13652 Human mel	475	95.6	8.3	1062	5	ABL05353	AbL05353 Drosophi1
403	97.2	8.4	1062	4	AAH47298	AAH47298 Human mel	476	95.6	8.3	1062	5	ABL05353	AbL05353 Drosophi1
404	97.2	8.4	1062	5	ABT197900	ABT197900 Non-endog	477	95.6	8.3	1062	5	ABT197912	Abt197912 Non-endog
405	97.2	8.4	1062	5	ABT197924	ABT197924 Non-endog	478	95.6	8.3	1062	5	ABT197927	Abt197927 Non-endog
406	97.2	8.4	1062	6	ABT197924	ABT197924 Non-endog	479	95.6	8.3	1062	5	ABT197909	Abt197909 Non-endog
407	97.2	8.4	1062	6	ABT197924	ABT197924 Non-endog	480	95.6	8.3	1062	5	ABT197918	Abt197918 Non-endog
408	97.2	8.4	1062	6	ABT197924	ABT197924 Non-endog	481	95.6	8.3	1062	5	ABT197921	Abt197921 Non-endog
409	97.2	8.4	1062	7	AAZ45795	AAZ45795 Human mel	482	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
410	97.2	8.4	1062	7	AAZ45795	AAZ45795 Human mel	483	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
411	97.2	8.4	1062	8	AAZ45795	AAZ45795 Human mel	484	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
412	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	485	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
413	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	486	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
414	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	487	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
415	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	488	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
416	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	489	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
417	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	490	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
418	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	491	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
419	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	492	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
420	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	493	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
421	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	494	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
422	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	495	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
423	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	496	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
424	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	497	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
425	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	498	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
426	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	499	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
427	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel	500	95.6	8.3	1062	5	AAZ45795	Aaz45795 Human mel
428	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
429	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
430	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
431	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
432	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
433	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
434	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
435	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
436	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
437	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
438	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
439	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
440	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
441	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
442	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
443	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
444	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
445	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
446	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
447	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
448	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
449	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
450	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
451	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
452	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
453	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
454	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
455	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
456	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
457	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
458	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
459	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
460	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							
461	97.2	8.4	1062	9	AAZ45795	AAZ45795 Human mel							

XX 19-DEC-2000; 2000US-0257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burner GC, Roush CL, Brown JP;
XX WPI: 2003-046718/04.
XX P-PDB: ABP81832.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure: Fig 1; 523pp: English.

XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention

XX Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.3%; Score 1146; DB 7; Length 1182;
Best Local Similarity 99.6%; Pred. No. 1.9e-271;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGATCCAGATCTTCCGCGGGAGCCGCGCCCTTACCTGCGCCCGAGCGCC 60
DB 14 ATGAGATCCCGATTCAGATCTTCCGCGGGAGCCGCGCTTACCTGCGCCCGAGCGCC 73
QY 61 TGCCTGCCCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGGAGCCGCAACGAGCC 120
DB 74 TGCCTGCCCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGGAGCCGCAACGAGCC 133
QY 121 AAGCGCGGCTCGAGAGAGCGGAGCTGAGCCCGGCGCATCTCCCGGCGCATCCCGGCTC 180
DB 134 AAGCGCGGCTCGAGAGAGCGGAGCTGAGCCCGGCGCATCTCCCGGCGCATCCCGGCTC 193
QY 181 ATCATCAGCGGCGTCTACTCCGTAGTGTGTCGTGCGGCGTGGTGGGCAACTCGCTGATC 240
DB 194 ATCATCAGCGGCGTCTACTCCGTAGTGTGTCGTGCGGCGTGGTGGGCAACTCGCTGATC 253
QY 241 ATGTCGTGATCATCCGATACACAAAGATGAGACGCAACCAACTTTATCATATTTAAC 300
DB 254 ATGTCGTGATCATCCGATACACAAAGATGAGACGCAACCAACTTTATCATATTTAAC 313
QY 301 CTGGCTTGGAGATGCTTAACTTAAACCAACGCTTGAAGTACGCGTCTACTTG 360
DB 314 CTGGCTTGGAGATGCTTAACTTAAACCAACGCTTGAAGTACGCGTCTACTTG 373

QY 361 ATGAATTCCTGGACCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
DB 374 ATGAATTCCTGGACCTTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 433
QY 421 AACATGTTACAGACATCTTACCTTGACCATGATGAGCGGCAACCGCTACATGGCGTG 480
DB 434 AACATGTTACAGACATCTTACCTTGACCATGATGAGCGGCAACCGCTACATGGCGTG 493
QY 481 TGCAACCCCGTGAAGGCTTTGGACTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 540
DB 494 TGCAACCCCGTGAAGGCTTTGGACTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 553
QY 541 TGCAATGAGCTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGAAGGCAACAA 600
DB 554 TGCAATGAGCTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGAAGGCAACAA 613
QY 601 GTCAAGGAAGACCTTCATGATGATGAGGCTCTTGAAGTCCGAGATGATGATCACTCC 660
DB 614 GTCAAGGAAGACCTTCATGATGATGAGGCTCTTGAAGTCCGAGATGATGATCACTCC 673
QY 661 TGTGAGGACCTCTTCATGAGATCTGCGTCTTCACTTTCCTTGTGATCCGTGCTC 720
DB 674 TGTGAGGACCTCTTCATGAGATCTGCGTCTTCACTTTCCTTGTGATCCGTGCTC 733
QY 721 ATCATCATGCTGTGCTACACCTTGATGATCTGCTGCTCAAGACGCTCCGCTCTTCT 780
DB 724 ATCATCATGCTGTGCTACACCTTGATGATCTGCTGCTCAAGACGCTCCGCTCTTCT 793
QY 781 GGCCTCCGAGAGAAAGATCGCAACCTGCTAGATGATCAGACTGCTGCTGCTGCTG 840
DB 794 GGCCTCCGAGAGAAAGATCGCAACCTGCTAGATGATCAGACTGCTGCTGCTGCTG 853
QY 841 GCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 854 GCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
QY 901 AGCAGCTTCCAGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 914 AGCAGCTTCCAGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 973
QY 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 974 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
QY 1021 TTCCGGGACCTTCTGCTTCCACTGAAGATGAGATGAGGCGGAGAGCACTAGAGATC 1080
DB 1034 TTCCGGGACCTTCTGCTTCCACTGAAGATGAGATGAGGCGGAGAGCACTAGAGATC 1093
QY 1081 CGAATTTACAGTTCAAGATCTGCTTCACTGAGGAGCATCGATGGGATGAATTAACAGTA 1140
DB 1094 CGAATTTACAGTTCAAGATCTGCTTCACTGAGGAGCATCGATGGGATGAATTAACAGTA 1153
QY 1141 TGACTAGTGTGGA 1154
DB 1154 TGACTAGTGTGGA 1167

RESULT 3
AAD58490
ID AAD58490 standard; DNA; 1182 BP.
XX
XX AAD58490;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human kappa opioid receptor 1 (KOR) DNA.
DB Human, urological disorder; urinary incontinence; gene therapy; cancer;
XX kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
XX urethra; overflow urinary incontinence; stress urinary incontinence;
KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
KW kappa opioid receptor 1; KOR; gene; de.
XX

OS Homo sapiens.
XX Key Location/Qualifiers
FT CDS 14..1156
FT /*tag=a
FT /product="Human kappa opioid receptor 1 (KOR)"
FT /note="The CDS is referred to as SEQ ID NO:21 in the
FT specification"
XX
XX WO2003061573-A2.
XX
XX 31-JUL-2003.
XX
XX 16-JAN-2003; 2003WO-US001450.
XX
XX 18-JAN-2002; 2002US-0349511P.
XX 28-FEB-2002; 2002US-0360500P.
XX 15-MAR-2002; 2002US-0365041P.
XX 19-APR-2002; 2002US-0374063P.
XX 14-AUG-2002; 2002US-0403468P.
XX 27-SEP-2002; 2002US-0414262P.
XX 21-OCT-2002; 2002US-0419986P.
XX 05-NOV-2002; 2002US-0423809P.
XX 26-NOV-2002; 2002US-0429797P.
XX
XX (MILL.) MILLENNIUM PHARM INC.
XX
XX S1105-Santiago I, Karichet V;
XX
XX WPI; 2003-598705/56.
XX P-P8DB; AAE38589.
XX
XX Identifying a compound for treating urological disorders, for example
XX PT urinary incontinence by assaying the ability of the compound to modulate
XX PT the nucleic acid expression or polypeptide activity.
XX
XX Dielosure; Page 149-151; Opp; English.
XX
XX The present relates to a method for identifying a compound for treating
XX CC urological disorders e.g., urinary incontinence including overactive/
XX CC overensitive bladder, overflow urinary incontinence, stress urinary
XX CC incontinence caused by dysfunction of the bladder, urethra or central or
XX CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
XX CC cancer of the prostate or kidney disorders. The method is also useful for
XX CC modulating hyperplasia in a cell and treating a subject having a
XX CC urological disorder. The invention is also used in gene therapy. The
XX CC present sequence is human kappa opioid receptor 1 (KOR) DNA
XX
XX Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;
XX
XX Query Match 99.3%; Score 1146; DB 9; Length 1182;
XX Best Local Similarity 99.6%; Pred. No. 1.9e-271;
XX Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 ATGAGCTCCCGCATCCAGATCTTCCGCGGAGAGCCGGGCTCACTCGGCCCGAGCGCC 60
XX 14 ATGAGATCCCGCATTCAGATCTTCCGCGGAGAGCCCTGAGCTTCCCGCCCGAGCGCC 73
XX
XX 61 TGCCCTGCCCCCAACAGACAGCGCTGATTCCCGGCTGGGCGGAGCCGAGCAAGAGCGC 120
XX 74 TGCCCTGCCCCCAACAGACAGCGCTGATTCCCGGCTGGGCGGAGCCGAGCAAGAGCGC 133
XX
XX 121 AGCGCCGAGCTCGAGAGACGCGAGCTGAGGCGCGGACATCTCCCGGCAATCCCGGTC 180
XX 134 AGCGCCGAGCTCGAGAGACGCGAGCTGAGGCGCGGACATCTCCCGGCAATCCCGGTC 193
XX
XX 181 ATCATCAGCGCGCTCTACTCCGTAAGTTCGTGCGGCTTGTGGGCAACTCGCTGTC 240
XX 194 ATCATCAGCGCGCTCTACTCCGTAAGTTCGTGCGGCTTGTGGGCAACTCGCTGTC 253
XX
XX 241 ATGTTCTGATCATCGATACCAAGATGAGAGACGCAACCACTTTACATATTTAAC 300
XX 254 ATGTTCTGATCATCGATACCAAGATGAGAGACGCAACCACTTTACATATTTAAC 313
XX
XX

QY 301 CTGGCTTTGGAGATGATCTTTAGTTACTCAACACATGACCCCTTTCAGAGTACGCTACTTGG 360
DB 314 CTGGCTTTGGAGATGATCTTTAGTTACTCAACACATGACCCCTTTCAGAGTACGCTACTTGG 373
QY 361 ATGAATCTCGGCTTTTGGGAGTGTGTGCAAGATAGTAATTTCAATTGATTAATCACTAC 420
DB 374 ATGAATCTCGGCTTTTGGGAGTGTGTGCAAGATAGTAATTTCAATTGATTAATCACTAC 433
QY 421 AACATGTTCAACAGATCTTCACTTTGACATGATGAGCGGTGACCCGCTACATTGGCCGTC 480
DB 434 AACATGTTCAACAGATCTTCACTTTGACATGATGAGCGGTGACCCGCTACATTGGCCGTC 493
QY 481 TGCCACCCCGTGAAGGCTTTTGGACTTCCGACACACCTTGAAGGCAAGATCATATATC 540
DB 494 TGCCACCCCGTGAAGGCTTTTGGACTTCCGACACACCTTGAAGGCAAGATCATATATC 553
QY 541 TGCACTGTGAGCTGTGTGATCTGTGAGCATCTGTGCAATATGCTTGGAGGACCAAA 600
DB 554 TGCACTGTGAGCTGTGTGATCTGTGAGCATCTGTGCAATATGCTTGGAGGACCAAA 613
QY 601 GTCAAGGAAAGCTGTGATGTCAATTGAGTCTCTTGCAGTTCCAGATGATGACTACTTC 660
DB 614 GTCAAGGAAAGCTGTGATGTCAATTGAGTCTCTTGCAGTTCCAGATGATGACTACTTC 673
QY 661 TGCTGGGACCTTTCATGAAGATCTGCGCTTCACTTTGCTGATATCCCTGTCC 720
DB 674 TGCTGGGACCTTTCATGAAGATCTGCGCTTCACTTTGCTGATATCCCTGTCC 733
QY 721 ATCATCATGCTGTGTCAACCTGTATGATCTGTGCTCAAGAGGCTCGGCTCTTCT 780
DB 734 ATCATCATGCTGTGTCAACCTGTATGATCTGTGCTCAAGAGGCTCGGCTCTTCT 793
QY 761 GGGTCCGAGAAAGATGCAAGCTGTGAGATACCAAGCTGCTGTGTGTGTG 840
DB 794 GGGTCCGAGAAAGATGCAAGCTGTGAGATACCAAGCTGCTGTGTGTGTG 853
QY 841 GCAATCTTCGT 900
DB 854 GGGT 913
QY 901 AGCACTCCCAAGACAGACAGTGTCTCTTCAAGATTAATTTGATGATGCTTGAAGCTAT 960
DB 914 AGCACTCCCAAGACAGACAGTGTCTCTTCAAGATTAATTTGATGATGCTTGAAGCTAT 973
QY 961 ACCAAGAGT 1020
DB 974 ACCAAGAGT 1033
QY 1021 TTCCGGGACTTGT 1080
DB 1034 TTCCGGGACTTGT 1093
QY 1081 CGAATTAAGT 1140
DB 1094 CGAATTAAGT 1153
QY 1141 TGACTTGT 1154
DB 1154 TGACTTGT 1167
XX
XX RESULT 4
XX ADE84861
XX ID ADE84861 standard; DNA; 1182 BP.
XX
XX ADE84861;
XX
XX 29-JAN-2004 (first entry)
XX
XX Farnesyl transferase inhibitor modulated leukemia associated gene #80.
XX
XX 88; cyclostatic; farnesyl transferase inhibitor; gene expression;
XX
XX

KW quinoline; leukemia; cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO2003038129-A2.
 XX
 PD 08-MAY-2003.
 XX
 PP 30-OCT-2002; 2002MO-US034784.
 XX
 PR 30-OCT-2001; 2001US-0338997P.
 PR 30-OCT-2001; 2001US-0340081P.
 PR 30-OCT-2001; 2001US-0340938P.
 PR 30-OCT-2001; 2001US-0341012P.
 XX
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PI Rapont M;
 XX
 DR WPI; 2003-513497/48.
 XX
 PT Determining whether a patient will respond to treatment with a farnesyl
 PT transferase inhibitor, by analyzing the expression of gene that is
 PT differentially modulated in the presence of the inhibitor.
 XX
 PS Disclosure; SEQ ID NO 80; 346bp; English.
 XX
 CC The invention relates to a method of determining whether a patient will
 CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
 CC analyzing the expression of gene that is differentially modulated in the
 CC presence of an FTI. The method is useful for determining whether a
 CC patient will respond to treatment with a FTI such as (B)-6-(lamino(4-
 CC chlorophenyl)-(1-methyl-1H-imidazol-5-yl)methyl)-4-(3-chlorophenyl)-1-
 CC methyl-2-(1H-quinoline), monitoring the therapy of a patient, treating a
 CC patient with leukemia with FTI if the analysis indicates that the patient
 CC will respond. This sequence corresponds to a gene whose expression may be
 CC modulated in the presence of FTI.
 XX
 SO Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;
 Query Match 99.3%; Score 1146; DB 9; Length 1182;
 Best Local Similarity 99.6%; Pred. No. 1.9e-271;
 Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCGGCGCTTACCTGCGGCCCGAGCGCC 60
 DB 14 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCGCTTACCTGCGGCCCGAGCGCC 73
 QY 61 TGCCCTGCCCCCAAGAGAGAGCGCTGTTTCCCGGCTGGGCGAGCCCGAGCAAGCAAGC 120
 DB 74 TGCCCTGCCCCCAAGAGAGAGCGCTGTTTCCCGGCTGGGCGAGCCCGAGCAAGCAAGC 133
 QY 121 AGCGCGGCTGGAGAGAGCGGAGCGGAGCGGCGGACATCTTCCCGGCGCATCCCGGTC 180
 DB 134 AGCGCGGCTGGAGAGAGCGGAGCGGAGCGGCGGACATCTTCCCGGCGCATCCCGGTC 193
 QY 181 ATCATCAGGCGGCGCTTACCTCCGTAAGTTCGTCGCGGCTGGTGGGCAACTCGCTGTC 240
 DB 194 ATCATCAGGCGGCGCTTACCTCCGTAAGTTCGTCGCGGCTGGTGGGCAACTCGCTGTC 253
 QY 241 ATGTTCTGATCATCCGATACCAAGATGAAGAGAGCAACCAATTTACATATTATAC 300
 DB 254 ATGTTCTGATCATCCGATACCAAGATGAAGAGAGCAACCAATTTACATATTATAC 313
 QY 301 CTGGCTTTGGCAGATGCTTTAGTACTACACCAATGCGCTTTCAGAGTACGCTTACTTG 360
 DB 314 CTGGCTTTGGCAGATGCTTTAGTACTACCAACCAATGCGCTTTCAGAGTACGCTTACTTG 373
 QY 361 ATGAATTCCTGGGCTTTGGGAGATGCTGTCGCAAGATGAATTTCCATGATTAATAC 420
 DB 374 ATGAATTCCTGGGCTTTGGGAGATGCTGTCGCAAGATGAATTTCCATGATTAATAC 433
 QY 421 AACATGTTCAACGAGATCTTCACTTGACATGATGAGCGTGAACCGCTACATTCGCGTG 480

DB 434 AACATGTTCAACGAGATCTTCACTTGACATGATGAGCGTGAACCGCTACATTCGCGTG 493
 QY 481 TGCCACCCCGTGAAGGCTTTGAGCTTCCGCAACCCCTTGAAGGCAAAATGATCAATATC 540
 DB 494 TGCCACCCCGTGAAGGCTTTGAGCTTCCGCAACCCCTTGAAGGCAAAATGATCAATATC 553
 QY 541 TGCACTGGCTGCTGCTGCTCATCTGTTGGACATCTCTGCATATGCTCTTGAAGGCAACAA 600
 DB 554 TGCACTGGCTGCTGCTGCTCATCTGTTGGACATCTCTGCATATGCTCTTGAAGGCAACAA 613
 QY 601 GTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 614 GTCAAGGAAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 673
 QY 661 TGCTGGGAGCTCTTCATGAAGATGAGGCTCTTCACTTCTTGGCTTGGATGATGATGATGAT 720
 DB 674 TGCTGGGAGCTCTTCATGAAGATGAGGCTCTTCACTTCTTGGCTTGGATGATGATGATGAT 733
 QY 721 ATCATCATGCTGCTGCTACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 734 ATCATCATGCTGCTGCTACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 793
 QY 781 GGCCTCCGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 794 GGCCTCCGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 853
 QY 841 GCAGCTTCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 854 GCGGTTTCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913
 QY 901 AGCACTCCCAAGAGAGAGCTGCTCTCTCACTATTAATTTCTGATGATGATGATGATGATGAT 960
 DB 914 AGCACTCCCAAGAGAGAGCTGCTCTCTCACTATTAATTTCTGATGATGATGATGATGATGAT 973
 QY 961 ACCAAGTACCTGATATCCATTTCTTACGCTTTCTTGAATGAATTTCAAGCGGTGT 1020
 DB 974 ACCAAGTACCTGATATCCATTTCTTACGCTTTCTTGAATGAATTTCAAGCGGTGT 1033
 QY 1021 TTCGGGAGCTTCTGCTTCCACTGAAGATGAGATGAGAGCGGCGAGCACTGAGCAAGTC 1080
 DB 1034 TTCGGGAGCTTCTGCTTCCACTGAAGATGAGATGAGAGCGGCGAGCACTGAGCAAGTC 1093
 QY 1081 CGAATACAGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGATGAATTAACAGTA 1140
 DB 1094 CGAATACAGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGATGAATTAACAGTA 1153
 QY 1141 TGACTAGTGTGGA 1154
 DB 1154 TGACTAGTGTGGA 1167
 RESULT 5
 AAT9098
 ID AAT9098 standard; cDNA; 1143 BP.
 XX
 AC AAT9098;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human kappa opioid receptor cDNA.
 XX
 KW Selective target cell activation; G protein-coupled receptor; RASL;
 KW gene therapy; cell proliferation; kappa opioid receptor; human;
 KW transgenic animal; arrhythmia; bone disease; seizure;
 KW vascular contraction; disease model; ss.
 OS Homo sapiens.
 XX
 PN WO9735478-A1.
 XX
 PD 02-OCT-1997.
 XX

PF 25-MAR-1997; 97WO-US005334.
XX
XX 26-MAR-1996; 96US-00622348.
XX
PA (REBC) UNITV CALIFORNIA.
XX
XX Conklin BR;
XX
DR MPI: 1997-502739/46.
DR P-PSDB; AAM30297.
XX
PT Selective activation of target cell expressing modified G protein coupled
PT receptor - allows control of cellular proliferation, especially for
PT amplification of transfected cells in gene therapy.
XX
PS Example 1, Page 74-76; 117pp; English.
XX
XX This cDNA sequence comprises the coding region for human kappa opioid
XX receptor (KOR, see AAM30297), a G protein-coupled receptor implicated in
XX neurotransmission. A novel method for selectively activating a target
XX cell (TC) comprises: (i) introducing into the cell a nucleic acid
XX sequence (1) that expresses a G protein-coupled receptor (A) modified to
XX be activated superiorly by a synthetic ligand (RASSL); and (ii) exposing
XX the transfected cell to small synthetic molecules (B) that bind to and
XX activate (A), inducing the G protein coupled cellular response associated
XX with receptor activation. (A) has: (a) decreased binding affinity for a
XX selected natural ligand of the native receptor; (b) binding affinity for
XX (B); and (c) is activated by binding (B) sufficiently to produce the
XX required cellular response. Also new are: (1) transgenic cells including
XX heterologous (1) in the genome; (2) cellular implants comprising a TC
XX transfected with (1); (3) isolated (1); and (4) transgenic non-human
XX animals expressing (A). Activation of (A) results, in vitro or in vivo,
XX in cellular proliferation, or secretion of a cellular product,
XX particularly a heterologous therapeutic protein encoded by a second
XX inserted nucleic acid sequence. Particularly it is used to expand the
XX relatively few cells that are successfully transfected during gene
XX therapy procedures. Other responses that can be regulated are cell
XX migration and contraction, or pigment production. In transgenic animals,
XX expression or stimulation of (A) is designed to develop cardiac
XX arrhythmia, symptoms of bone disease, seizures, vascular contractions,
XX dementia, neurodegeneration etc., for use as models of these diseases
XX (claimed). The transgenic animals are also used for production of
XX improved food products (e.g. increased calcium content in eggshells or
XX altered fat/lean ratios) or to control fertility or induce labour. A
XX RASSL derived from KOR, designated RASSL ORI (see AAM30299), was
XX generated by mutation of the KOR cDNA sequence
SQ Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T; 0 U; 0 Other;
Query Match 99.0%; Score 1143; DB 2; Length 1143;
Best Local Similarity 100.0%; Fred. No. 1e-270;
Matches 1143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 CTGGCTTTGGAGAGATGCTTTAGTACTACAAACCATGCCCTTTCAGATGAGGTACTTTG 360
DB 301 CTGGCTTTGGAGAGATGCTTTAGTACTACAAACCATGCCCTTTCAGATGAGGTACTTTG 360
QY 361 ATGAATTCCTGGACCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTAATAC 420
DB 361 ATGAATTCCTGGACCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTAATAC 420
QY 421 AACATGTTACACAGATCTTACCTTTGACCAATGATGAGGTGAGACCGCTACATTCGCGG 480
DB 421 AACATGTTACACAGATCTTACCTTTGACCAATGATGAGGTGAGACCGCTACATTCGCGG 480
QY 481 TSCCACCCTGTAAGGCTTTGAGACTTCCGACACCTTGAAGGCAAAAGATCAATATTC 540
DB 481 TSCCACCCTGTAAGGCTTTGAGACTTCCGACACCTTGAAGGCAAAAGATCAATATTC 540
QY 541 TGCATCTGGCTGCTGTGCTCATCTGTGACATCTGTGCAATATGCTCTTGGAGGACCAAA 600
DB 541 TGCATCTGGCTGCTGTGCTCATCTGTGACATCTGTGCAATATGCTCTTGGAGGACCAAA 600
QY 601 GTCAAGGAAGAGTGAATGTCATTGAGTCTCTTGCAGTTCCTCCAGATGATGACTATCC 660
DB 601 GTCAAGGAAGAGTGAATGTCATTGAGTCTCTTGCAGTTCCTCCAGATGATGACTATCC 660
QY 661 TGGTGGAGACTCTTCATGTAAGATGCGCTTCATCTTGGCTTGGATCCCTGCTGCTC 720
DB 661 TGGTGGAGACTCTTCATGTAAGATGCGCTTCATCTTGGCTTGGATCCCTGCTGCTC 720
QY 721 ATCATCATGCTGTGCTACACCTGTATGATCTGTGCTCAAGAGGCTCGGCTCTTCT 780
DB 721 ATCATCATGCTGTGCTACACCTGTATGATCTGTGCTCAAGAGGCTCGGCTCTTCT 780
QY 781 GGGTCCCGAAGAAAGATGCAACCTGGGTAGATCAACAGCTGCTCTGTTGGTGGTG 840
DB 781 GGGTCCCGAAGAAAGATGCAACCTGGGTAGATCAACAGCTGCTCTGTTGGTGGTG 840
QY 841 GGAATCTTGTGTGCTGTGAGTCCCATTCATATTCATCTGTTGAGAGGCTCTGGGG 900
DB 841 GGAATCTTGTGTGCTGTGAGTCCCATTCATATTCATCTGTTGAGAGGCTCTGGGG 900
QY 901 AGCAGCTCCACAGACAGAGCTGCTCTCCAGACTTATCTTGTGATGCGCTTAAAGCTAT 960
DB 901 AGCAGCTCCACAGACAGAGCTGCTCTCCAGACTTATCTTGTGATGCGCTTAAAGCTAT 960
QY 961 ACCAAGATGAGCTTAATCCCATCTTCAAGCTTTGTGATGAAGAACTTCAAGGCGTGT 1020
DB 961 ACCAAGATGAGCTTAATCCCATCTTCAAGCTTTGTGATGAAGAACTTCAAGGCGTGT 1020
QY 1021 TTCCGGGACTCTGCTTCCACTGAAGATGAGAGCGGCGACAGCACTGACAGAGTC 1080
DB 1021 TTCCGGGACTCTGCTTCCACTGAAGATGAGAGCGGCGACAGCACTGACAGAGTC 1080
QY 1081 CGAATATGAGTTCAGAGATCTGCTTACCTGAGGAGCATATGAGATGAATTAACAGTA 1140
DB 1081 CGAATATGAGTTCAGAGATCTGCTTACCTGAGGAGCATATGAGATGAATTAACAGTA 1140
QY 1141 TGA 1143
DB 1141 TGA 1143
RESULT 6
AAT12550 standard; cDNA, 1142 BP.
ID AAT12550
XX AAT12550;
XX
AC AAT12550;
XX
DT 03-SEP-1996 (first entry)
XX
XX Human kappa opioid receptor cDNA.
XX
XX Human kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; de.

```
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..1142
XX FT /*tag= a
XX FT /product= "kappa opioid receptor"
XX FT /note= "incomplete termination codon"
XX
XX MO9601898-A1.
XX
XX 25-JAN-1996.
XX
XX 07-JUL-1995; 95WO-FR000912.
XX
XX 11-JUL-1994; 94FR-00008531.
XX
XX (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX
XX Kieffer B, Simonin F;
XX
XX WPI, 1996-097628/10.
XX P-PSDB; AAR8722.
XX
XX New nucleic acid encoding the human Kappa opioid receptor - useful in
XX diagnosis and therapy, and for isolating receptor ligands and modulators.
XX
XX Claim 3; Page 13-15; 30pp; French.
XX
XX This sequence codes for the human kappa opioid receptor and was obtained
XX from two overlapping cDNA fragments isolated from a human placental cDNA
XX library. The fragments were amplified from the library using PCR primers
XX based on the sequence of human genomic clones which hybridised with a
XX murine delta receptor cDNA probe. Nucleotide probes derived from the
XX kappa opioid receptor coding sequence are useful for diagnosis of
XX neurological, cardio- vascular and psychiatric disorders associated with
XX opioid receptors
XX
XX Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 1142; DB 2; Length 1142;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-270;
XX Matches 1142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCGGATCCAGATCTTCGCGGGAGCGCGGCCCTCACTGCGCCCGGAGCGCC 60
DB 1 ATGAGCTCCCGGATCCAGATCTTCGCGGGAGCGCGGCCCTCACTGCGCCCGGAGCGCC 60
QY 61 TGCCGCCCCCAACAGAGCGCGCTGTTTCCGGCTGGGCGAGCCCGACAGCAACGGC 120
DB 61 TGCCGCCCCCAACAGAGCGCGCTGTTTCCGGCTGGGCGAGCCCGACAGCAACGGC 120
QY 121 AGCGCGGCTGGAGAGCGCGAGCTGAGCCCGGCAACATCTCCCGGCCATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGCGCGAGCTGAGCCCGGCAACATCTCCCGGCCATCCCGGTC 180
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTTCGTCGGGCTTGGTGGCACTCGTGTC 240
DB 181 ATCATCAGGCGGCTTACTCCGTAAGTTCGTCGGGCTTGGTGGCACTCGTGTC 240
QY 241 ATGTCGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTC 300
DB 241 ATGTCGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTC 300
QY 301 CTGGCTTTGGAGATGCTTTAGTTACTCAACCAATGCGCTTTCAGAGTACGCTTACTTG 360
DB 301 CTGGCTTTGGAGATGCTTTAGTTACTCAACCAATGCGCTTTCAGAGTACGCTTACTTG 360
QY 361 ATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTAC 420
DB 361 ATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTAC 420
QY 421 AACATGTTACACAGCATCTTCACTTGACCATGATGAGCGTGAGCCGCTACATGCGGTG 480
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DB 421 AACATGTTACACAGCATCTTCACTTGACCATGATGAGCGTGAGCCGCTACATGCGGTG 480
QY 481 TGCCACCCCGTGAAGGCTTTGAACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 540
DB 481 TGCCACCCCGTGAAGGCTTTGAACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 540
QY 541 TGCAATCGGCGCTGCTGCTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGACCAAA 600
DB 541 TGCAATCGGCGCTGCTGCTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGACCAAA 600
QY 601 GTCAAGGAAGAGCTGATGATGATGAGTCTCTTGCAGTTCAGATGATGATGATGATGATG 660
DB 601 GTCAAGGAAGAGCTGATGATGATGAGTCTCTTGCAGTTCAGATGATGATGATGATGATG 660
QY 661 TGCTGGGACCTCTTCATGAGATCTGCGTCTTCACTCTTGGCTTGGATCCCTGCTCTC 720
DB 661 TGCTGGGACCTCTTCATGAGATCTGCGTCTTCACTCTTGGCTTGGATCCCTGCTCTC 720
QY 721 ATCATCATGCTGCTGCTACACCTGATGATCTGCTGCTCAAGAGGCTCGGCTCTTCT 780
DB 721 ATCATCATGCTGCTGCTACACCTGATGATCTGCTGCTCAAGAGGCTCGGCTCTTCT 780
QY 781 GGCCTCCGAGAGAAAGATCGCAACCTGCGTAGATCAACAGACTGCTCTGCTGCTG 840
DB 781 GGCCTCCGAGAGAAAGATCGCAACCTGCGTAGATCAACAGACTGCTCTGCTGCTG 840
QY 841 GCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 GCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 AGCACTCTCCAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 AGCACTCTCCAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 ACCAAGTACCTGTAATCCCATCTCTACGCTTCTTGAATGAATCTTCAAGCGGTGT 1020
DB 961 ACCAAGTACCTGTAATCCCATCTCTACGCTTCTTGAATGAATCTTCAAGCGGTGT 1020
QY 1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGAGATGAGAGCGGCGAGACATGAGATC 1080
DB 1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGAGATGAGAGCGGCGAGACATGAGATC 1080
QY 1081 CGAATACAGTTGAGATCTCGCTTACCTGAGGGACATGAGATGAGATGAGATGAGATG 1140
DB 1081 CGAATACAGTTGAGATCTCGCTTACCTGAGGGACATGAGATGAGATGAGATGAGATG 1140
QY 1141 TG 1142
DB 1141 TG 1142
RESULT 7
AAT90999
ID AAT90999 standard; cDNA; 1284 BP.
XX
XX AAT90999;
DE 14-APR-1998 (first entry)
XX
XX Human kappa opioid receptor modified cDNA.
XX
XX Selective target cell activation; G protein-coupled receptor; RASL;
XX gene therapy; cell proliferation; kappa opioid receptor; human;
XX transgenic animal; arrhythmia; bone disease; seizure;
XX vascular contraction; disease model; ss.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX sig_peptide 1..90
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PT      /+tag= a
PT      /product= "prolactin signal sequence"
PT      mat_peptide
PT      91..1284
PT      /+tag= b
PT      /product= "FLAG-KOR-HA fusion"
XX      WO9735478-A1.
XX      02-OCT-1997.
XX      25-MAR-1997; 97WO-US005334.
XX      26-MAR-1996; 96US-00622348.
XX      (REGC ) UNIV CALIFORNIA.
XX      Conklin BR;
XX      WPI; 1997-502739/46.
XX      P-PsDB; AAW30298.
PT      Selective activation of target cell expressing modified G protein coupled
PT      receptor - allows control of cellular proliferation, especially for
PT      amplification of transfected cells in gene therapy.
XX      Example 1; Page 77-79; 117pp; English.
XX      This cDNA sequence encodes a polypeptide (see AAW30298) comprising the
XX      human G protein-coupled kappa opioid receptor (KOR) (see also AAW30297)
XX      flanked by sequences that facilitate the detection and purification of
XX      recombinant KOR, and especially KOR RASSLS (see AAW30299), i.e. a
XX      receptor activated superiorly by a synthetic ligand. A novel method for
XX      selectively activating a target cell (TC) comprises: (i) introducing into
XX      the cell a nucleic acid sequence (I) that expresses a RASSL (A) and (ii)
XX      exposing the transfected cell to small synthetic molecules (B) that bind
XX      to and activate (A), inducing the G protein coupled cellular response
XX      associated with receptor activation. (A) has: (a) decreased binding
XX      affinity for a selected natural ligand of the native receptor; (b)
XX      binding affinity for (B); and (c) is activated by binding (B)
XX      sufficiently to produce the required cellular response. Also new are:
XX      CC transgenic cells including heterologous (I) in the genome; cellular
XX      implants comprising a TC transfected with (I); isolated (I); and
XX      CC transgenic animals expressing (A). Activation of (A) results, in vitro or
XX      in vivo, in cellular proliferation, or secretion of a cellular product,
XX      particularly a heterologous therapeutic protein encoded by a second
XX      CC inserted nucleic acid sequence. Particularly it is used to expand the
XX      CC relatively few cells that are successfully transfected during gene
XX      CC therapy procedures. Other responses that can be regulated are cell
XX      CC migration and contraction, or pigment production. In transgenic animals,
XX      CC expression or stimulation of (A) is designed to develop cardiac
XX      CC arrhythmia, symptoms of bone disease, seizures, vascular contractions,
XX      CC dementia, neurodegeneration etc., for use as models of these diseases
XX      CC (claimed). The transgenic animals are also used for production of
XX      CC improved food products (e.g. increased calcium content in eggshells or
XX      CC altered fat/lean ratios) or to control fertility or induce labour
XX      CC
XX      Sequence 1284 BP; 265 A; 377 C; 322 G; 320 T; 0 U; 0 Other;
SQ      Query Match          98.6%; Score 1137.8; DB 2; Length 1284;
SQ      Best Local Similarity 99.8%; Pred. No. 2.1e-269;
SQ      Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      182 TCATCAGCGGCGGTCTACTCCAGTAGTGTGCTGCGGCTTGGGCGCAACTGGCTGTCA 241
QY      293 TCATCAGCGGCGGTCTACTCCAGTAGTGTGCTGCGGCTTGGGCGCAACTGGCTGTCA 352
QY      242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTATCATATTTAAC 301
QY      353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTATCATATTTAAC 412
QY      302 TGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCTTTCAAGTACGCTTACTTGA 361
QY      413 TGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCTTTCAAGTACGCTTACTTGA 472
QY      362 TGAATTCCTGGGCTTTGGGCGATGCTGTGCAAGATGATATTTCCATTGATTTACTACA 421
QY      473 TGAATTCCTGGGCTTTGGGCGATGCTGTGCAAGATGATATTTCCATTGATTTACTACA 532
QY      422 ACATGTTACACGACATCTTACCTTGACCATGATGACGCTGACCGCTACATTGCCGTG 481
QY      533 ACATGTTACACGACATCTTACCTTGACCATGATGACGCTGACCGCTACATTGCCGTG 592
QY      482 GGCACCCCGTGAAAGCTTTGACCTTCCGACACCCCTTGAAAGCAAGATCATATATCT 541
QY      593 GGCACCCCGTGAAAGCTTTGACCTTCCGACACCCCTTGAAAGCAAGATCATATATCT 652
QY      542 GCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY      653 GCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
QY      602 TCAGGAGAGACGTCGATGTCATTTGATGTCCTTGCAGTTCGACAGATGATGATCTCT 661
QY      713 TCAGGAGAGACGTCGATGTCATTTGATGTCCTTGCAGTTCGACAGATGATGATCTCT 772
QY      662 GGTGGACCTCTTCATGAAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
QY      773 GGTGGACCTCTTCATGAAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
QY      722 TCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY      833 TCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
QY      782 GCTCCGAGAGAAAGATGCAACCTGCGTAGATGACAGACTGCTGCTGCTGCTGCTGCT 841
QY      893 GCTCCGAGAGAAAGATGCAACCTGCGTAGATGACAGACTGCTGCTGCTGCTGCTGCT 952
QY      842 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901
QY      953 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
QY      902 GCACTCTCCACAGCAGACTGCTCTCTCAGCTATTACTTCTGCACTGCTTAGGCTATA 961
QY      1013 GCACTCTCCACAGCAGACTGCTCTCTCAGCTATTACTTCTGCACTGCTTAGGCTATA 1072
QY      962 CCAACGATGAGCTGATCCATCTCTGAGCTTCTTGAATGAATCAAGCGGTGT 1021
QY      1073 CCAACGATGAGCTGATCCATCTCTGAGCTTCTTGAATGAATCAAGCGGTGT 1132
QY      1022 TCCGGAGCTTCTGCTTCCACTGAAGATGAGATGAGAGCGGACGACTAGCAGAGTCC 1081
QY      1133 TCCGGAGCTTCTGCTTCCACTGAAGATGAGATGAGAGCGGACGACTAGCAGAGTCC 1192
QY      1082 GAAATACGTTCAAGATCTGCTTCACTGAGGGAATGATGGAATGAATTAACCACTAT 1141
QY      1193 GAAATACGTTCAAGATCTGCTTCACTGAGGGAATGATGGAATGAATTAACCACTAT 1252
QY      1142 G 1142
QY      1253 G 1253
Db      1253 G 1253
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RESULT 8
ABI98011
ID ABI98011 standard; cDNA; 1143 BP.

XX AB198011;
AC 18-FEB-2002 (first entry)
XX Non-endogenous human GPCR cDNA, SEQ ID NO: 542.
DT
DE
XX
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease; ss.
OS
XX Homo sapiens.
XX Synthetic.
XX WO200177172-A2.
XX
XX 18-OCT-2001.
XX
XX 05-APR-2001; 2001WO-US011098.
XX
XX 07-APR-2000; 2000US-0195747P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Bruinema K, Liaw CW, Lin I;
XX WPI; 2001-648759/74.
XX P-PsDB; ABB56375.
XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
XX Example 2; Page 344; 394dp; English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence encodes a non-endogenous version of a known human GPCR
XX
XX Sequence 1143 BP; 238 A; 332 C; 284 G; 289 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 1131.8; DB 5; Length 1143;
Best Local Similarity 99.4%; Pred. No. 5.9e-268;
Matches 1136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGGAATCCCGATCCAGATCTTCCGCGGAGAGCCGCGCTTACTCTGCGCCCGAGCGCC 60
Db 1 ATGGAATCCCGATCCAGATCTTCCGCGGAGAGCCGCGCTTACTCTGCGCCCGAGCGCC 60
QY 61 TGGCTGCCCCCAAGAGAGAGCGGCTGTTTCCCGGCTGCGCGAGCCCGAGAGAGAGCGC 120
Db 61 TGGCTGCCCCCAAGAGAGAGCGGCTGTTTCCCGGCTGCGCGAGCCCGAGAGAGAGCGC 120
QY 121 AGCGCCGCGCTCGAGAGAGCGGAGCGGAGCGGAGCATCTCCCGGCGCATCCCGGCTC 180
Db 121 AGCGCCGCGCTCGAGAGAGCGGAGCGGAGCGGAGCATCTCCCGGCGCATCCCGGCTC 180
QY 181 ATCATACAGGCGGTCTACTCTCGTAGTGTTCGTGCGGAGCTGTGAGGAGCATCTGCTG 240
Db 181 ATCATACAGGCGGTCTACTCTCGTAGTGTTCGTGCGGAGCTGTGAGGAGCATCTGCTG 240
QY 241 ATGTTTCGATCATCCGATACCAAAAGTGAAGAGAGAGACCAACATTTATATTTTAAAC 300
Db 241 ATGTTTCGATCATCCGATACCAAAAGTGAAGAGAGAGACCAACATTTATATTTTAAAC 300
QY 301 CTGCGTTTGGAGAGATGCTTTAGTTACTACTCAACCAATGCCCTTTCAGAGAGAGGCTACTG 360
Db 301 CTGCGTTTGGAGAGATGCTTTAGTTACTACTCAACCAATGCCCTTTCAGAGAGAGGCTACTG 360
QY 361 ATGAATTCCTGGCTTTTGGGAGATGTGCTGTGCAAGATGATTAATTCATGATTACTAC 420

Db 361 ATGAATTCCTGGCTTTTGGGAGATGTGCTGTGCAAGATGATTAATTCATGATTACTAC 420
QY 421 AACATGTTACACAGATCTTACCTTGACATGATGAGCGTGAGCCGCTACATGCGGTG 480
Db 421 AACATGTTACACAGATCTTACCTTGACATGATGAGCGTGAGCCGCTACATGCGGTG 480
QY 481 TGGCAACCCCGGAGAGGCTTTGAGATCTTCGAGACACCTTTGAAGGCAAAATCATATTC 540
Db 481 TGGCAACCCCGGAGAGGCTTTGAGATCTTCGAGACACCTTTGAAGGCAAAATCATATTC 540
QY 541 TGCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGAGAGAGCAAA 600
Db 541 TGCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGAGAGAGCAAA 600
QY 601 GTCAAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GTCAAGGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 TGGTGGAGAGCTTTCATGAGAGATCTGCGTCTTCAATCTTGGCTTGTGATCCCTGCTC 720
Db 661 TGGTGGAGAGCTTTCATGAGAGATCTGCGTCTTCAATCTTGGCTTGTGATCCCTGCTC 720
QY 721 ATCATCATCTGCTGCTACACCCCTGATGATCTGCGCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATCATCTGCTGCTACACCCCTGATGATCTGCGCTCAAGAGCGTCCGCTCTTCT 780
QY 781 GGCCTCCGAGAGAAAGATCGCAACCTCGTAGATGATGATGATGATGATGATGATGATG 840
Db 781 GGCCTCCGAGAGAAAGATCGCAACCTCGTAGATGATGATGATGATGATGATGATGATG 840
QY 841 GCGATCTTCGCTGCTGCTGAGAGCTCCATTCATTCATTCATTCATTCATTCATTCATTC 900
Db 841 GCGATCTTCGCTGCTGCTGAGAGCTCCATTCATTCATTCATTCATTCATTCATTCATTC 900
QY 901 AGCACTCCCAACAGAGAGCTGCTCTGCACTATTCCTGATGATGATGATGATGATGATG 960
Db 901 AGCACTCCCAACAGAGAGCTGCTCTGCACTATTCCTGATGATGATGATGATGATGATG 960
QY 961 ACCAAGTAGTACCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1020
Db 961 ACCAAGTAGTACCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1020
QY 1021 TTCCGGAGCTTCTGCTTCCAGTGAAGATGAGATGAGAGGAGAGAGAGAGAGAGAGAG 1080
Db 1021 TTCCGGAGCTTCTGCTTCCAGTGAAGATGAGATGAGAGGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CGAATATCAGTTTCAAGATCTGCTTACCTGAGGAGCATTCATGAGATGAGATGAGAT 1140
Db 1081 CGAATATCAGTTTCAAGATCTGCTTACCTGAGGAGCATTCATGAGATGAGATGAGAT 1140
QY 1141 TGA 1143
Db 1141 TGA 1143
RESULT 9
ID AAT92601 standard; cDNA; 1275 BP.
XX AAT92601;
XX
DT 14-APR-1998 (first entry)
XX
DE Human kappa opioid receptor prototype RASSL ORI DNA.
XX
XX Selective target cell activation; G protein-coupled receptor; RASSL;
KW gene therapy; cell proliferation; kappa opioid receptor; human;
KW transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model; ss.
XX
XX Homo sapiens.
OS Synthetic.

OS	Chimeric.
XX	
FH	Key
FT	sig_peptide
FT	/tag= a
FT	1..90
FT	/product= "prolactin signal sequence"
FT	91..1284
FT	/tag= b
FT	/product= "FLAG-modified KOR-HA fusion"
FT	702..787
FT	/tag= c
FT	/note= "delta opioid receptor sequence"
XX	
PN	M09735478-A1.
XX	
PD	02-OCT-1997.
XX	
PP	25-MAR-1997; 97WO-US005334.
PR	26-MAR-1996; 96US-00622348.
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Conklin BR;
XX	
KI	WPI; 1997-502739/46.
DR	P-PADB; AAM30299.
PT	Selective activation of target cell expressing modified G protein coupled
PT	receptor - allows control of cellular proliferation, especially for
PT	amplification of transfected cells in gene therapy.
XX	
XX	Example 1; Page 80-82; 117pp; English.
PS	
CC	This CDNA sequence encodes RASBL ORI (see AAM30299) a G protein-coupled
CC	receptor that is activated superiorly by synthetic ligands. ORI comprises
CC	human G protein-coupled kappa opioid receptor (KOR) (see also AAM30297)
CC	modified at 17 amino acid positions to contain the corresponding amino
CC	acid of the delta opioid receptor. The ORI polynucleotide was obtained by
CC	site-directed mutagenesis of native human KOR cDNA (see AAT90998) and
CC	includes flanking sequences that encode signal and epitope peptides to
CC	facilitate the detection and purification of recombinant ORI. A novel
CC	method for selectively activating a target cell (TC) comprises: (1)
CC	introducing into the cell a nucleic acid sequence (I) that expresses a
CC	RASBL (A) and (II) exposing the transfected cell to small synthetic
CC	molecules (B) that bind to and activate (A), inducing the G protein
CC	coupled cellular response associated with receptor activation. (A) has:
CC	(a) decreased binding affinity for a selected natural ligand of the
CC	native receptor; (b) binding affinity for (B); and (c) is activated by
CC	binding (B) sufficiently to produce the required cellular response. Also
CC	new are: transgenic cells including heterologous (I) in the genome;
CC	cellular implants comprising a TC transfected with (I); isolated (I); and
CC	transgenic animals expressing (A). Activation of (A) results, in vitro or
CC	in vivo, in cellular proliferation, or secretion of a cellular product,
CC	particularly a heterologous therapeutic protein encoded by a second
CC	inserted nucleic acid sequence. Particularly it is used to expand the
CC	relatively few cells that are successfully transfected during gene
CC	therapy procedures. Other responses that can be regulated are cell
CC	migration and contraction, or pigment production. In transgenic animals,
CC	expression or stimulation of (A) is designed to develop cardiac
CC	arrhythmia, symptoms of bone disease, seizures, vascular contractions,
CC	dementia, neurodegeneration etc., for use as models of these diseases
CC	(claimed). The transgenic animals are also used for production of
CC	improved food products (e.g. increased calcium content in eggshells or
CC	altered fat/lean ratios) or to control fertility or induce labour
XX	
SQ	Sequence 1275 BP; 266 A; 373 C; 318 G; 318 T; 0 U; 0 Other;
Query Match	86.7%; Score 1001; DB 2; Length 1275;
Best Local Similarity	93.1%; Pred. No. 8.5e-236;
Matches 1062; Conservative	0; Mismatches 70; Indels 9; Gaps 1

Db	113	TCGACTCCCCGATCCAGATCTTTCGCGGGGAGCCGGGCTTAACTGCGCCCGAGCGCT	172
QY	62	GCTGCCCCCAACAGCAGCCGCTGGTTCCTCCGGCTGGGCGGAGCCGACAGCAACGCA	121
Db	173	GCTGCCCCCAACAGCAGCCGCTGGTTCCTCCGGCTGGGCGGAGCCGACAGCAACGCA	232
QY	122	GCGCGGCTCGGAGGAGCGCGCAGCTGGAGCCCGGACATCTCCCCGGGCACTCCCGGTCA	181
Db	233	GCGCGGCTCGGAGGAGCGCGCAGCTGGAGCCCGGACATCTCCCCGGGCACTCCCGGTCA	292
QY	182	TCATCAGGGGGGTCTACTCCGAGTGTTCGTGTGGGCTGGTGGGCAACTGCTGGTCA	241
Db	293	TCATCAGGGGGGTCTACTCCGAGTGTTCGTGTGGGCTGGTGGGCAACTGCTGGTCA	352
QY	242	TGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAAC	301
Db	353	TGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAAC	412
QY	302	TGGCTTTGGCAGATGCTTTAGTACTACAAACATGCCCTTTCAAGTACGCTTACTTGA	361
Db	413	TGGCTTTGGCAGATGCTTTAGTACTACAAACATGCCCTTTCAAGTACGCTTACTTGA	472
QY	362	TGAATTCCTGGACCTTTGGGGATGCGTGTGCAGATGTAATTCATGTATCTTCA	421
Db	473	TGAATTCCTGGACCTTTGGGGATGCGTGTGTGCAGATGTAATTCATGTATCTTCA	532
QY	422	ACATGTTCCACAGCATCTTTCACCTTGCACATGATAGCGTGGACCGTACATTTGCCGT	481
Db	533	ACATGTTTACAGCATATTTACCTTGCACATGATAGTGGACCGTACATTTGCCGT	592
QY	482	GCCACCCCGTAAAGGCTTTGGAATTCGCGCACACCTTTAAGGCAAAGATCATATTTCT	541
Db	593	GCCACCCCGTAAAGGCTTTGGAATTTCCGAAACACCTTTAAGGCAAAGATCATCAATCTT	652
QY	542	GCATTCGGCTCTGTCTGCATCTGTGTGCATCTCTGAAATGTCTTGGAGGCCAACAAAG	601
Db	653	GCATTTGGCTACTGGCATCTATCTGTGTATATACGCATATGCTTGGAGGACCCAAAC	712
QY	602	TCAGGGAAGAGTGCATGTCATATTAAGTCTCTCTTCAGTCTCCAGATGATGTACTCTCT	661
Db	713	CCCGGGAATGAGAGCAAGTGTATGCAACGCTCCAGTTCGCCAGGCC-----CAGTGGT	763
QY	662	GATGGAGCTCTTCAATGAAGATCTGCGCTTCATCTTTGCTCTGTATCCTGTCTCTCA	721
Db	764	ACTGGGACACTGTGACCAAGATCTGCGCTTCATCTTTGCTCTGTATCCTGTCTCTCA	823
QY	722	TCATCATGTCTGTCTACACCTGTATGATCTTCCGCTCAAGAGCCTCCGGCTCTTTCTG	781
Db	824	TCATCATGTCTGTCTACACCTGTATGATCTTCCGCTCAAGAGCCTCCGGCTCTTTCTG	883
QY	782	GCTCCCGAGAAAGATGCAACCTGCGTAAAGATCACCAAGATGTCCTGCTGGTGGTGG	841
Db	884	GCTCCCGAGAAAGATGCAACCTGCGTAAAGATCACCAAGATGTCCTGCTGGTGGTGG	943
QY	842	CAGTCTTGCTGCTGTCTGAACTCCCATTCACATATTCATCTCGGTGAGAGCTCTGGGA	901
Db	944	CAGTCTTGCTGCTGTCTGAACTCCCATTCACATATTCATCTCGGTGAGAGCTCTGGGA	1001
QY	902	GCACTTCCCAACAGCAGCTGTCTCTCAAGTATTAATTCCTGCATTCGCTTAAGCTTAA	961
Db	1004	GCACTTCCCAACAGCAGCTGTCTCTCAAGTATTAATTCCTGCATTCGCTTAAGCTTAA	1061
QY	962	CCAAAGTAGGCTGAATCCCAATTCCTAAGCCTTTCTTGATGAATACTTCAAGCGGTGT	1021
Db	1064	CCAAAGTAGGCTGAATCCCAATTCCTAAGCCTTTCTTGATGAATACTTCAAGCGGTGT	1122
QY	1022	TCCGGAGCTTGTCTTTTCACTGAAGATGAGAGTAGAGCCGAGAGCACTAGCAAGTCC	1081
Db	1124	TCCGGAGCTTGTCTTTTCACTGAAGATGAGAGTAGAGCCGAGAGCACTAGCAAGTCC	1181
QY	1082	GAAATACGTTCCAGATCTGTCTTAACCTGAGGAGATGATGGATGAAATTAACCAATAT	1141

Db 1184 GAAATACAGTTCAGATCTGCTTACTGAGGAGCATGATGATGAATAAACAGATAG 1243
QY 1142 G 1142
Db 1244 G 1244

RESULT 10
AAV49254
ID AAV49254 standard; DNA; 1408 BP.
XX AAV49254;
AC AAV49254;
XX 28-OCT-1998 (first entry)
DT 28-OCT-1998 (first entry)
XX Mouse kappa opiate receptor gene.
DE Mouse kappa opiate receptor gene.
XX Mouse; kappa opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect; ds.
XX
OS Mus sp.
XX Key Location/Qualifiers
FH 184.1326
FT CDS /tag=a
FT /product="kappa opiate receptor"
FT
XX WO9802534-A2.
XX 22-JAN-1998.
XX PD 11-JUL-1997; 97WO-FR001282.
XX PF 15-JUL-1996; 96FR-00008810.
XX PR (CNRS) CENT NAT RECH SCI.
XX PA
XX Kieffer BL, Matches HMD, Simonin F, Dierich A, Lemeur M;
XX WPI; 1998-110582/10.
DR P-PSDB; AAM44939.
XX
XX Transgenic animals defective in one type of opioid receptor - used to
PT identify agents for treatment of pain, drug addiction and transplant
PT rejection, lacking side effects of known opiate(s).
XX
XX Disclosure; Fig 13; 58pp; French.
XX
XX This sequence represents the gene encoding the mouse kappa opiate
XX receptor protein. The sequence is used to generate a transgenic non-human
XX mammal for identifying agents for treating disorders associated with
XX opiate receptors. In the mammal, the expression of the gene encoding the
XX opiate receptor is modified, particularly by the deletion of an exon
XX and/or insertion of a marker gene, e.g. the neomycin resistance gene,
XX into the sequence. Especially the expression of the gene is altered in
XX nervous tissue. The agents are potentially useful for treating severe
XX pain (chronic or acute), drug addiction and/or prevention or treatment of
XX transplant rejection (as immunosuppressants). The method may isolate and
XX identify powerful analgesics that lack morphine-like side effects
XX

Sequence 1408 BP; 322 A; 359 C; 336 G; 391 T; 0 U; 0 Other;
Query Match 78.9%; Score 910.8; DB 2; Length 1408;
Best Local Similarity 86.8%; Pred. No. 1.3e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGGATCCAGATCTCCGCGGAGACCGGCGCTTACTGCGCCCGAGCGCC 60
Db 184 ATGAGTCCCGCATTCAGATCTTCGAGAGATCCAGGCGCTTACTGCTGCCAGTCT 243
QY 61 TGCTGCGCCCAACAGAGCGCTGTTTCCCGGCTGGCGGAGCCGAGCAAGCAACGCG 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 244 TGCTTTCGCCAACAGACGCTTGTGTTCCCACTGGGAGATCCGACGATATGGC 303
QY 121 AGCGCGGCTCGGAGAGAGCGCAGTGGAGCGCCGCGCAGCATCTCCCGGCGCATCCGGTC 180
Db 304 AGTGGGAGCTGAGAGATCAGCAGCTGGAGTCCGCGCAGATCTCCGCGCATCTCTTT 363
QY 181 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGAGGCTTGTGGGCAACTCGCTGCTC 240
Db 364 ATCATCAGCGGCTTACTCTGTGTATTTGTGTGGCTTAGTGGGCAATCTCTGCTC 423
QY 241 ATGTTGATCATTCGATACACAAAGTGAAGACAGCAACCAATTCATATTTTAA 300
Db 424 ATGTTGATCATTCGATACACAAAGTGAAGACAGCAACCAATTCATATTTTAA 483
QY 301 CTGGCTTGGAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGCTACTTG 360
Db 484 CTGGCTTGGAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGCTACTTG 543
QY 361 ATGAATTCCTGGCCCTTTGGGATGTGCTGCAAGATAGTAATTTCCATGATTTACTAC 420
Db 544 ATGAATTCCTGGCCCTTTGGGATGTGCTGCAAGATAGTAATTTCCATGATTTACTAC 603
QY 421 AACATGTTACACAGCATCTTACCTTGACCATGATGAGCGTGAACCGCTACATTTGCGTG 480
Db 604 AACATGTTACACAGCATATTCACCTTGACCATGATGAGTGGACCGCTACATTTGCGTG 663
QY 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGACACACCTTTGAAGGCAAGATCATATATC 540
Db 664 TGCCACCCCGTGAAGGCTTTGAGCTTCGACACACCTTTGAAGGCAAGATCATATATC 723
QY 541 TGCAATGCGCTGCTGTGCTGATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAAA 600
Db 724 TGCAATGCGCTGCTGTGCTGATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAAA 783
QY 601 GTCAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 784 GTCAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843
QY 661 TGTGAGGACCTTTCATGAGATGCTGCGCTTTCATCTTGGCTTCGAGATCCGCTGCTC 720
Db 844 TGTGAGGACCTTTCATGAGATGCTGCGCTTTCATCTTGGCTTCGAGATCCGCTGCTC 903
QY 721 ATCATCATGCTCTGCTACACCCCTGATGATCCGTGCTCAAGAGCTCCGCTCTTCT 780
Db 904 ATCATCATGCTCTGCTACACCCCTGATGATCCGTGCTCAAGAGCTCCGCTCTGCT 963
QY 781 GGCCTCCGAGAAAGATGCGAAGCTGATGATGATGATGATGATGATGATGATGATGAT 840
Db 964 GGCCTCCGAGAAAGATGCGAAGCTGATGATGATGATGATGATGATGATGATGATGAT 1023
QY 841 GCAATCTTTCGCTGCTGATCTCCCATTCATTCATTCCTGCTGAGGCTCTGGGG 900
Db 1024 GCAATCTTTCATCTGCTGATCTCCCATTCATTCATTCCTGCTGAGGCTCTGGGA 1083
QY 901 AGCAGCTCCCAACAGAGCTGCTCTCCAGCTATTACTTCTGATGCTTGGGCTAT 960
Db 1084 AGCAGCTCCCAACAGAGCTGCTCTCCAGCTATTACTTCTGATGCTTGGGCTAT 1143
QY 961 ACCAAGATAGCTGAATTCCTATTCAGCCCTTTTGTATGAAAACTTCAAGCGGTGT 1020
Db 1144 ACCAAGATAGCTGAATTCCTATTCAGCCCTTTTGTATGAAAACTTCAAGCGGTGT 1203
QY 1021 TTCGGGACTTTCCTTTCATGAAATGAGATGAGAGCGGCGAGACCTAGAGAGTC 1080
Db 1204 TTTTGGGACTTTCCTTTCATGAAATGAGATGAGAGCGGCGAGACCAATAGAGTT 1263
QY 1081 CGAATATCAAGTTCAGATTCGCTTACCTGAGGAGCATGATGAGATGAAATTAACAGATA 1140
Db 1264 AGAATCAAGTTCAGATTCGCTTACCTGAGGAGCATGATGAGATGAAATTAACAGATA 1323
QY 1141 TGAATAGTGTGA 1154
Db 1324 TGAATAGTGTGA 1337

RESULT 11
AA075926 standard; DNA, 1410 BP.
AA075926;
25-MAR-2003 (revised)
17-AUG-1995 (first entry)
Mouse kappa opioid receptor MOR1 cDNA.
Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
truncate; chimeric; assay; probe; ss.
Mus musculus.
Key Location/Qualifiers
FT CDS 186..1328
FT /tag= a
FT /product= "mouse kappa opioid receptor"
MO9428132-A2.
08-DEC-1994.
20-MAY-1994; 94MO-US005747.
20-MAY-1993; 93US-00066296.
30-JUL-1993; 93US-00100694.
05-NOV-1993; 93US-00147592.
(ARCH-) ARCH DEV CORP.
Bell GI, Retsine T, Yeauda K;
WPI; 1995-022804/03.
P-PSDB; AAR67669.
Polynucleotides and peptides derived from opioid receptor polypeptides -
for use in therapeutic compositions and in screening assays for useful
drug substances.
Claim 10; Page 207-211; 300bp; English.
The nucleotide sequence of the novel mouse kappa opioid receptor gene
MOR1. The gene was isolated from a mouse brain cDNA library using a
fragment (amplified from the cDNA library with primers AA075929-30) as a
probe. The primers are based on the conserved sequences present in the
second and third transmembrane domains of somatostatin (SRI) receptor
subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb part fragment from the mouse
kappa opioid receptor clone, lambda mal-1, was subcloned into the CMV
promoter-based expression vector pCMV-6b. The resultant construct pCMV-
mal-1 was transfected into COS-1 cells for protein production. The gene
encoding the opioid receptor can be used to produce complete, truncated
or chimeric opioid receptor proteins. The opioid receptors thus produced
are useful for the development of novel assays designed to select or
improve substances, capable of interacting with the opioid receptor
proteins, for use in diagnosis, drug design and therapeutic applications.
(Updated on 25-MAR-2003 to correct FN field.)
Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T; 0 U; 0 Other;
Query Match 78.9%; Score 910.8; DB 2; Length 1410;
Best Local Similarity 86.8%; Pred No. 1.3e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCCGATCCAGATCTTCCGCGGAGACCGGCGCTACCTGCGCCCCGAGCGCC 60
DB 186 ATGAGTCCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCAGTGTCT 245

QY 61 TGCCTGCCCCCAACAGACGCGCTGTGTTTCCCGGCTGGGCGGACCGGACAGAACGCGC 120
DB 246 TGCCTTCTCCCAACAGACGCTGTGTTTCCCAACTGGGCGGAATCCGACGTATATGGC 305
QY 121 AGCGCGGCTGGAGAGACGCGACGCTGAGAGCCCGGCAATCTCCCGGCAATCCGGTTC 180
DB 306 AGTGTGGGCTCAGAGATCAGACGCTGAGAGTCCGGCGCAATCTCTCCGCGCAATCCCTGTT 365
QY 181 ATCATCAGCGGCTTACTCCGTAGTGTTCGTCGCGGGCTGGTGGGCGCAATCCGCTGCTC 240
DB 366 ATCATCAGCGGCTTACTCCGTAGTGTTCGTCGCGGGCTGGTGGGCGCAATCCGCTGCTC 425
QY 241 ATGTTGATCATCCGATACACAAAGATGAGAGAGAACCAACATTATTAATTTAAC 300
DB 426 ATGTTGATCATCCGATACACAAAGATGAGAGAGAACCAACATTATTAATTTAAC 485
QY 301 CTGGCTTTGGCAGATGCTTTAGTTAATAACCAATGCGCTTTCAGAGTACGCTTACTTG 360
DB 486 CTGGCTTTGGCAGATGCTTTAGTTAATAACCAATGCGCTTTCAGAGTACGCTTACTTG 545
QY 361 ATGAATTCGCGCTTTGGGAGATGCTGTCGCAAGATGATTAATTTCAATTAATAC 420
DB 546 ATGAATTCGCGCTTTGGGAGATGCTGTCGCAAGATGATTAATTTCAATTAATAC 605
QY 421 AACATGTTCAACGAGATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTG 480
DB 606 AACATGTTCAACGAGATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTG 665
QY 481 TGCACCCCGTGAAGGCTTTGGACTTTCGCAACCCCTTGAAGGCAAGATCATCAATATC 540
DB 666 TGCACCCCGTGAAGGCTTTGGACTTTCGCAACCCCTTGAAGGCAAGATCATCAATATC 725
QY 541 TGCATCTGGCTGCTGCTGATCTGTTGGACATCTCTGCAATGCTCTTGGAGGCAACAA 600
DB 726 TGCATCTGGCTGCTGCTGATCTGTTGGACATCTCTGCAATGCTCTTGGAGGCAACAA 785
QY 601 GTCAGAGAAAGCGTGCATGTCATGATGCTGCTTGCAGATGATGATGATGATGATGATG 660
DB 786 GTCAGAGAAAGCGTGCATGTCATGATGCTGCTTGCAGATGATGATGATGATGATGATG 845
QY 661 TGGTGGGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTCCTTCGTCGATTCCTGCTCT 720
DB 846 TGGTGGGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTCCTTCGTCGATTCCTGCTCT 905
QY 721 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTTCAGAGCGCTCGGCTCTTCT 780
DB 906 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTTCAGAGCGCTCGGCTCTTCT 965
QY 781 GGCCTCCGAGAAAGATCGCAACCTGGTGGATGATGATGATGATGATGATGATGATGATG 840
DB 966 GGCCTCCGAGAAAGATCGCAACCTGGTGGATGATGATGATGATGATGATGATGATGATG 1025
QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 1026 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
QY 901 AGCACTTCCACAGACAGCTGCTTCTTCACGCTTACCTTTCATGCTGCTTTCATGCTT 960
DB 1086 AGCACTTCCACAGACAGCTGCTTCTTCACGCTTACCTTTCATGCTGCTTTCATGCTT 1145
QY 961 ACCAAGATGAGCTGAATCCCATCTCTACGCTTCTTGAAGAAACCTTCAAGGGGTGT 1020
DB 1146 ACCAAGATGAGCTGAATCCCATCTCTACGCTTCTTGAAGAAACCTTCAAGGGGTGT 1205
QY 1021 TTCCGGAGCTTCTGCTTTCACCTGAAGATGAGATGAGCGGACAGACCTAGCAGATGC 1080
DB 1206 TTCCGGAGCTTCTGCTTTCACCTGAAGATGAGATGAGCGGACAGACCTAGCAGATGC 1265
QY 1081 CGAAATTAAGATGAGATGCTGCTTACCTGAGGAGCATGATGAGATTAATTAACAGTA 1140
DB 1266 AGAAACACAGATGAGATGCTGCTTACCTGAGGAGCATGATGAGATTAATTAACAGTA 1325
QY 1141 TGACTAGTGTGGA 1154

Db 1326 TGACTAGTCGTGA 1339

RESULT 12

AA086725
ID AA086725 standard; cDNA; 2481 BP.

AC AA086725;

DT 01-DEC-1995 (first entry)

DE Mammalian kappa opioid receptor protein cDNA.

KM Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.

OS Rattus rattus.

Key Location/Qualifiers

FT CDS 111..1253

FT /tag= a

FT /product= "kappa opioid receptor"

PN JP07070191-A.

PD 14-MAR-1995.

PF 30-JUL-1993; 93JP-00190261.

PR 09-JUL-1993; 93JP-00170591.

PA (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1995-144857/19.

DR P-PsDB; AAR72591.

PT Kappa opioid receptor protein and cells expressing it - useful for the screening of compounds for analgesic and hypnotic properties.

PS Claim 2; Page 9-10; 15pp; Japanese.

XX The nucleotide sequence of the novel mammalian kappa opioid receptor cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA by reverse transcriptase-PCR (RT-PCR) using primers AA086726-7 derived from the mouse delta opioid receptor gene. This fragment was cloned into the plasmid pCR11 to produce pR11. The plasmid pR11 was used to probe a rat brain DNA library in lambda ZAPII to obtain a clone of the rat kappa opioid receptor gene, designated pKOPR2. This clone was introduced into E.coli JM109 for production of the receptor protein. The receptor protein is useful for screening of analgesic and hypnotic compounds including peptides and proteins

XX Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T; 0 U; 0 Other;

Query Match 78.9%; Score 910.8; DB 2; Length 2481;

Best Local Similarity 86.8%; Pred. No. 1.6e-213; Indels 0; Gaps 0;

Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGGATCCAGATCTTCCGCGGAGACCGGCGCTTACCTGCGCCCGAGCGCC 60

Db 111 ATGAGTCCCGCATCATGATTTTCCGCGGAGAGCGGCGCTTACCTGCGCTCCAGTGTCT 170

QY 61 TGCCTGCCCCCAAGACGAGCGCTGTTTCCCGGCTGGGCGGAGCCGACGACGAAAGGC 120

Db 171 TGCCTACTCCCAACAGACGCTCTTGTTTCCCAACTGGGCGGAATCGGACGCAATGCG 230

QY 121 AGCGCGGCTGGAGAGCGGAGCTGGAGCGGCGGACATCTCCCGGCGATCCCGGCTC 180

Db 231 AGTTGGGCTCCGAGAGACGAGCTGGAGCGGCGGACATCTTCCAGCCATCCCTGTT 290

QY 181 ATCATCAGGCGGTCTACTCCGTAGTGTCTGCTGGGCTTGGGAGCAATCGCTGTCTC 240

Db 291 ATCATCAGGCGGTCTACTCCGTAGTGTCTGCTGGGCTTGGGAGCAATCCGTGTCTC 350

QY 241 ATGTTGATCATCCGATACCAAGATGAAGACAGACCAACCATTTATATTTTAAAC 300

Db 351 ATGTTGATCATCCGATACCAAGATGAAGACAGACCAACCATTTATATTTTAAAC 410

QY 301 CTGGCTTTGGAGATGCTTTAGTTACTCAACCATGCGCTTCAAGATACGGTCTACTTG 360

Db 411 CTGGCTTTGGAGATGCTTTAGTTACTCAACCATGCGCTTCAAGATACGGTCTACTTG 470

QY 361 ATGAATTCCTGGCTTTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTGATTAAC 420

Db 471 ATGAATTCCTGGCTTTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTGATTAAC 530

QY 421 AACATGTTCAACAGATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATGTCGCTG 480

Db 531 AACATGTTCAACAGATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATGTCGCTG 590

QY 481 TGCCACCCCGTGAAGGCTTTGGAAGCTTCCGACACCCCTTGAAGGCAAGATCATATATC 540

Db 591 TGCCACCCCGTGAAGGCTTTGGAAGCTTCCGACACCCCTTGAAGGCAAGATCATATATC 650

QY 541 TGCACTTGGCTGCTGTCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600

Db 651 TGCACTTGGCTGCTGTCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 710

QY 601 GTCAAGGGAAGAGTGTGATGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATG 660

Db 711 GTCAAGGGAAGAGTGTGATGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATG 770

QY 661 TGTGGGAGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

Db 771 TGTGGGAGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 830

QY 721 ATCATCATCTGTCTGATACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 780

Db 831 ATCATCATCTGTCTGATACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 890

QY 781 GGCCTCCGAGGAAAGATGCAACCTGGTGAATGATGATGATGATGATGATGATGATGATG 840

Db 891 GGCCTCCGAGGAAAGATGCAACCTGGTGAATGATGATGATGATGATGATGATGATGATG 950

QY 841 GCAGTCTTCTGTCTGTGACTCCCATTTTCAATATTCATCTGTGAGAGCTCTGAGG 900

Db 951 GCAGTCTTCTGTCTGTGACTCCCATTTTCAATATTCATCTGTGAGAGCTCTGAGG 1010

QY 901 AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGATGATGATGATGATG 960

Db 1011 AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGATGATGATGATGATG 1070

QY 961 ACCAAGATGAGCTGAATCCCATTTCTTAAGGCTTTCTTAAGGCTTTCTTAAGGCTTTCT 1020

Db 1071 ACCAAGATGAGCTGAATCCCATTTCTTAAGGCTTTCTTAAGGCTTTCTTAAGGCTTTCT 1130

QY 1021 TTCCGGGACTTCTGTCTTCACTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1080

Db 1131 TTTCGGGACTTCTGTCTTCACTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1190

QY 1081 CGAAATATCATGTTCAAGATCTGCTTCACTGAGGAGATGATGAGATGATGATGATGATG 1140

Db 1191 AGAAACACAGTTCAAGATCTGCTTCACTGAGGAGATGATGAGATGATGATGATGATG 1250

QY 1141 TGACTAGTCGTGA 1154

Db 1251 TGACTAGTCGTGA 1264

RESULT 13

AA075931

ID AA075931 standard; DNA; 1000 BP.

XX AA075931;

XX


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FT      /transl_except= (pos: 169, .171, aa: Pro)
FT      /transl_except= (pos: 232, .234, aa: Gly)
XX      US6225080-B1.
XX      PD
XX      PD 01-MAY-2001.
XX      PF 28-APR-1995; 95US-00430286.
XX      PR 23-MAR-1992; 92US-00855286.
XX      PR 26-FEB-1993; 93US-00026140.
XX      PR 11-JUN-1993; 93US-00075447.
XX      PA (UHLG/) UHL G. R.
XX      PA (EPPL/) EPLER C. M.
XX      PA (WANG/) WANG J.
XX      PI Uhl GR, Epller CM, Wang J;
XX      DR WPI; 2001-342395/36.
XX      DR P-PSDB; AAB68440.
XX      PT Novel isolated DNA encoding mu-subtype opioid receptor protein which is
XX      PT useful for identifying other receptor subtypes, screening for mu opioid
XX      PT ligands and for understanding mechanisms of opioid action.
XX      PS Claim 1; Col 17-20; 51pp; English.
XX      CC The present sequence encodes a rat mu-subtype opioid receptor. The
XX      CC polynucleotide sequence is useful for producing a mu-type opioid receptor
XX      CC by standard recombinant techniques. The encoded protein is useful for
XX      CC producing monoclonal or polyclonal anti-receptor antibodies and to
XX      CC identify patterns of post-translational modifications and to elucidate
XX      CC associated G proteins. Mu receptor polynucleotides and polypeptides are
XX      CC useful in identifying other receptor subtypes, in screening for new
XX      CC opioid ligands and for understanding mechanisms of opioid action e.g.,
XX      CC drug addiction
XX      SQ Sequence 2135 BP, 541 A, 590 C, 441 G, 563 T, 0 U; 0 Other;

Query Match      38.8%; Score 448; DB 5; Length 2135;
Best Local Similarity 67.0%; Pred. No. 8.1e-100;
Matches 669; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

QY      110 ACAGCAACGCGACCGCGCTCGAGAGACCGCAGCTGAGACCGCGGCACATCTCCCGG 169
DB      167 ACCGCAACCGGCGCTTGGCGGAGACAGACCTGTGACCTCAGACCGGACCGCTTCATG 226
QY      170 CCATCCCGGTCATCATCAGCGCGGTCTACTCCGTAGTGTTCGTGCGGCGCTTGGTGGCA 229
DB      227 TCACAGCATTTACATCATGCGCCTCTACTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTG 286
QY      230 ACTCGGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 289
DB      287 ACTTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
QY      290 ACATATTATTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 349
DB      347 ACATTTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
QY      350 CGGTCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 409
DB      407 TCACATCTACCTGAGGAGCAATGCGCCTTGGGAACATCTCTGTCAAGATGTGATCTCA 466
QY      410 TTGATTACTACCAATGTTCACACGATCTTCACTTGAACCATGATGAGGTGACCGCT 469
DB      467 TAGATTACTACCAATGTTCACACGATTTCAACCTCTGTCAACATGAGGTGACCGCT 526
QY      470 ACATTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
DB      527 ACATTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 586
QY      530 TCATCAATATCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589

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DB      587 TCGTCAACGTCTGCAATGTGATCTCTCTCTGTGCACTGCGCTGTGATGTTCATGG 646
QY      590 GAGGCAACCAAGTACGAGGAAGACGTGCATGTCTATTGATGTCTCTTGACATGCCAATG 649
DB      647 CAACCAACAAATATACAGCAGGCGGTC-----CATGATGTGACCTTCACTTCCACC 700
QY      650 ATGACTACTCTCTGTGTGGGACCTCTTTCATGAAATCTGCTGTTCATCTTTCCTTGTGA 709
DB      701 CAACCTGTACTGTGAGAACTGTCTC---AAATCTGTGTCTTATCTTGTGCTTTCATCA 757
QY      710 TCCTGTCTCATCATCATCATGTCTGTCTTACACCTGTGATGTCTGTCTTCAAGCGCTCC 769
DB      758 TGCGGTCTCATCATCATCATGTCTGTCTTACGCGCTGTGATGTCTTCACTCAAGCGCTTC 817
QY      770 GGTCTCTTTTGTGTCTCCGAGAGAAATGTCCAACTCGGTGAGATCACCAAGCTGTGTC 829
DB      818 GCATGCTATCGGGCTCCAAAGAAAGACAGAAATCTGTGCGAGATCACCGGATGTGTG 877
QY      830 TGTGTGTGTGTGGAGTCTGTCTGTGTGTGACTCCCATTTACATATTCATCTGTGTG 889
DB      878 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
QY      890 AGGCTTGTGGAGACCTTCCACAGCACAGCTGTCTTCCAGCTATTTACTTGTGCATG 949
DB      938 AAGGCTGATCAGATTCAGAAACCAATTTACAGACCGTTCTGTGGACATTTGTGCATG 997
QY      950 CCTTAGGCTATACCAACAGTATGCGTGAATCCCATTTCTAGCGCTTCTTATGAAAAC 1009
DB      998 CTTGTGGTATACCAACAGTATGCGTGAATCCCATTTCTTATGCGCTTCTGTGATGAAAAC 1057
QY      1010 TCAAGCGGTGTGTTCGCGGACTTGTCTTTCATCTGAAGATGAGATGAGGCGGACAGCA 1069
DB      1058 TCAAGCATGTCTTACAGAGATTTGTGATCCCACTGTGTCCAGATGAAAGAAAAC 1117
QY      1070 CTAGCAAGTCCGAATATCAAGTTACAGATCTCTGTAC 1107
DB      1118 CCATCGAGTCCGTTCAGAACTAGGGAACATCCCTCC 1155

RESULT 15
AA089222
ID      AA089222 standard; cDNA, 1618 BP.
XX
XX      AA089222;
AC      25-MAR-2003 (revised)
DT      20-OCT-1995 (first entry)
XX
XX      Rat mu opioid receptor cDNA.
DE      Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
XX
XX      Rattus sp.
OS
XX
XX      Key Location/Qualifiers
FH      CDS 214..1410
FT      /*tag= a
XX
XX      WO9507983-A1.
PD      23-MAR-1995.
XX
XX      PF 13-SEP-1994; 94WO-US010358.
XX
XX      PR 13-SEP-1993; 93US-00120601.
XX
XX      PA (INDV ) UNIV INDIANA FOUND.
XX
XX      PI Yu L;
XX
XX      WPI; 1995-131351/17.
DR      P-PSDB; AAR71964.

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XX New nucleic acid encoding new human mu opioid receptor - and related
PT vectors, transformed cells, antibodies etc., useful in diagnosis.
PT treatment and drug screening.

XX Disclosure: Page 190-194; 266pp; English.

XX A 365 bp fragment of the mouse delta opioid receptor was used to screen a
CC rat brain cDNA library under low stringency conditions. One positive
CC clone included the sequence given in AA089222, encoding a mu opioid
CC receptor, MOR-1 (AAR71964). MOR-1 was stably expressed in transfected CHO
CC cells. (Updated on 25-MAR-2003 to correct FN field.)
XX

SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 U; 0 Other;

Query Match 38.7%; Score 446.4; DB 2; Length 1618;

Best Local Similarity 66.9%; Pred. No. 1.8e-99;

Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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QY 110 ACAGCAAGCGGCGCGCTCGGAGACGCGCAGCTGAGACCGCGCAGCATCTCCCGG 169
DB 350 ACCGACCGGGCTTGGCGGAAAGACAGCTGTGCTCAGACCGGACGCTTCCATGG 409
QY 170 CCATCCCGGTATCATCAAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGTGGCA 229
DB 410 TCACAGCATTAACATCATAGGCGCTTACTCTATGTGTGTATGTGGGCTTTCGAA 469
QY 230 ACTCGCTGTATGTTCTGTATCATCCATACACAAAGATGAAAGACAGCAACCATTT 289
DB 470 ACTTCTGTGTATGTATGTATGTATGATACACAAATGAAAGCTGCACCAATCT 529
QY 290 ACATTTTAACCTGGCTTGGAGATGCTTATGATTAACAAACCATGCTTTCAGATTA 349
DB 530 ACATTTTAACCTGTCTGCGAGAGCGCTTACGACACGATACACTGCGCTTTCAGATG 589
QY 350 CGGTCTACTGTATGATTCCTGCGCTTGTGGGATGTCTGTGCAAGATAGTATTTCCA 409
DB 590 TCACTACTGATGAGGAACATGCGCTTTCGAAACATCTCTGCAAGATGATGATCTCA 649
QY 410 TTGATTAACAAATGTTCAACGACATCTTCACTTCAACATGATGAGCGTCA 469
DB 650 TAGATTAACAAATGTTCAACGACATTTCACTTCAACATGATGAGCGTCA 709
QY 470 ACATTTGCGGTGCGACCGCGTGAAGGCTTGGACTTCCGACACCTTTGAAGGCAAGA 529
DB 710 ACATTTGCGGTGCGACCGCGTGAAGGCTTGGACTTCCGACACCTTTGAAGGCAAGA 529
QY 470 ACATTTGCGGTGCGACCGCGTGAAGGCTTGGACTTCCGACACCTTTGAAGGCAAGA 529
DB 710 ACATTTGCGGTGCGACCGCGTGAAGGCTTGGACTTCCGACACCTTTGAAGGCAAGA 529
QY 530 TCATCAATATCTGCACTGCGCTGTGTGTATCTGTTGGACATCTCTGCAATAGCTTGG 589
DB 770 TCGTCAAGCTGTGCACTGAGATCTCTCTTCTGCAATGAGTGTGCTGTAATGTTCAATG 829
QY 590 GAGGACCAAAAGTACGAGGAAGCGTGTATGATGATGATGATGATGATGATGATGATG 649
DB 830 CAACCAAAATTAACGAGGAGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 883
QY 650 ATGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 709
DB 884 CAACCTGTACTGAGGAGAACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940
QY 710 TCCCTGCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769
DB 941 TCCCATCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1000
QY 770 GAGCTCTTCTGAGCTCCGAGAGAAAGATTCGCAACCTGCGATGATGATGATGATGAT 829
DB 1001 GCATCTATTCGAGGCTCCAAAGAAAGAGACAGGAATCTGGGAGATGATGATGATGAT 1060
QY 830 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
DB 1061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
QY 890 AGGCTCTGGGAGCACTCCGACAGACAGCTGTCTCTCCAGCATTAATCTTCTGATCG 949

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DB 1121 AAGCGTGTATCATGATTCAGAAACCATATTTACAGACCGTTCCTGCACTTCTGATTC 1180
QY 950 CCTTAGGCTATACCAACAGTAGCTGATTCATTCATTCATTCATTCATTCATTCATTCAT 1009
DB 1181 CTTTGGGTTTACACGAAAGCTGCTGAAATCCAGTCTTTTACCGCTTCTGATGAAACT 1240
QY 1010 TCAAGCGGTGTTTCCGAGACTTCTGCTTTCACACTGAAGATGAGATGAGCGGAGAGCA 1069
DB 1241 TCAGCGATGCTTTCAGAGAGTTTTCATTCCTCAACTCTGTCACGATCGAAGCAAACT 1300
QY 1070 CTAGCAGATCGGAATACAGTTTCAGATCTGCTTAC 1107
DB 1301 CCACTCGAGTCCGTCAGAAACACTAGGAAACATCCCTCC 1338

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RESULT 16

AA089223

ID AA089223 standard; cDNA; 1618 BP.

XX AA089223;

XX AC 25-MAR-2003 (revised)

XX DT 20-OCT-1995 (first entry)

XX XX

XX DE Transcription regulatory protein cDNA.

XX KM Mu opioid receptor; MOR-1; gene therapy; diagnostic;

XX KW transcription regulatory protein; ss.

XX OS Rattus sp.

XX XX

XX FH Key

XX FT CDS location/Qualifiers

XX FT CDS 339..1235

XX FT /*tag= a

XX PN MO9507983-A1.

XX PD 23-MAR-1995.

XX PF 13-SEP-1994; 94WO-US010358.

XX PR 13-SEP-1993; 93US-00120601.

XX PA (INDV) UNIV INDIANA FOUND.

XX PI Yu L;

XX DR MPI; 1995-131351/17.

XX DR P-P8DB; AAR71965.

XX PT New nucleic acid encoding new human mu opioid receptor - and related

XX PT vectors, transformed cells, antibodies etc., useful in diagnosis,

XX PT treatment and drug screening.

XX PS Disclosure: Page 199-203; 266pp; English.

XX CC A 365 bp fragment of the mouse delta opioid receptor was used to screen a

XX CC rat brain cDNA library under low stringency conditions. One positive

XX CC clone included the sequence given in AA089222, encoding a mu opioid

XX CC receptor, MOR-1 (AAR71964). Sequence analysis revealed an alternative

XX CC reading frame (AA089223) encoding a zinc finger-containing transcrip

XX CC tional protein (AAR71965). (Updated on 25-MAR-2003 to correct FN

XX CC field.)

XX SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 U; 0 Other;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

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XX

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XX

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XX

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QY 110 ACAGCAAGCGGCGCGCTCGGAGACGCGCAGCTGAGACCGCGCAGCATCTCCCGG 169
DB 350 ACCGACCGGGCTTGGCGGAAAGACAGCTGTGCTCAGACCGGACGCTTCCATGG 409

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QY 170 CCATCCGGTATCATCAGGCGGCTTACTCCGATGTTGCTGCTGGCTTGGTGGCA 229
Db 410 TCACAGCATTCATCATATGCCCCCTTACTATCGTGTGTGTGTGGCCCTCTTGGAA 469
QY 230 ACTGCGTGTATGTTGCTGATTCATCCGATACACAAAGATGAAGACAGCAACCAATTT 289
Db 470 ACTTCCTGGTATGATGTGATGTGATGATACCAAAATAGAGCTGCCACCAACATCT 529
QY 290 ACATATTTAACCTGGCTTGGCAAGATGCTTTAGTTACTACAAACATGCTTTTCAAGATA 349
Db 530 ACATTTTAACTCTGCTGCGACAGCGCTTACGACACAGTACACTGCTTTCAAGATG 589
QY 350 CGGTCTACTGATGAATTCCTGGCCCTTTTGGGAGATGCTGTGCAAGATGATTAATTTCA 409
Db 590 TCAACTTACTGATGGGAACATGGCCCTTCGGAACCATCTCTGCAAGATGCTGATCTCA 649
QY 410 TTGATTACTACAACTGTTTCCAGACATCTTCACTTACATGATGATGAGCGTGAACGCT 469
Db 650 TAGATTACTACAACTGTTTCCAGACATCTTCACTTACATGATGATGAGCGTGAACGCT 709
QY 470 ACATTGCGGTGTCACCCCGTGAAGGCTTGGACTTCCGACACCTTTGAAGCAAGA 529
Db 710 ACATTGCTGTCTGCCACCCAGTCAAGCCCTGGAATTCCTGATCCCGGAATGCAAAA 769
QY 530 TCATCAATATCTGATCTGGCTGTGCTGCTCATCTGTTGGCATCTTGCATATGCTCTTG 589
Db 770 TCGTCAGCTGCAACTGAGTCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
QY 590 GAGGACCAAAATCAGGGAAGACGTGATGTCATTTGAGTGTCTTGGACCTTCCAGATG 649
Db 830 CAACACAAATAACAGGAGGAGGCTC-----CATGATTTGACCTTCACTTCTCCAC 883
QY 650 ATGACTACTCTCTGTGGGACCTTCTTCAATGATGATGCTGCTTCAATCTTTGCTTGTGA 709
Db 884 CAACCTGGTACTGGGAGAACTGTCTC---AAATCTGTGTCTTATCTTCTGCTTATCA 940
QY 710 TCCCTGTCTCATCATCATCTGTCTGTACACCTGATATCTCTGGCTTCAAGAGGCTC 769
Db 941 TCCCATCTCTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1000
QY 770 GGTCTCTTCTGTGCTCCGAGAGAAAGATCGCAACTCGTGTGATGATCAACGACTGTCTC 829
Db 1001 GATGCTATCGGCTCTCAAGAAAGAGAGAGATCTGGGAGGATCAACCGGATGTGTC 1060
QY 830 TGGTGTGTGTCAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
Db 1061 TGGTGTGTGTCAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
QY 890 AGGCTTGGGAGACCTCCCAAGACAGCTGTCTTCAAGCTATTAATCTTGTGATCG 949
Db 1121 AAGCGTGTATCAAGATTCAGAAACCAATTCAGACCGTTTCTGTGGCACTTCTGATGG 1180
QY 950 CCTTAGCTATATCAACAGTAGCTGATATCCCATTTCTTACAGCTTCTTGTGAAACT 1009
Db 1181 CTTTGGTATACAGAACAGCTGTGATATCCAGTTCTTACGCTTCTTGTGATGAAACT 1240
QY 1010 TCAAGCGTGTTCGGGACTTCTGTCTTCTCACTGAAGATGAGATGAGCGGAGAGA 1069
Db 1241 TCAAGCGATGCTTCAAGAGATCTGTGATCCCAACTGTGTCAAGATGAAACGAAACT 1300
QY 1070 CTAGAGAGATCGGAAATACAGTTCAAGATCTGCTTAC 1107
Db 1301 CCACTGAGTCTGTGAGAACACTAGGAAATCTCTCC 1338

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RESULT 17
ID AAAS9499
XX AAAS9499 standard; cDNA; 1618 BP.
AC AAAS9499;
XX
DT 14-NOV-2000 (first entry)

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XX cDNA encoding a mu opioid receptor polypeptide.
DE
XX
XX mu opioid receptor; transcription regulatory polypeptide;
KM opioid receptor-like polypeptide; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 214..1410
XX FT /*tag= a
XX FT /product= "mu opioid receptor (AAB07864)"
XX FT 339..1235
XX FT /*tag= b
XX FT /note= "alternative reading frame which encodes a
XX polypeptide (AAB07865) with a zinc finger motif"
XX
XX US6103492-A.
XX
XX 15-AUG-2000.
XX
XX 07-JUL-1997; 97US-00889108.
XX
XX 08-MAR-1993; 93US-00056886.
XX PR 13-SEP-1993; 93US-00120601.
XX PR 13-SEP-1994; 94US-00305518.
XX
XX (INDV ) UNIV INDIANA.
XX
XX Yu L;
XX
XX MPI; 2000-542550/49.
XX P-PSDB; AAB07864, AAB07865.
XX
XX Novel nucleic acids encoding mu opioid receptor for expressing large
XX quantities opioid receptors which are useful for screening and evaluating
XX subtype-selective drugs and as probes or primers.
XX
XX Example 1; Col 89-92; 86pp; English.
XX
XX The present sequence encodes a mu opioid receptor protein. The
XX specification also describes a transcription regulatory polypeptide and
XX an opioid receptor-like polypeptide. Human mu opioid receptor
XX polynucleotides are useful as a source of probes and primers, which may
XX be used as diagnostic tools to detect normal and abnormal DNA sequences
XX in DNA derived from patients cells. They are also used as a means for
XX detecting and isolating other members of the polypeptide family and
XX related polypeptides from a DNA library potentially containing such
XX sequences. The polynucleotide is used for preparing large quantities of
XX opioid receptor which on expression in microorganism can be useful for
XX evaluating subtype-selective drugs
XX
XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 U; 0 Other;
XX
XX Query Match 38.7%; Score 446.4; DB 3; Length 1618;
XX Best Local Similarity 66.9%; Pred. No. 1.8e-99;
XX Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
XX
QY 110 ACAGCAAGGAGGCGGCGGCTCGAGGAGCGGAGCTGAGACCGCGGACATCTCCCGG 169
Db 350 ACCGCAAGGCGGCTTGGCGGAGACAGACCTGTGCTTCAACCGGAGCGCTTCCATGG 409
QY 170 CCATCCGGTATCATCAGGCGGCTTACTCCGATGTTGCTGCTGGCTTGGTGGCA 229
Db 410 TCACAGCATTCATCATATGCCCCCTTACTATCGTGTGTGTGTGGCCCTCTTGGAA 469
QY 230 ACTGCGTGTATGTTGCTGATTCATCCGATACACAAAGATGAAGACAGCAACCAATTT 289
Db 470 ACTTCCTGGTATGATGTGATGTGATGATACCAAAATAGAGCTGCCACCAACATCT 529
QY 290 ACATATTTAACCTGGCTTGGCAAGATGCTTTAGTTACTACAAACATGCTTTTCAAGATA 349
Db 530 ACATTTTAACTCTGCTGCGACAGCGCTTACGACACAGTACACTGCTTTCAAGATG 589

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Oy	350	CGGCTCTATTGATGAATTCCTGGCCCTTTTGGGAGTGTCTGTGCAAGATATTAATTTCCA	403
Db	590	TCAACTACTCTATGGGAACTAGGCCCTTCGGAAACCATCTCTCGCAAGATCGTGAATCTCA	649
Oy	410	TTGATTTATCAAACTATGTTTCAACAGCATCTTTCACCTTGACCATGATGAGCGTGAACGCT	469
Db	650	TAGATTTATCAAACTATGTTTCAACAGCATATTTCAACCTCTCGACATGAGCGTGAACGCT	709
Oy	470	ACATTTGCCGTGTGCCACCCCGGTGAAGGCTTTGACTTCCGACACACCTTGAAGGCMAAGA	529
Db	710	ACATTTGCTGTCTGCCACCCAGCAAGGCCCTGGAATTTCCGTAACCCCCGAATGCAAAA	769
Oy	530	TCATCAATATCTGCAATCTGGCGTGTGTGTCAATCTGTTGGCAATCTCTGCATATAGTCTTG	589
Db	770	TCGTCAAGTGTGCAACTGGAATCTCTCTTTCTGCACATGAGTCTGTGCTGTAAATGTTCAATG	829
Oy	590	GAGGCACCAAAAGTCAAGGAGACGTCGATGTCATTTAGTGGTCCCTTGAGTATCCCAATG	649
Db	830	CAAACCAAAAATACAGGCAAGGGGTC-----CATGATTTGCAACCTTCAACGTTCTCCACC	883
Oy	650	ATGACTACTCTGTTGGGAGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGCTCCTCGTA	709
Db	884	CAACTGGTACTGGGAGAAACCTGCTC---AAATCTGTGTCTTTATCTTCGCTTTCATCA	940
Oy	710	TCCCTGTCTCTATATCATCATGCTCTGCTACACCTGTATATCTCGTGTCTCAAGACGCTCC	769
Db	941	TGCCGATCTCTATCATATCACTGTGTGTACGGCTGTGATATCTTTCAGACTCAAGACGTTTC	1000
Oy	770	GAGCTCCTTTCTGGCTCCCGAGAGAAAGATGCGCACTCTGATAGATTCACCAAGACTGCTCC	829
Db	1001	GCAATGCTATCGGGCTCCAAAGAAAAGACAGAAATCTGCGCAGATCAACCGGATGCTGC	1066
Oy	830	TGTGTGTGTGGCACTCTTCGTGTCTGTCTGTGAGACTCCCATTTCACTATTCATCTGTGTG	889
Db	1061	TGTGTGTGTGGCTGTATTTATTCGTCTGTGAGACCCCATCATCACTACGTCATCATCA	1120
Oy	890	AGGCTCTTGGGAGACCTTCCCAAGCAACAGCTGCTCTCTCCAGCTATTAATCTTCTGCATCG	949
Db	1121	AAGGCTGTATCAAGATTCACAGAAACCAATTTCAACACGTTTCCGCGACCTTCTGCATTTG	1180
Oy	950	CCTTAGGCTATACCAACAGTAGCTGATGCCATCTCTACGCGCTTTTGTATGAAACT	1009
Db	1181	CTTTGGGTTTACAGAACGCTGCTGAAATCCAGTTCTTTAGGCTTCTTGATGAAACT	1240
Oy	1010	TCAAACGGGTGTTTCCGGGACTTCTGCTTTTCACTGAAGATGAGATGAGAGCGGACAGACA	1069
Db	1241	TCAAACGATGCTTCAAGAGAGTTCTGTCATCCCAACTGTCACAGATGAAACGCAAAACT	1300
Oy	1070	CTAGCAGAGTCCGAAATACAGTTTACAGATCTCTGCTTAC	1107
Db	1301	GCACCTCAGTCCGTCAAGAACTATGAGGAAATCTCCCTCC	1338

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RESULT 18
AAQ79199
ID      AAQ79199 standard; cDNA; 2070 BP.
XX
XX
AC      AAQ79199;
XX
DT      25-MAR-2003 (revised)
DT      19-APR-1995 (first entry)
XX
XX      Rat mu-subtype opioid receptor cDNA.
XX
XX      Mu-subtype opioid receptor; MSOR; drug addiction; ds.
OS      Rattus rattus.
XX
XX      Key
FH      CDS
FT      Location/Qualifiers
FT      /*tag= a
FT      /product= "Mu-subtype opioid receptor"
FT

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XX	EP612845-A2.
PN	
XX	
PD	31-AUG-1994.
XX	
XX	
PF	09-FEB-1994; 94EP-00101968.
XX	
PR	26-FEB-1993; 93US-00026140.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
PI	Eppler CM, Shieh H, Zysk JR, Corbett MJ;
XX	
XX	WPI: 1994-265963/33.
DR	P-PsDB; AAR65188.
XX	
PT	Pure mu-type opioid receptor protein - and nucleic acid coding for it.
PS	Claim 1; Fig 11, 39pp; English.
CC	AAR65188 is the rat mu-subtype opioid receptor protein purified from rat brain membranes, with biotinyl-b-endorphin (AAR56666) as its ligand. It is encoded by the nucleotide sequence AAQ79199 which was synthesized using AAQ101022 and AAQ101023 as PCR primers. AAR65188 is useful for identifying other receptor subtypes, for screening new opioid ligands, and for studying mechanisms of opioid action, e.g. drug addiction.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 U; 0 Other;
Query Match	38.4%; Score 443.4; DB 2; Length 2070;
Best Local Similarity	66.6%; Pred. No. 1.le-98;
Matches 668; Conservative	0; Mismatches 326; Indels 9; Gaps 2;
OY	105 GCCCGACAGCAACGGCAGCGCGGCTGGAGSAGCGGAGCTGGAGCCGGGCACATCTC 164
Db	97 GTCTGAACCGACCGCGGCTTGGCGGAAACGACAGCCTGTGCCCTCAGACGGAGCCCTTC 156
OY	165 CCCCGACATCCCGGTATCATCACGGCGGTACTCCGTAGTGTTCTGTCGGGCTTGGT 224
Db	157 CATGTCACAGCCATTACCATCATAGGCCCTCTACTCTATGCTGTGTAGTGGGCTCTT 216
OY	225 GGCGAACCTCGTGTCATGTTCTGTGATCATCCGATPACAAAAGATGAAGACAGCAACCA 284
Db	217 CGGAAACTCTCGTGATCATGTATGTGATGTGAATGATACACAAAATGAAGACTGCCACCA 276
OY	285 CATTTACATATTTAAACCTGGCTTTGGCAGATGCTTAGTTACTAACACATGCCCTTTCA 344
Db	277 CATCTACATTTTCAACCTTGTCTGGGACGAGCGCTTAGCGACAGTAACCTGCCCTTTTCA 336
OY	345 GAGTACGGGTCTACTTGATGAATTTCTGGGCTTTTGGGGATGTGCTGTSCAAGATAGTAA 404
Db	337 GAGTGTCAACTACTGTATGGGAATAAGGCCCTTGGAAACAATCCTCTGTGCAAGATGTAT 396
OY	405 TTCCATTGATTACTPACAAACATGTTCAACGAGCATCTTCACTTGAACATGATGAGCTGGA 464
Db	397 CTCAATAGATTACTACAAACATGTTCAACGAGCATATACCCTCTGACACATGAGGCTGGA 456
OY	465 CCGCTACATCTCCGTGTGCCACCCCCGTAAGAGCTTTGGAATCTCCGACACACCTTGAAGGC 524
Db	457 CCGGTACATCTGCTGTGCCACCCAGTCAAAAGCCCTGATTTCCGTACCCCCGAAAGAAGC 516
OY	525 AAAATCATCAATATTCGATCTGTGGCTGTGTCATCTTTGGCATCTCTGCATAATAGT 584
Db	517 CAAAATGTCAAGCTGTGCAACTGSAATCTCTCTTGTGCCATCGGTCTGCTGTAAATGTT 576
OY	585 CCTTGGAGGCAACCAAAGTCAGGAAAGAGTCGATGTCAATTGATGCTTCTTGACAGTTCCC 644
Db	577 CATGGCAACCACAAAAATACAGGAGGGGATC-----ATAGATTGCAACCTTCAGTCTTC 630
OY	645 AGATGATGATCTACTCTCGTGTGGACCTTCTTATGAAGATCTGCGTCTTCAATCTTTCCTT 704
Db	631 CCACCCAACCTGTGATCTGGGAGAACCTGCTC---AAATCTGTGTCTTTATCTTGTGCTTT 687

QY	705	CGTATCCCTGCTCCCAATCATCATGCTGTGCTCAACCGTGATGATCTGCAGCTCAACAG	764
Db	688	CATCATGCCGGTCTCTCATCACTCTGTGTGTTACGGCCTGATGATCTTACGACTCAAG	747
QY	765	CGTCCGGCTCTTCTTGCTCCCGAGAGAAAGATGCAACTGCGTAGAATCACCAACT	824
Db	748	CGTTCCGATGCTATCGGGCTCCAAAGAAAGACAGAAATCTGGCAGATCACCCGGAT	807
QY	825	GGTCTCGTGGTGGTGGGCAATCTTGTGTCTGTCTGGACTCCCATTCATATTCATCT	884
Db	808	GGTCTGGTGGTGGGCTGTAATTAATGTCTGTGGAACCCCATCAATCTACGTAT	867
QY	885	GGTGAAGGCTCGGGGAGACACCTCCACAGCAGCTGCTCTCCAGCTATTAATCTG	944
Db	868	CATCAAGGCTTGATCAGCATTCAGAAACCAATTTAGACCGTTTCTGGCACTTCTG	927
QY	945	CATGCGCTTAAAGCTATATCAACAGTAGGCTGATCCCATTCCTTCAAGCCTTCTTGATGA	1004
Db	928	CATTGCTTTGGGTTACAGAAAGGTGCTGATCCAAATTCATTTAAGCCTTCTGGATGA	987
QY	1005	AAACTTCAGGGGTGTTTCCGGGACTTTGCTTTCCACTGAAGATGAGATGAGCGGCA	1066
Db	988	AAACTTCAGGGAGTCTTCAGAGGTTCTGCATCCCACTGTCTCAAGATCGAAGCA	1047
QY	1065	GAGCACTAGCAGATCGGAAATPACAGTTCAGAGTCTGACTTA	1107
Db	1048	AAACTTCAGTGGAGTCTCGTCAAGACCTAGGAGAAATCTTCTC	1090

XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B;
XX
XX
DR WPI; 1998-437487/37.
XX
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
PT e.g. to predict pre-disposition to addiction and for development of
PT analgesics, anaesthetics and anti-addiction agents.
PS
PS Claim 8; Page; 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1154 of the wild-type sequence represented in
CC AAV61984 is replaced by an A. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism. Note: This sequence is not
CC represented in the specification and has been constructed from the wild-
CC type sequence represented in AAV61984 in accordance with the
CC specification

Qy 872 ACATATTCATCTGCTGGAGGCTCTGGGGAGCACTCCACAGACAGCTGCTCTTCCA 931
Db 890 ACATTAGCATCATTTAAAGCTTGGTATCAATCCAGAAACTGCTTCCAGACTGTT 949
Qy 932 GCTATTACTTCTGCATGCGCTTAGGCTATACCAAGTAGCGCTGAATCCATTCTTAG 991
Db 950 CTGGCAGCTTCTGCATGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG 1009
Qy 992 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCACTGAAGTGA 1051
Db 1010 CATTCTGGATGAAACTTCAACGATCTTCAAGAGGTCTGTATCCCAACTTTTCCA 1069
Qy 1052 GGATGAGCGGAGAGCACTAGACAGTCCGAAATA 1087
Db 1070 ACATTGAGCAACAAACTCCACTGGAATTCGTGAGA 1105

RESULT 21
ABS54813
ID ABS54813 standard; cDNA; 1245 BP.
XX
AC ABS54813;
XX
DT 11-DEC-2002 (first entry)
XX
DE cDNA encoding human mu2 opioid receptor fused to mu1 2KB sequence.
XX
KW Human; mu1; opioid receptor; gene; ss; morphine; receptor;
KW intracellular calcium.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1245
FT /"tag= a
FT /product= "Mu1/mus opioid receptor fusion protein"
FT /transl_except= (pos:1185..1187,aa:Leu)
XX
PN W0200268594-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002MO-US005452.
XX
PR 22-FEB-2001; 2001US-0270479P.
PR 05-DEC-2001; 2001US-0336677P.
XX
PA (RESU-) RES FOUND SUNY.
XX
PI Cadet P, Stefano GB;
XX
PS WPI: 2002-706977/76.
PS P-PSDB; AB932260.
XX
PT New isolated nucleic acid molecule encoding a polypeptide having mu3
PT opiate receptor activity, useful as research tools for exploring the
PT interactions, molecular mechanisms and relationship of morphine with the
PT mu3 opiate receptor.
XX
PS Claim 5; Page 29-30; 52pp; English.
XX
PS This invention relates to a novel nucleic acid molecule encoding a
CC polypeptide having mu3 opiate receptor activity. Mu opioid receptors
CC exhibit a high binding specificity for morphine. The invention also
CC comprises a method for identifying a mu3 opiate receptor agonist or
CC antagonist. The nucleic acids and polypeptides of the invention are
CC useful as research tools for exploring the interactions of morphine
CC with the mu3 opiate receptor, the molecular mechanisms by which morphine
CC induces intracellular calcium concentration changes and the relationship
CC of mu3 opiate receptors with other mu opioid receptors. They are also
CC useful for identifying a mu3 opiate receptor agonist or antagonist. THE

CC Present sequence represents a cDNA sequence encoding human mu1/mu2 opioid
CC receptor fusion protein of the invention
XX
SQ Sequence 1245 BP; 308 A; 356 C; 248 G; 333 T; 0 U; 0 Other;
Query Match 37.7%; Score 434.8; DB 6; Length 1245;
Best Local Similarity 66.3%; Pred. No. 1,2e-96;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
Qy 92 CCGGCTGGGCGGAGCCGAGCAACGCGAGCCGCTGAGAGAGCGGACGTGAGC 151
Db 125 CCGAGCCCATGCGGCTCCAGACCGACCGACTGGGCGGAGAGACAGCTGCGCTCCGA 184
Qy 152 CCGGAGCAATCTCCCGGCGCATCCGGTCAATCAACGGGGGTCTACTCCGTAGTGTG 211
Db 185 CCGGCACTCCCTCCATGATATACGCGCATACGATACGCGCTCTACTCATGTGTGCG 244
Qy 212 TCGTGGGCTTGTGGGCACTCGCTGGTCAATGTTGATCATCCGATACACAAAGTGA 271
Db 245 TGGTGGGGCTCTTGGGAACTTCTGGTCAATGATGATGATGATGATGATGATGATG 304
Qy 272 AGACAGCAACCAACATTTACATATTTAACTGCTTTGGCAGATGCTTTAGTTACAA 331
Db 305 AGACTGCCAACCAATCTACATTTTCAACCTTGCTGCGCAGATGCTTAGCCACAGTA 364
Qy 332 CCAATGCCCTTTGAGAGAGGCTCTACTGTGTAATTCCTGGGCTTTTGGGGATGTGCT 391
Db 365 CCTGCGCTTCCAGAGTGAATTAACCTAATGAGAAACATGACCATTTGAAACCATCTT 424
Qy 392 GCAAGATAGTAATTTCAATGATTTACTAACAATGTTCAACAGACATTTCACTGACA 451
Db 425 GCAAGATAGTATCTCATATGATTTACTATTAACATGTTCAACAGCATATTCACCTT 484
Qy 452 TGATGACGTTGACCGCTACATTTGCGTGGCCACCCCGTGAAGGCTTTGGAATTCG 511
Db 485 CCAATGAGTGTGATTCATATTTGACGCTGCGACCCCTTCAAGGCTTAGATTCGTA 544
Qy 512 CACCTTGAAGGAAAGATCATATATATGCAATCGGCGCTGTCATGCTGTTGGA 571
Db 545 CTCCTCCGAAATGCGAAATTTATCAATGTCTGCAACTGATCTCTTTAGCCATTTGTC 604
Qy 572 TCTCTGCAATAGTCTTGGAGGCAACCAAGTCAGGAGAACGTGATGATTTGAGTGT 631
Db 605 TTCCTGTAAATGTTCAATGCTTACCAACAAATATACAGGCAAG-----TTCCAT 658
Qy 632 CCTTGAAGTTCGCAATGATGACTACTCTGTGGGACCTTTTATGAAGATCTGCTCT 691
Db 659 CACTAACATTTCTCATTCACACCTGGTACTGGGAAACCTGCG---TGAAGATCTGTG 715
Qy 692 TCATCTTTGCGTTGCGATCCGTCCTCATCATCATGCTGCTACACCCGATGAGATCC 751
Db 716 TCATCTTGCCTTCAATTAATGCAATGCTCATATTAACGATGCTGATGAGATGATCT 775
Qy 752 TGGCTTCAAGAGCGTCCGCTCTTCTTGAGCTCCGAGAGAAAGATCGCAACTGCTGA 811
Db 776 TGGGCTTCAAGAGTGCAGATGCTCTCTGCTCCAAAGAAAGGACAGGAATCTTCGAA 835
Qy 812 GGATACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
Db 836 GGATACCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
Qy 872 ACATATTCATCTGCTGGAGGCTCTGGGAGCACTCCACAGACAGCTGCTCTTCCA 931
Db 896 ACATTAGCATCATTTAAAGCTTGGTATCAATCCAGAAACTGCTTCCAGACTGTT 955
Qy 932 GCTATTACTTCTGCATGCGCTTAGGCTATACCAAGTAGAGCTGAATCCATTCTTAG 991
Db 956 CTGGCAGCTTCTGCATGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG 1015
Qy 992 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCACTGAAGTGA 1051
Db 1016 CATTCTGGATGAAACTTCAACGATGCTTCAAGAGGTCTGTATCCCAACTCTTCCA 1075

Query Match	37.7%	Score 414.8	DB 6	Length 1431
Best Local Similarity	66.3%	Pred. No. 1.2e-96		
Matches 660	Conservative 0	Mismatches 327	Indels 9	Gaps 2

Query	152	CGCGGACATCTCCCGGCGCATCCCGGTCATCATCAGCGGCTTACTCCGTAATGTTTCG	211
DB	1076	ACATTGAGCAACAAACTCTCACTCGAATTCGTGAGA	1111

Query	92	CCGCGTGGGCGGAGCCGACAGCAACGCGAGCCGCGTCCGAGAGACGCGAGCTGAGAC	151
DB	311	CCGACCCATGCGGTCTCGAACCGACACGACTGCGGCGGAGAGACAGCTGTGCTCCCGCA	370

Query	152	CGCGGACATCTCCCGGCGCATCCCGGTCATCATCAGCGGCTTACTCCGTAATGTTTCG	211
DB	1076	ACATTGAGCAACAAACTCTCACTCGAATTCGTGAGA	1111

Db		371	CCGGCAGTCCCTCCATGATCAAGCGGCATCAGCATATGGCCCTCTAATCTCATCTGTGGG	430
Qy		212	TCTGGGGCTTGGTGGGCAACTCGCTGTGCATGTTGGTATCATCCGATACACAAAGATGA	271
Db		431	TGGTGGGGCTCTTGGGAACTTCCGTGTCATCTATGTAATGTGCAGATACACCAAGATGA	490
Qy		272	AGACAGCAACCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTTACA	331
Db		491	AGACTGCCACCAACATCTACATTTTCAACTTGTCTCTGGCAGATGCTTTAGCCACAGTA	550
Qy		332	CCATGCCCTTTCAGAGTACGGTCTTACTGATGTAATTTCCGGGCTTTTGGGAGATGTCGTG	391
Db		551	CCCTGCCCTTCCAGAGTGAATTAACCTATATGGAAATGGCCATTTGGAAACCATCTTT	610
Qy		392	GCAAGATAGTAAATTTCCATTTGATTTACTACAACATGTTCCACAGCATCTTCACCTTGACCA	451
Db		611	GCAAGATAGTATCTTCCATAGATTCTATTAACAATGTTCACAGCATATTCAACCTCTGCA	670
Qy		452	TGATGAGCGTGAACCGCTACATTTGCCGTGTGTCACCCCGGTGAAGGCTTTGACCTTCGCA	511
Db		671	CCATGAGTGTGATGATATACATTTGACATCTGCAACCTCTGCAAGGCTTAGATTTCGTA	730
Qy		512	CACCTTGAAGGCAAAAGATTCATCATATCTGATCTGGTGTGTGTCATCTGTTGGCA	571
Db		731	CTCCCGCAATGCGCAAAATTAATCAATGCTTGCACATGATCTCTCTTTAGCCATTGGTC	790
Qy		572	TCTGCAATATGTCCTTTGGAGGACCAAAAGTCAGGGAAGACGTGATCTATTGATGATGT	631
Db		791	TTCTCTATATGTTCTATGCTACACAAATAACAGGCAAG-----TTCCATATGATTTGA	844
Qy		632	CCTTGACAGTCCCAAGATGATGACTACTCCTGTGTGGACCTCTTCAATGAAGATCTGCGTC	691
Db		845	CACATAACATTCCTCATCCAACCTGGTACTGGGAAACCTGC---TGAAGATCTGTGTTT	901
Qy		692	TCATCTTTGCTTGTGTGATCCCTGTCTCATATCATATGTCCTGTCTACACCTCGATGATCC	751
Db		902	TCATCTTGGCTTCAATTAATGCAAGTCTCATATTACCGTGTGCTATGGAATGATGATCT	961
Qy		752	TGCGCTCAAGAGCCTCGGCTCTTTCTGGCTCCGAGAGAAAGATCGCAACTGTCGTA	811
Db		962	TGCGCTCAAGAGTTCGCGATGCTCTCTGTGCTCCAAAGAAAGACAGGAATCTTTCGA	102
Qy		812	GGATCACCAGACTGTGCTCTGTGTGTGTGGCAGTCTTGTGCTGTGTGGAATCCCATTC	871
Db		1022	GGATCACCAGAGT	108
Qy		872	ACATTTTATCTGTGTGAGAGGCTCTGGGGAGCACTCCACAGCAGACGCTGCTCTTCCA	931
Db		1082	ACATTTATGTCATCATCTTAAGGCTTTGGTTACATCCCAAAACTACGTTCCAGACTGTTT	114
Qy		932	GCTATTACTTTCGCATCTGCGCTTAAGGCTTATCCAAACAGTAGTGCAGATCCCATTTCTACG	991
Db		1142	CTTGGACCTTCTGCATGTGCTCTAGGTTACAAACAGCTGCTTCAACCAAGTCTTTATG	120
Qy		992	CCTTCTCTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCATCGAAGATGA	105
Db		1202	CATTTCTGAGTGAATACTTCAAAAGATGCTCAGAGAGTTCTGTATCCAAACCTTTCA	126
Qy		1052	GGATGAGCGGACAGCACTAGCAGAGTCCGAATA	1087
Db		1262	ACATTGAGCAACAAAATCTCACTCGAATTCGTGAGA	1297
RESULT 23				
AA089226				
ID AA089226 standard; cDNA, 1610 BP.				
AC	AA089226;			
XX				
DT	25-MAR-2003 (revised)			
DT	20-OCT-1995 (first entry)			
XX				

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DE Human mu opioid receptor cDNA.
XX Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 239..1441
XX FT /*tag= a
XX PN
XX MO507983-A1.
XX PD 23-MAR-1995.
XX PF 13-SEP-1994; 94W0-US010358.
XX PR 13-SEP-1993; 93US-00120601.
XX PA (INDV ) UNIV INDIANA FOUND.
XX PI Yu L;
XX DR MPI: 1995-131351/17.
XX DR P-PSDB; AAR71966.
XX PT New nucleic acid encoding new human mu opioid receptor - and related
XX PT vectors, transformed cells, antibodies etc., useful in diagnosis,
XX PT treatment and drug screening.
XX PS Claim 5; Page 208-210; 266pp; English.
XX CC A cDNA library constructed from human caudate nucleus mRNA was screened
XX CC with rat mu opioid receptor cDNA under conditions of low stringency. One
XX CC positive clone included the sequence given in A089226, encoding a mu
XX CC opioid receptor MOR (AAR71964). The cDNA is used for prodn. of
XX CC recombinant MOR, in gene therapy, etc. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 U; 0 other;

Query Match 37.7%; Score 434.8; DB 2; Length 1610;
Best Local Similarity 66.3%; Pred. No. 1.3e-96;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAAGCAAGCGAGCGGCGTGGAGAGAGCGGAGCTGGAGC 151
DB 363 CCGAGCCAGTGGGTCGAGCCGACCGACCTGGCGGAGAGAGAGAGAGAGAGAGAGAG 422
QY 152 CCGGCGCAATCTCCCGGCGCATCCGGTCAATCATCAGCGCGGTCTACTCGGTAGTGTTCG 211
DB 423 CCGGCAATCTCCCGTCAATCATCAGCGCGCATCAGATCATGCGCTCTACTCATCGTGTGCG 482
QY 212 TCGGTGGGCTTGTGGGCACTCGCTGTGCATGTTCCGATCCTCCGATACCAAGATGA 271
DB 483 TGGTGGGCTTGTGGGCACTCGCTGTGCATGTTCCGATCCTCCGATACCAAGATGA 542
QY 272 AGACAGCAACCAATTATACATATTTAACTGGCTTGGAGAGAGCTTTAGTACTACAA 331
DB 543 AGACTGCAACCAATTATACATATTTAACTGGCTTGGAGAGAGCTTTAGTACTACAA 602
QY 332 CCAATGCCCTTTCAGAGTACGCTCTACTGTATGAATTCCTGGCTTTGGGAGATGTGCT 391
DB 603 CCTTGGCTTTCAGAGTACGCTCTACTGTATGAATTCCTGGCTTTGGGAGATGTGCT 662
QY 392 GCAAGATAGTAATTTCCATGATTTACTACAAAGTTCACACAGATCTTACCTTGACCA 451
DB 663 GCAAGATAGTAATTTCCATGATTTACTACAAAGTTCACACAGATCTTACCTTGACCA 722
QY 452 TGAATGACGTTGACCGCTATACCTGCTGTGCAACCCGTTGAAGCTTTGACTTCGCA 511
DB 723 CCAATGAGTGTGTATGATATCATTTGAGTGTGCAACCCGTTGACTTCGCA 782
QY 512 CACCTTTGAAGGCAAGATCATCAATATCTGATCTGGCTGTCTGTCTATCTGTTGGCA 571

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DB 783 CTCCCGAATATGCAAAATTAATCAATCTCTGCAACTGGATCTCTTCCAGCCATTGCTC 842
QY 572 TCTTGAATATGCTCTTGGAGGCAACCAAGTCAGAGAGAGAGAGAGATGATGATGATGCT 631
DB 843 TTCCATGTAATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896
QY 632 CCTTGAAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 897 CACTAATATCTCTCATTCACCACTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
QY 692 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 954 TCATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013
QY 752 TGGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
DB 1014 TGGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
QY 812 GGATCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871
DB 1074 GGATCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
QY 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
DB 1134 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1193
QY 932 GCTATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
DB 1194 GCTATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
QY 992 CTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
DB 1254 CATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
QY 1052 GGATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
DB 1314 ACATGAGCAACAAACTCCATCGAATTCGTAGA 1349

RESULT 24
AAA59503
ID AAA59503 standard; cDNA; 1610 BP.
XX AAA59503;
AC 14-NOV-2000 (first entry)
DE cDNA encoding a human mu opioid receptor polypeptide.
XX mu opioid receptor; transcription regulatory polypeptide;
KM opioid receptor-like polypeptide; ss.
XX Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 239..1441
XX FT /*tag= a
XX FT /product= "mu opioid receptor"
XX PN US6103492-A.
XX PD 15-AUG-2000.
XX PF 07-JUL-1997; 97US-00889108.
XX PR 08-MAR-1993; 93US-00056886.
XX PR 13-SEP-1993; 93US-00120601.
XX PR 13-SEP-1994; 94US-00305518.
XX PA (INDV ) UNIV INDIANA.
XX PI Yu L;

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Qy	392	CCAAGATGTGTAATTTCCATTGATTAATTAATTAACAACATTTACACAGATCTTCAACCTTGACA	451
Db	637	GCAAGATGTGATCTCCATAGATTACTTAACATATTTACACAGCAATATTCACCCCTTGCA	696
Qy	452	TGATGAGCGTGGACCGCTACATTTGCCGATGGCCACCCCGTGAGGCTTTGCACTTCCGCA	511
Db	697	CCATGAGTGTGATGATACATATGCAATGTGCACCCGTCAAGGCCCTTAAGTTTCCGTA	756
Qy	512	CACCTTTGAAGGCACAAAGATCATCAATATCTGCATCTGGCTGTGTCGTATCTGTTGGCA	571
Db	757	CTCCCCGAAATGCCAAAATTAATTCATATGCTGCAATGTGATCCTCTCTTTCAGCAATTTGCTC	816
Qy	572	TCTGTCAATATAGTCTTTGAGGCAACAAAGTACGGAAGAAGCTGCATGTCATTTAGTGTCT	631
Db	817	TTCTGTATATGTCAATGTGCTACACAAATAATACGGCAAG-----TTCCATATAGTTGTA	870
Qy	632	CCTTGCAATTCACAGATAGTACTACTCTGTGTGGACCTCTTCAATGAAGATCTGCGTCT	691
Db	871	CACCTAACATTTCTCTCATCCAACTGTGTACTGGGAAACCTCG--TGAAGATCTGTGTTT	927
Qy	692	TCATTTTGGCTTGTGTGATTCCTGTGCTCATATGATGTCGTGCTACACCGTATGATGCC	751
Db	928	TCATTTTGGCTTCTTAATGCGAGTGTCAATCATTAACGTGTGCTATAGCATGATGATCT	987
Qy	752	TGCGTCTCAAGAGCGTCCGCGTCTTTCTGGCTCCGAGAGAAAGTGCACAACCTGCTA	811
Db	988	TGCGGCTCAAGAGTGTCCGCAATGCTCTGTGGCTCAAAAGAAAGACAGGAATCTTGAA	1044
Qy	812	GGATTCACAGACTGTCCTGTGTGTGTGTGGACGTCTTGTGTGTCTGTGTGACTCCCATTC	871
Db	1048	GGATTCACAGAGTGTGTGTGTGTGTGGTGTGTGTATGTCGTGTGGAATCTCCATTC	1107
Qy	872	ACATATTCATCTGTGTGAGGCTCTGGGGAGACCTCCACACGACACAGCTGCTCTCTCA	931
Db	1108	ACATTTAGTCAATCTTAAGCTTGTGTTACATCCAGAAACATACGTTCCAGACTGTTT	1167
Qy	932	GCTATTAATTTCTGTGCATGTGCTTAAGGCTATTAACAAGTAAGCTGTAATCCATTTCTTACG	991
Db	1168	CTTGACATTTCTGCATTTGCTCTCAAGGTATACAAAGACGTGCTCAACCAAGCTCTTATG	1227
Qy	992	CCTTCTCTGATGAAAACCTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCACATGAAGATGA	1051
Db	1228	CATTTCTGGAATGAATACTTCAACAGATGCTTCAAGAGATTCTGTATCCCAACTCTTCCA	1287
Qy	1052	GGATGAGCGGACAGCACTACAGACATGCCAATA	1087
Db	1288	ACATTTGAGCAACAAATCTCACTCAAAATTCGTCACA	1323

RESULT	27
AAV61995	
ID	AAV61995 standard; cDNA; 2162 BP.
XX	
XX	AAV61995;
XX	
DT	11-JAN-1999 (first entry)
XX	
DE	Human mu-opioid receptor cDNA variant 11.
XX	
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	
FT	Key
CDS	Location/Qualifiers
FT	213..2040
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FT	/product= "mu-opioid receptor"
FT	502..503
FT	misc feature

FT		/+tag= b
FT		/note= "Site of intron 1"
FT	misc_feature	855..856
FT		/+tag= c
FT		/note= "Site of intron 2"
FT	misc_feature	1376..1377
FT		/+tag= d
FT		/note= "Site of intron 3"
FT	mutation	1613
FT		/+tag= e
FT		/note= "Wild type G is replaced by C"
PN		
PN	W09833937.A2.	
PD		
PD	06-AUG-1998.	
PF		
PF	02-FEB-1998;	98WO-DE000382.
PR		
PR	03-FEB-1997;	97DE-01003925.
PA		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PI		
PI	Hoehe M, Wendel B;	
XX		
XX	WPI; 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g., to predict pre-disposition to addiction and for development of	
PT	analgesics, anaesthetics and anti-addiction agents.	
PS		
PS	Claim 8; Page; 26pp; German.	
CC	This sequence encodes a novel human mu-opioid receptor in which a G	
CC	nucleotide at position 1613 of the wild-type sequence represented in	
CC	AAV61984 is replaced by a C. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anaesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism. Note: This sequence is not	
CC	represented in the specification and has been constructed from the wild-	
CC	-type sequence represented in AAV61984 in accordance with the	
CC	specification	
SQ		
SQ	Sequence 2162 BP; 562 A; 566 C; 457 G; 575 T; 0 U; 2 Other;	
	Query March 37.7%; Score 434.8; DB 2; Length 2162;	
	Best Local Similarity 66.3%; Pred. No. 1.4e-96;	
	Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;	
OY		
OY	92 CCGGCTGGGCGCAGACCCGCAGCAAGCAGCGCGGCTCGAGAGACGCGAGCTGAGC	151
DB		
DB	337 CCGACCATTGGGTGCCAACCGCACCAACTGGGCGGGAAGAACAAGCTTGCCCTCCGA	396
OY	152 CCGGCGCATTCGCCGCGCATCCCGGTATCATCAGCGCGGTCTTACTCGTAAGTTTCG	211
DB		
DB	397 CCGGCAAGTCCTCATGATCATCGGCGCATCATGAGTATGCGCTTACTCATCTGTGTCG	456
OY	212 TCCTGGGCTTGGTGGCACTCGTGTGCATGTTCTGGATCATTCGATATCCGATATCAAGAATGA	271
DB		
DB	457 TGCTGGGGCTCTTGGAAAATCTCTGTGTCATGATGATGATTTGTAGATATCCAAAGATGA	516
OY	272 AGATAGCAACCAATTATATATTTAACCCTGGCTTTGGCAGATGCTTTAGTACTACAA	331
DB		
DB	517 AGACTGCCACCAATCTACTATTTTCAACCTGTGCTGCGAAGTCCCTTAGCCACACATA	576
OY	332 CCATGCCCCCTTCAGAGTACGGTCTACTGATGAATTCCTGGCCCTTTTGGGANTGTGCTGT	391

[illegible]

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FT	/product= "mu-opioid receptor"	
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FT	/tag= b	
FT	/note= "Site of intron 1"	
FT	misc_feature	855..856
FT	/tag= c	
FT	/note= "Site of intron 2"	
FT	misc_feature	1376..1377
FT	/tag= d	
FT	/note= "Site of intron 3"	
XX		
PX	WO9833937-A2.	
XX		
PD	06-AUG-1998.	
PF	02-FEB-1998;	98WO-DE000382.
PR	03-FEB-1997;	97DE-01003925.
XX	(DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PI	Hoehe M, Wendel B;	
DR	WPI; 1998-437487/37.	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g. to predict pre-disposition to addiction and for development of	
PS	analgesics, anaesthetics and anti-addiction agents.	
PS	Claim 8; Page; 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor in which a C	
CC	nucleotide at position 80 of the wild-type sequence represented in	
CC	AAV61984 is replaced by a T. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism. Note: This sequence is not	
CC	represented in the specification and has been constructed from the wild-	
CC	-type sequence represented in AAV61984 in accordance with the	
CC	specification	
XX		
SQ	Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 0 U; 2 Other;	
	Query Match 37.7%; Score 434.8; DB 2; Length 2162;	
	Best Local Similarity 66.3%; Pred. No. 1.4e-96;	
	Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2	
OY	92 CGCGTGGGCGCAGGCCGACAGCAACGGCAGCGCTGCAGAGACCGCAGCTGAGC	151
Db	337 CCGACCATTGCGGTCCGAACCGCACCAAACCTGGCGGAGAGACAGCCTGTCCTCCGA	396
OY	152 CGCGGCAATCTCCCCGGCCCATCCCGGCATCATCAACGCGCGTCTACTCCGTAAGTTGG	211
Db	397 CGCGCAATCTCTCATATGATCAACGSCCATCAAGATATAGGCCCTTACTTCATCGTGACG	456
OY	212 TCCTGGGCTTGGTAGGCAACTCGCTGTCATGTTCTGTATCATCGATACCAAGAATGA	271
Db	457 TGCTGGGGCTCTTGAAAACCTTCTGTGCATGTAATGTGATTTGTCAATACCAAGAATGA	516
OY	272 AGAACAACAACAATTTACTATTTAACTGCGCTTGGCGAGATGCTTTAGTTACTAAC	331
Db	517 AGACTGCACCAACAATCTAACATTTTCAACCTGTCTGGCAGAGCCCTTACCAACAGTA	576
OY	332 CCAATGCCCTTCAAGTACGGTCTACTATGTAANTCCTGGCCTTTTGGGAGATGTCGT	391

QY 332 CCATGCCCTTTAGAGTACGGTCTACTTGATGAAATTCCTGGCTTTGGGGATGCTGT 391
 Db 577 CCTGCCCTTCCAGAGTGTGAATTTACTAATGGAACATGGCACTTTGGAAACATCTTT 636
 QY 392 GCAAGATAGTAATTTCCATTGATTCTACACATGTTCAACGACATCTTCACTTGACCA 451
 Db 637 GCAAGATAGTATCTCCATAGATTACTAATCATGTTCAACGACATTTCACTTCTCA 696
 QY 452 TGATGAGCGTGGACCGCTACATTCGGTGGCCACCCCGTGAAGGCTTTGACCTTCGCA 511
 Db 697 CCATAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
 QY 512 CACCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGCTGCTGCTGCTGCTGCTGCA 571
 Db 757 CTCCCGAAATGCCAAATTTATCAATGCTGCAATGATGATGATGATGATGATGATGATG 816
 QY 572 TCTCGCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGAGTGCATGCTCAATGAGTCT 631
 Db 817 TTCTGTATGTATGATGCTTACAAACAAATACAGGCAAGG-----TTCCATGATGTA 870
 QY 632 CTTGACATTCCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 Db 871 CACTAACATTTCTTCATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
 QY 692 TCATCTTGTCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751
 Db 928 TCATCTTGTCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987
 QY 752 TGGCTTCAAGAGGCTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
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 Db 1108 ACATATTCATCTCTGAGGCTCTGAGGACCTCCACAGACAGCTGCTCTTCCA 1167
 QY 932 GCTATTCCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
 Db 1168 CTGGACCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
 QY 992 CTTTCTGATGAAATCTTCAAGCGGCTGCTTCCGGAATCTTCTGCTTCCA CTGAAGATGA 1051
 Db 1228 CATTTCTGATGAAATCTTCAAGCGGCTGCTTCCGGAATCTTCTGCTTCCA CTGAAGATGA 1287
 QY 1052 GGATGAGCGGCGAGCACTAGCAGAGTCCGAATA 1087
 Db 1288 ACATTTAGCAACAACTCCACTGCAATGCTGTGCA 1323
 RESULT 30
 ID AAV61984 standard; cDNA; 2162 BP.
 XX AAV61984;
 AC
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA.
 XX
 DE Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KM prediction; addition; analgesic; anaesthetic; anti-addictive;
 KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
 KM cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT 502..503
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 FT 1376..1377
 FT /*tag= d
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 XX
 XX W09833937-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 02-FEB-1998; 98MO-DE000382.
 XX
 XX 03-FEB-1997; 97DE-01003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 XX Hoehe M, Wendel B;
 XX
 XX WPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
 PT e.g. to predict pre-disposition to addiction and for development of
 PT analgesics, anaesthetics and anti-addiction agents.
 XX
 PS Claim 8; Page 14-15; 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor. This sequence and
 CC its variants, polymorphisms and mutants are used in a method for
 CC detecting predisposition to disease, particularly addictive disease, by
 CC isolating DNA from a sample, genotyping selected positions and comparing
 CC with a reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmacological agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism
 XX
 SQ Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 0 U; 2 Other;
 Query Match 37.7%; Score 434.8; DB 2; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1.4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
 QY 92 CCGGCTGGGCGGAGCCGACAGCAACGGAGGCGGCTCGGAGAGGACGGCGAGCTGAGC 151
 Db 337 CCGAGCCATGCGGTCCGAACCGACCAACCTGGGCGGAGAGACAGCTGCGCTCCGA 396
 QY 152 CCGGCAATCTCCCGGCGCATCCGCTCATATGACGCGGCTTACTCCAGTAGTTCG 211
 Db 397 CCGGAGTCCCTCCATGATCAAGGCATATGAGCCCTTACTCATCGTGTGG 456
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 QY 272 AGACAGCAACCAACATTAATTAATTAACCTGCTTGGAGAGAGCTTAACTTACTACAA 331
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 Db 637 GCAAGATAGTATCTCCATAGATTACTAATCATGTTCAACGACATTTCACTTCTCA 696

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Oy 452 TGATGAGCGTGAACCGCTACATTCGCCGTGTCACACCCCGTAGAGCTTTGGACTTCCGCA 511
    |||||
Db 697 CCAATGAGTGTGATCGATACATTCAGTCTCCACCCCTGTCAAGCCCTTAATTTCCGTA 756
Oy 512 CACCTTGGAGCAAGATCATCAATATCTGCATCTGGCTGCTGCTCATCTGTGGCA 571
    |||||
Db 757 CTCCCCGAAATGCGAAATATTCATATGCTCAATGGATCCTCTTCAACCAATGGTTC 816
Oy 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGAGTGCATTTAGTGCCT 631
    |||||
Db 817 TTCCGTAAATGTTATGAGCTCAACAAATAAGCAAGG-----TTCCATGAATTTGTA 870
Oy 632 CCTTGACAGTTCCAGATGATGACTACTCCTGAGGAGACCTTTCATGAAAGATGCGCT 691
    |||||
Db 871 CACTACATTTCTTCATTCGAACCTGTACTGGGAAACCTGG---TGAAGATCTGTGTTT 927
Oy 692 TCATCTTTGACCTTGGATGCCCTGCTCTCATCATCATGTCGTGCTACACCCCTGATGCC 751
    |||||
Db 928 TCATCTTGGCTTCAATATGCGAGTGTCTCATATTAACGCTGTGCTATGGAATGATCT 987
Oy 752 TGCCTTCAAGAGCGTCCGCTCTTTTGGCTCCGAGAGAAAGATGCAACTGGGTA 811
    |||||
Db 988 TGCCTTCAAGAGCGTCCGCTCTTCTGCTCCAAAGAAAGACAGAAATCTTGGAA 1047
Oy 812 GGATCACCAGACTGCTCTGGTGGTGGTGCAGTCTTGTGCTGCTGAGCTCCCATTC 871
    |||||
Db 1048 GGATCACCAGAGTGTGCTGGTGGTGGTGCAGTCTTGTGCTGCTGAGCTCCCATTC 1107
Oy 872 ACATATTCATCTCGTGGAGGCTCTGGGAGACACCTCCACAGACAGCTGCTCTTCCA 931
    |||||
Db 1108 ACATATTCATCTCGTGGAGGCTCTGGTGGAGACACCTCCACAGCTGCTTTC 1167
Oy 932 GCTTACTTTCATCTGCTGCTTGAAGCTTATACCAACAGTACCTGATCTTCTTACG 991
    |||||
Db 1168 CTTCGCACTTCTGATGCTCTGAGTTTACCAACAGCTGCTCAACCCAGTCTTATATG 1227
Oy 992 CCTTCTTGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGAAGATA 1051
    |||||
Db 1228 CATTTCTGAGTGAATACTTCAACGATGCTTCAAGAGATCTCTTATCCAACTTCTTCA 1287
Oy 1052 GGATGAGCGGCGAGGACACTAGACAGTCCGAAATA 1087
    |||||
Db 1288 ACATTTGAGCAACAAACTCCACTGGAATTGCTGAGA 1323
```

RESULT 31

AAV61987 standard; cDNA; 2162 BP.

```
XX AAV61987;
XX
XX 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 3.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX predilection; addiction; analgesic; anaesthetic; anti-addictive;
XX psychopharmacological agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; aa.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX mutation 102
XX CDS 213..2040
XX /note= "Wild type C is replaced by T"
XX /tag= a
XX /product= "mu-opioid receptor"
XX /tag= b
XX /note= "Site of intron 1"
```

```
FT misc_feature 855..856
FT /tag= c
FT /note= "Site of intron 2"
FT misc_feature 1376..1377
FT /tag= d
FT /note= "Site of intron 3"
PN MO983937-A2.
PD 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-DE000382.
XX
XX 03-FEB-1997; 97DE-01003925.
XX
XX (DELB-) DELBRUECK CBNT MOLEKULARE MEDIZIN MAX.
XX
XX Hoehe M, Wendel B;
XX
XX WPI; 1998-437487/37.
XX
XX
XX This sequence encodes a novel human mu-opioid receptor in which a C
XX nucleotide at position 102 of the wild-type sequence represented in
XX AAV61984 is replaced by a T. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predilection to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmacological agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug, opiate, or
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism. Note: This sequence is not
XX represented in the specification and has been constructed from the wild-
XX type sequence represented in AAV61984 in accordance with the
XX specification
XX
XX Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 0 U; 2 Other;
XX
XX Query Match 37.7%; Score 434.8; DB 2; Length 2162;
XX Best Local Similarity 66.3%; Pred. No. 1.4e-96;
XX Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
Oy 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCGGAGCGGCTGGAGAGCGCGAGCTGAGC 151
    |||||
Db 337 CCGAGCCATGCGGTGCTCCAGACCGCACCACTGGCGGAGAGAGACGCTGCTCCGA 396
Oy 152 CCGGCAATCTCCCGGCGCATCCGGATCATCAAGCGGCTGTAATCTGAGTGTTCG 211
    |||||
Db 397 CCGGAGTCTCTTCATATATACGCGCATCAAGATCAAGCGGCTTATCTCATCTGTGCG 456
Oy 212 TCGTGGGCTTGTGGGCACTCGCTGTGATGTTCTGATCATGCAATCAAAAGATGA 271
    |||||
Db 457 TCGTGGGCTTGTGGAAACTTCTGGTCAATGATGATGATGATGATGATGATGATGATG 516
Oy 272 AGACAGCAACCAATTTACATTTTAACTGGCTTTGGCAGATGCTTTAATTACTACA 331
    |||||
Db 517 AGACTGCGCACCAACATCTACATTTTCAACCTGCTGCGCAGATGCTTACCCACAGTA 576
Oy 332 CCATGCCCTTTCAAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATG 391
    |||||
Db 577 CCTGCGCTTCCAGAGTGTGATTTAATCTAATGGAACATGCGCATTTGGAACTCTTTT 636
Oy 392 GCAAGATGATTAATTTCAATGATTTACTACAACATGTTCCACGAGATCTTCACTTGACA 451
    |||||
Db 637 GCAAGATGATGATTTCCATGATTTACTATTAACATGTTCAACAGCATATTGACCTCTGCA 696
```

QY 452 TGATGAGGCTGAGACCGCTACATGTCGCTGTCACCCCGTGAAGCTTTGAGCTTCGCA 511
 Db 697 CCATGAGGTGTTGATGATACATGAGTCTGACCCCTGTGACGGCTTAATATTTCCGTA 756
 QY 512 CACCTTGAAGCAAAAGATCATCATATCTGCATCTGCTGCTGCTCATCTGTGGCA 571
 Db 757 CTCCCCGAAATGCCAAATTAATCAATGCTGCACTGGAATCTCTTCAACCAATGGTC 816
 QY 572 TCTTGCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGAGCTGATGTCATTAGTCT 631
 Db 817 TTCCTGTAATGTTGATGCTACCAACAAATAACAGCAAGG-----TTCCTAATAGTGA 870
 QY 632 CCTTGACAGTTCGAGATGATGACTCTGCTGGGAGCTTCTGATGAAGATGCGGCT 691
 Db 871 CACTACATCTCTCATCAACCTGTGACTGGAAACCTG---TGAAGATCTGTGTTT 927
 QY 692 TCATCTTTGCTGCTGATGCTGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCT 751
 Db 928 TCATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
 QY 752 TGCCTTCAGAGAGGCTCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
 Db 988 TGCCTTCAGAGAGGCTCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
 QY 812 GGATCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 Db 1048 GGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
 QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
 Db 1108 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
 QY 932 GCTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
 Db 1168 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
 QY 992 CTTTCTGATGAAACCTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
 Db 1228 CATTCTGATGAAACCTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
 QY 1052 GGATGAGCGGACAGACTGACAGAGTCCGAAATA 1087
 Db 1288 ACATGAGCAACAAACTCCACTGGAATGCTGCA 1323

RESULT 32
 AAV61990 standard; cDNA; 2162 BP.
 AAV61990;
 11-JAN-1999 (first entry)
 Human mu-opioid receptor cDNA variant 6.
 Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 addiction; analgesic; anesthetic; anti-addictive;
 psychopharmacological agent; diagnostic; side effect; drug; opiate;
 cocaine; inherited alcoholism; human; ss.
 Homo sapiens.
 Synthetic.
 Location/Qualifiers
 CDS 213..2040
 /tag= a
 /product= "mu-opioid receptor"
 mutation 330
 /tag= e
 /note= "Wild type A is replaced by G"
 misc_feature 502..503
 /tag= b

FT /note= "Site of intron 1"
 FT misc_feature 855..856
 FT /tag= c
 FT /note= "Site of intron 2"
 FT misc_feature 1376..1377
 FT /tag= d
 FT /note= "Site of intron 3"
 PN W0983937-A2.
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98MO-DE000382.
 XX
 PR 03-FEB-1997; 97DE-01003925.
 XX
 PA (DELB-) DELBRUCK CENT MOLEKULARE MEDIZIN MAX.
 PI Hoehe M, Wendel B;
 XX WPI; 1998-437487/37.
 DR
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
 PT e.g. to predict pre-disposition to addiction and for development of
 PT analgesics, anaesthetics and anti-addiction agents.
 XX
 PS Claim 8; Page; 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which an A
 CC nucleotide at position 330 of the wild-type sequence represented in
 CC AAV61984 is replaced by a G. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anesthetic,
 CC anti-addictive and psychopharmacological agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism. Note: This sequence is not
 CC represented in the specification and has been constructed from the wild-
 CC type sequence represented in AAV61984 in accordance with the
 CC specification
 CC
 SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 0 U; 2 Other;
 Query Match 37.7%; Score 434.8; DB 2; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1,4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
 QY 92 CCGGCTGGGCGGACCCGACGACGAGCGCGGCTGCGAGAGCGGCGGCTGAGGC 151
 Db 337 CCGACCCATGCGGCTCGAACCACCAACCTGGGAGAGACAGCTGCTCCGCA 396
 QY 152 CCGGCGACATCTCCCGGCGCATCCGGTATCATACGGCGGCTACTCCGATGTTGG 211
 Db 397 CCGGAGTCTCTCATGATACGGCCATACATCATGCGCTTCACTCATGCTGCGG 456
 QY 212 TCGTGGGCTTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
 Db 457 TGGTGGGCTTTCGAAACCTTCGTGCTATGATGATGATGATGATGATGATGATGATGAT 516
 QY 272 AGACAGCAACCAATTTACATTTTAACTGGCTTGGAGATGCTTACTACAA 331
 Db 517 AGACTGCGCAACCAATTTACATTTTAACTGGCTTGGAGATGCTTACTACAA 576
 QY 332 CCATGCGCTTGAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
 Db 577 CCTGCGCTTTCAGAGTGTGATTTACCTBATGGAACTGGCAATTTGAAACATCTTT 636
 QY 392 GCAGATGTAATTTCAATTTACTACACATGTTACAGCATCTTCACTTGAACA 451

Db 637 GCAAGATAGTACTCCATAGATTACTATACATGTTCCACGACATATTCACCTCTGCA 696
 Qy 452 TGATGACCGTGGACCGCTACATTGCCGTGTCACCCCGTAAAGCTTTGACCTTCGCA 511
 Db 697 CCAAGAGTGTGATCGATACATTCATGCACTCCGACCCCTGTCAAGCCCTTAATATTCGCTA 756
 Qy 512 CACCCCTGGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGCTCATCTGTGGCA 571
 Db 757 CTCCCGAATATGCCAAATTTCAATGCTGCAATGATCTCTCTTCAGCCATGTGTC 816
 Qy 572 TCTGTCAATAGTCTTGGAGGACCAAGTCAAGGAAAGACGTGATCATTTAGTGTCT 631
 Db 817 TTCCTGTAATGTTCATGGCTACCAACAAATACAGGCAAGG-----TTCATATGATGTGA 870
 Qy 632 CTTGCAAGTTCACAGATGATGATGATCTCTGCTGGAGACCTCTTCATGAAATCTGGCT 691
 Db 871 CACTAACATTCCTCATTCACCACTGTGATCTGGGAAACCTGG---TGAAGATCTGTGTTT 927
 Qy 692 TCATCTTGTGCTTGTGATCCCTGTGCTCATCATCATGCTGTGCTACACCTGATGATCC 751
 Db 928 TCATCTTGTGCTTGTGATCCCTGTGCTCATCATCATGCTGTGCTATGGAATGATGATCT 987
 Qy 752 TGCCTCAAGAGCGCTCGGCTCTTCTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
 Db 988 TGGCCCTCAAGAGTGTCCGATGCTCTGTGCTCCAAAGAAAGACAGAAATCTTGAA 1047
 Qy 812 GGATCACCAGACTGCTCTGTGTGTGTGGCACTCTTCTGTGCTGCTGCACTCCATTC 871
 Db 1048 GGATCACCAGAGT 1107
 Qy 872 ACATATTCATCTCTGTGAGGCTCTGGGAGACACCTCCACAGACAGCTGCTCTTCCA 931
 Db 1108 ACATATTCATCTCTGTGAGGCTCTGGGAGACACCTCCACAGACAGCTGCTCTTCCA 1167
 Qy 932 GCTATTCATCTCTGTGAGGCTCTGGGAGACACCTCCACAGACAGCTGCTCTTCCA 991
 Db 1168 CTTGGCACTTCTGATGCTCTGATGCTCTGATGCTCTGATGCTCTGATGCTCTGATGCTCT 1227
 Qy 992 CTTTCTTGTGATGAAACTTCAAGGGGTGTTCGGGACTTGTGCTTTCACCTGAAGATGA 1051
 Db 1228 CATTTCGATGAGAAACTTCAAGGAGTCTTCAAGAGATCTGTATCCCAACTCTTCCA 1287
 Qy 1052 GGATGAGCGGCGAGAGCACTGACAGATCGGAATA 1087
 Db 1288 ACATTGAGCAACAAACTCCACTCGAATTCGTGACA 1323

RESULT 33

AAV61985 standard; cDNA; 2162 BP.

AAV61985;

11-JAN-1999 (first entry)

Human mu-opioid receptor cDNA variant 1.

Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KM predileposition; addiction; analgesic; anaesthetic; anti-addictive;
 KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.

Homo sapiens.

OS Synthetic.

Location/Qualifiers

/tag= e

/note= "Wild type G is replaced by T"

/tag= a

/product= "mu-opioid receptor"

misc_feature

502..503

FT FT /tag= b
 FT /note= "Site of intron 1"
 FT misc_feature
 FT 855..856
 FT /tag= c
 FT /note= "Site of intron 2"
 FT misc_feature
 FT 1376..1377
 FT /tag= d
 FT /note= "Site of intron 3"
 XX W0983937-A2.
 XX 06-AUG-1998.
 XX 02-FEB-1998; 98WC-DE000382.
 XX 03-FEB-1997; 97DE-01003925.
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PI Hoehe M, Wendel B;
 XX WPI; 1998-437487/37.
 DR
 XX
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
 PT e.g. to predict pre-disposition to addiction and for development of
 PT analgesics, anaesthetics and anti-addiction agents.
 XX
 PS Claim 8; Page; 26pp; German.
 XX
 XX This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 41 of the wild-type sequence represented in
 CC AAV61984 is replaced by a T. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predileposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
 CC anti-addictive and psychopharmacological agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism. Note: This sequence is not
 CC represented in the specification and has been constructed from the wild-
 CC type sequence represented in AAV61984 in accordance with the
 CC specification
 CC
 CC
 XX Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 0 U; 2 Other;
 SQ
 Query Match 37.7%; Score 434.8; DB 2; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1.4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
 Qy 92 CCGGCTGGGCGAGCCGAGAGCAACCGAGCCGCTCGAGAGACGCGAGCTGAGC 151
 Db 337 CCGAGCCATGGGCTGCGAGCCGAGCAACCTGGGCGGAGAGACAGCTGTGCCCGCA 396
 Qy 152 CCGGCAATCTCCCGGCAATCCCGGTATCATCAGCGGCGTTACTCCGTAGTTCG 211
 Db 397 CCGGCAATCTCCCGGTATCATCAGCGGCGTTACTCCGTAGTTCG 456
 Qy 212 TCGTGGGCTTGTGGGCAATCGGTGATGCTGTGATCATCGATCGATCAACAAAGATGA 271
 Db 457 TGTGGGCTTGTGGGCAATCTGTGATGCTGTGATCATCGATCGATCAACAAAGATGA 516
 Qy 272 AGACAGCAACCAATTTAATATTTAATCTGCTTGGAGATGCTTATGTTACTCA 331
 Db 517 AGACTGCCAACAATATTTAATCTGCTTGGAGATGCTTATGTTACTCA 576
 Qy 332 CCATGCTTTCAGAGTACGCTACTGTGAATTTCTGCGCTTTGGGAGTGTCTGT 391
 Db 577 CCGTGGCTTTCAGAGTACGCTACTGTGAATTTCTGCGCTTTGGGAGTGTCTGT 636
 Qy 392 GCAAGATAGTAATTTCAATGATTACTTACCAACATGTTCCACAGACTTTACCTGACA 451

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Db      637  GCAAGATGATGATCCATAGATTACTATAACATGTTACACAGATATTGACCCCTGCA 696
Qy      452  TGATGAGGTGAGACCGCTACATTTGCCGTGGCCACCCCGTGAAGGCTTTGGACTTCGCA 511
Db      697  CCATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
Qy      512  CACCTTGAAGGCAAAAGATCATCATATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 571
Db      757  CTCCCCGAAATGCCAAATTTTCAATGCTGCAACTGATCTCTCTTCAAGCCATTGCTC 816
Qy      572  TCTTGCAATAGTCTTGAGAGCACCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
Db      817  TTCCGTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
Qy      632  CCTTGAGTTCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
Db      871  CACTAACATTTCTCATCTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927
Qy      692  TCATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
Db      928  TCATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
Qy      752  TGGCTCTGAGAGCGCTCCGCTCTCTTCTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
Db      988  TGGCTCTGAGAGCGCTCCGCTCTCTTCTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
Qy      812  GGATCACAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db      1048  GGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy      872  ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db      1108  ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
Qy      932  GCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db      1168  CTTGGACATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
Qy      992  CCTTTCTGATGAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Db      1228  CATTTCTGATGAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
Qy      1052  GGATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
Db      1288  ACATGAGCAAACTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323

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RESULT 34
AAV61989
ID AAV61989 standard; cDNA; 2162 BP.
XX
AC AAV61989;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 5.
XX
OS Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX KM predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
XX KM cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT 229
FT mutation
FT /tag= e
FT /note= "Wild type C is replaced by T"

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FT      misc_feature 502..503
FT      /tag= b
FT      /note= "Site of intron 1"
FT      misc_feature 855..856
FT      /tag= c
FT      /note= "Site of intron 2"
FT      misc_feature 1376..1377
FT      /tag= d
FT      /note= "Site of intron 3"
FT      W09833937-A2.
FT      06-AUG-1998.
FT      02-FEB-1998; 98NO-DE000382.
FT      03-FEB-1997; 97DE-01003925.
FT      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
FT      Hoehe M, Wendel B;
FT      WPI; 1998-437487/37.
FT      New genomic and cDNA sequences encoding human mu-opioid receptor - used,
FT      e.g. to predict pre-disposition to addiction and for development of
FT      analgesics, anaesthetics and anti-addiction agents.
FT      Claim 8; Page; 26pp; German.
FT      This sequence encodes a novel human mu-opioid receptor in which a C
FT      nucleotide at position 229 of the wild-type sequence represented in
FT      AAV61984 is replaced by an T. The wild type receptor and its variants,
FT      polymorphisms and mutants are used in a method for detecting
FT      predisposition to disease, particularly addictive disease, by isolating
FT      DNA from a sample, genotyping selected positions and comparing with a
FT      reference DNA. Such sequences are used to develop analgesic, anaesthetic,
FT      anti-addictive and psychopharmacological agents, to construct genes and
FT      vectors, particularly for pharmaceutical development, to develop
FT      diagnostic kits for predicting risk of addiction, response to analgesics
FT      or anaesthetics, or development of side effects from a drug. Particular
FT      applications are to determine risk of addiction to opiates or cocaine, or
FT      of developing inherited alcoholism. Note: This sequence is not
FT      represented in the specification and has been constructed from the wild-
FT      type sequence represented in AAV61984 in accordance with the
FT      specification
XX
XX
XX
SQ      Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 0 U; 2 Other;
XX
XX
XX
Query Match 37.7%; Score 434.8; DB 2; Length 2162;
Best local Similarity 66.3%; Pred. No. 1.4e-96;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
Qy      92  CCGGCTGGGCGGACCCGACAGCAACGGGCGGCTGAGAGAGCGGAGCTGAGAC 151
Db      337  CCGAGCCATGCGGATCGGACCGCACCAACCTGGGCGGAGAGACAGCCCTGCCGA 396
Qy      152  CCGGCGACATCTCCCCGGGCAATCCGGGTATATATACAGCGGCTTACTCCGATGTTCCG 211
Db      397  CCGGCGATCCCTCCATGATCAAGGCGCATCAATGATGATGATGATGATGATGATGATGATGATG 456
Qy      212  TCGTGGGCTTGGTGGGCAACTGCTGATCATTTGATGATCATCGATGATCAAGAGATGA 271
Db      457  TGGTGGGCTCTTGGGAACTTCCGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
Qy      272  AGACAGCAACCAACATTTATGATTTTAACTGGCTTTGGAGATGCTTATGATCAAA 331
Db      517  AGACTGGCCACCAACATTTATGATTTTCAACTGCTGCGAGATGCTTATGATGATGATGATGATGAT 576
Qy      332  CCATGCGCTTTAGAGTACGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
Db      577  CCTGCGCTTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636

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QY 392 GCAAGATGTAATTTCCATTGATTACTACAAATGTCACAGCATCTTACCTTGACCA 451
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DB 637 GCAAGATGTAATTTCCATTGATTACTACAAATGTCACAGCATCTTACCTTGACCA 451
    |||||
QY 452 TGATGAGCGTGAACCGCTACATTCGCTGTCACACCCGCTGAAGCTTTGACCTGCA 511
    |||||
DB 697 CCATGAGTGTGATGATGATACATTCGATGTCGACCTGTCACAGCTTGAATTTCCGGA 756
    |||||
QY 512 CACCTTGAAGGCAAGATCATCATATTCGATCTGCTGTCGTCATCTGTTGCA 571
    |||||
DB 757 CTCCCGAAGTCCAAAATTATCAATGTCGCAATCGATCTCTTCAGCATTTGATC 816
    |||||
QY 572 TCTGCAATGATGCTTGAAGGACCAAGTGAAGGAAAGCTGATGATGATGCT 631
    |||||
DB 817 TTCTGTAATGTTCTGCTGCTACACAAATATGACGCAAGG-----TTCCATAGATTGA 870
    |||||
QY 632 CTTTCAGTCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
    |||||
DB 871 CACTTAACATTCCTGATCCAACTGCTGATGATGATGATGATGATGATGATGATGATGAT 927
    |||||
QY 692 TCATTTTTCCTTCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
    |||||
DB 928 TCATCTTTCCTTCTGATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
    |||||
QY 752 TGGCTTCAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
    |||||
DB 988 TGGCTTCAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
    |||||
QY 812 GGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
    |||||
DB 1048 GGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
    |||||
QY 872 ACATATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
    |||||
DB 1108 ACATATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
    |||||
QY 932 GCTATTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
    |||||
DB 1168 CTTGGCATTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
    |||||
QY 992 CTTTCTTGAAGAACTTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
    |||||
DB 1228 CATTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287
    |||||
QY 1052 GGATGAGCGGAGAGCACTAGACAGATGCTGCAATA 1087
    |||||
DB 1288 ACATTGAGCAACAAATCTCACTCGAATTCGTCGA 1323
    |||||

RESULT 35
AAZ88470
ID AAZ88470 standard; DNA; 2162 BP.
XX
AC AAZ88470;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human mu opioid receptor gene.
XX
KW Human; mu opioid receptor; hMOR1; diagnosis; addiction; constipation;
    diarrhoea; decreased immune response; stress; gastrointestinal motility;
    immune response; hypothalamus pituitary adrenal axis; gonadal axis; pain;
    alcohol; ds.
XX
OS Homo sapiens.
XX
PN WO200003024-A2.
XX
PD 20-JAN-2000.
XX
PF 10-JUL-1999; 99MO-US015707.
XX

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PR 10-JUL-1998; 98US-00113426.
PR 09-JUL-1999; 99US-00351198.
PA (UTRQ) UNIV ROCKEFELLER.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
Kreek MJ, Laforge KS, Yu L, Tischfield JA;
WPI, 2000-160930/14.
DR P-PSDB; AAY79945.
PT New human opioid mu receptor gene variant for determining susceptibility
    of a subject to addictive disorder, pain.
PS Claim 1; Page: 134pp; English.
XX
CC The present invention describes an isolated variant (V) of the human mu
    opioid receptor (hMOR1) gene with at least two variations A118G, C17T,
    CC G24X, G779A or G942A of the sequence of Genbank accession number U25119.
    CC Determination of increased or decreased susceptibility in a subject to at
    CC least one addictive disorder like opioid, cocaine, nicotine, barbiturate
    CC or sedative hypnotic, anxiolytic, alcohol addiction or addiction to
    CC others psychostimulants and to pain is done by determining the presence
    CC of (V) with variation A118G or C17T respectively in one and/or both
    CC alleles of (V) and it can also be done by determining the presence of the
    CC hMOR1 protein with variation AandAsp or Ala6val respectively.
    CC Therapeutically effective amount of pain reliever to induce analgesia or
    CC therapeutically agent to treat one addictive disorder is determined by
    CC determining the variations in the hMOR1 gene or protein and so increased
    CC or decreased susceptibility indicates an increased or decreased amount of
    CC pain reliever or therapeutic agent respectively. The determination of the
    CC hMOR1 gene with variation A118G or C17T also helps in the diagnosis of a
    CC disease or disorder like infertility constipation, diarrhoea, decreased
    CC immune response or decreased ability to withstand stress related to
    CC physiological function like sexual or reproductive function,
    CC gastrointestinal motility, immune response, or ability to withstand
    CC stress regulated by hypothalamus pituitary adrenal axis (HPA) or gonadal
    CC axis (HPG). The present sequence represents the hMOR1 gene. N.B. The
    CC present sequence is not given in the present invention but is referred to
    CC as the Genbank accession number U25119
    CC
SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 0 U; 2 Other;
    Query Match 37.7%; Score 434.8; DB 3; Length 2162;
    Best Local Similarity 66.3%; Pred. No. 1.4e-96;
    Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
QY 92 CCGGCTGGCCGAGCCGACAGCAACGGCAGGCGGCTCGGAGGACGCGAGCTGAGAC 151
    |||||
DB 337 CCGACCCATGCGGCTCCAAACGACCAACCTGGGGGAGAGACAGCCCTGCTCCGA 396
    |||||
QY 152 CCGGCGACATCTCCCGGCAATCCGGATCATCATGACGGCGGTCTACTCCGATGCTTGG 211
    |||||
DB 397 CCGGCAATGCTCCATGATCAACGGCCATCAAGATGATGATGATGATGATGATGATGATGAT 456
    |||||
QY 212 TCGTGGCTTGGTGGGCACTCGCTGCTGATGTTGATGATCCGATACAAAGATGA 271
    |||||
DB 457 TGGTGGGCTCTTCGGAATCTTCGATCATGATGATGATGATGATGATGATGATGATGATGAT 516
    |||||
QY 272 AGACAGCAACCAACATTTACATTTAATTTACCTGCTTGGAGATGCTTGAATGATCA 331
    |||||
DB 517 AGATGCGCAACCAACATTTACATTTTCAACCTTGTCTGCGACATGCTTGAACCAAGTA 576
    |||||
QY 332 CCATGCCCTTTCAAGATGCGGTCTACTGATGATTTCTGCGCTTTGGGAGTGTGCT 391
    |||||
DB 577 CCCTGCCCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
    |||||
QY 392 GCAAGATGTAATTTCCATTGATTACTACAAATGTCACAGCATCTTACCTTGACCA 451
    |||||
DB 637 GCAAGATGTAATTTCCATTGATTACTACAAATGTCACAGCATCTTACCTTGACCA 451
    |||||
QY 452 TGATGAGCGTGAACCGCTACATTCGCTGTCACACCCGCTGAAGCTTTGACCTGCA 511
    |||||

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Db 697 CCATGAGTGTGATGATACATTCAGTCTGCACCTGTCAAGGCTTAGATTTCCGTA 756
 Qy 512 CACCCCTTGAGGCAAGATCATCAATATGATCTGGTGTGTGTCATCTGTGGCA 571
 Db 757 CTCGCCGAATGCAAAATATCAATATGTCGAACTGAACTCTCTTCAGCAATGGTC 816
 Qy 572 TCTCTGCAATAGTCTCTTGAGGAGCAAAAGTCAGGAAAGCTGCATGATCTTAGAGTCT 631
 Db 817 TTCGTATATGTTCAATGCTACACAAATATAGGCAAG-----TTCATAGATTGTA 870
 Qy 632 CCTTGACAGTCTCCAGATGATGACTACTCTCTGTGGAGCTCTTCATGAAAGATCTGCGTCT 691
 Db 871 CACTACAACTTCTCTATCCAACTGTGTACTGGAAACCTCG---TGAAGATCTGTGTTT 927
 Qy 692 TCATCTTGGCTCTGCTGATGCCCTGTCCATCATGATGATGCTGACACCCGATGATGCC 751
 Db 928 TCATCTTGGCTCTTCAATATGTCAGTGTCTCATATTCATTCATGCTGATGAGTACT 987
 Qy 752 TGGCTCTCAAGAGCGTCCGCTCTCTTCTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
 Db 988 TGGCGCTCAAGAGTGTCCGCAATGCTCTGCGCTCAAGAAAGAACAGCAATCTTGAA 1047
 Qy 812 GGATCACCAGACTGCTCTGCTGTGTGTGTGGCAGTCTTGTGCTGTGACTGCCATTTC 871
 Db 1048 GGATCACCAGAGT 1107
 Qy 872 ACATATTCATCTGGTGTGAGGCTCTGGGAGAGCACTCCACAGCACTGCTCTCTCA 931
 Db 1108 ACATTTAGTATCATTTAAAGCTTTGGTTCAATTCAGAACTTAGCTTCCAGACTGTT 1167
 Qy 932 GCTATTTACTTGTGATCGCTTGAAGCTTATACCAACAGTGCCTGAATCCATTCCTACG 991
 Db 1168 CTGGCACTTCTGCACTTCTCTAGGTTACACAAAGCTGCTCAACCACTCTTATG 1227
 Qy 992 CCTTTCTGATGAAACTTCAAGCGGTCTTCCGGACTTCTGCTTCTCACTGAAGATGA 1051
 Db 1228 CATTCTGATGAAACTTCAAGCGGTCTTCAAGCGGTCTTCAAGCGGTCTTCAAGCGGT 1287
 Qy 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAATA 1087
 Db 1288 ACATTGAGCAACAAACTCCACTCGAATTCCTGCA 1323
 Db
 RESULT 36
 ABK14953
 ID ABK14953 standard; DNA; 2162 BP.
 XX
 AC ABK14953;
 XX
 DX 08-MAY-2002 (first entry)
 DT
 DX Human mu oploid receptor (hMOR) gene sequence.
 DB
 XX Human mu oploid receptor (hMOR) gene sequence.
 KW Human; mu oploid; receptor; MOR; gene; single nucleotide polymorphism;
 KW SNP; oploid addiction; infertility; constipation; diarrhoea;
 KW impaired immune responsiveness; stress; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..1415
 FT
 FT /tag= a
 FT /product= "Human mu oploid receptor protein"
 FT replace (229, T)
 FT
 FT /tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 FT /note= "Referred to in specification as C17T"
 FT variation replace (236, A)
 FT /tag= c
 FT /standard_name= "Single nucleotide polymorphism"
 FT /note= "Referred to in specification as G24A"
 FT variation replace (350, G)
 FT /tag= d

FT /standard_name= "Single nucleotide polymorphism"
 FT /note= "Referred to in specification as A118G"
 FT replace (91, A)
 FT /tag= e
 FT /standard_name= "Single nucleotide polymorphism"
 FT /note= "Referred to in specification as G779A"
 FT variation replace (1154, A)
 FT /tag= f
 FT /standard_name= "Single nucleotide polymorphism"
 FT /note= "Referred to in specification as G942A"
 FT
 PN US635168-B1.
 PD 01-JAN-2002.
 PF 09-JUL-1999; 99US-00351198.
 PR 10-JUL-1998; 98US-0092402P.
 PA (UYRO) UNITV ROCKEFELLER.
 PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 XX
 PI Kreek MJ, Iaforge KS, Yu L, Tischfield JA;
 DR WPI; 2002-163201/21.
 DR P-PSDB; AAU76034.
 XX
 PT Determining a susceptibility in a subject to oploid addiction, involves
 PT determining variation in the first allele of human mu oploid receptor
 PT gene or mu oploid receptor protein in the sample of the subject.
 PS
 XX Claim 1; Fig 4; 48pp; English.
 CC The present invention relates to a new method for determining
 CC susceptibility to oploid addiction in a subject. The method of the
 CC invention involves determining if the human mu oploid receptor (MOR) gene
 CC comprises a DNA sequence having at least one variation in a 2162
 CC nucleotide sequence, fully defined in the specification. The method also
 CC involves determining if the human MOR comprises a variation in a 400
 CC residue amino acid sequence, fully defined in the specification. The
 CC method is useful for determining susceptibility to oploid addiction in a
 CC subject. The method is also useful for identification of target
 CC prevention methods, early therapeutic intervention and improved treatment
 CC for oploid addiction, infertility, constipation, diarrhoea, impaired
 CC immune responsiveness and stress. The present nucleic acid sequence
 CC encodes the human mu oploid receptor (hMOR) protein of the invention
 CC
 SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 0 U; 2 Other;
 Query Match 37.7%; Score 434.8; DB 6; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1.4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
 Qy 92 CCGCGTGGGCGGAGCCCGACAGCAACGCGCGCGCTCGAGAGACGCGCAGCTGAGC 151
 Db 337 CCGAGCCATGCGGTCCGAGACCGCACCAACTGGCGGAGAGACAGCGTGTGCCCTCGA 396
 Qy 152 CCGCGACATCTCCCGGCGCATCCGCTCATATCAACGCGGCTTACTCGTATGTTG 211
 Db 397 CCGGAGTCCCTTCATGATCAACGCCATCAAGATCAATGCGCCCTTACTCTCATGTCG 456
 Qy 212 TCGTGGGCTTGGGCACTGCTGATCATGTGCGATCATCGATACACAAAGATGA 271
 Db 457 TGGTGGGCTCTTGGAACTTCTGCTCATGTATGATTTGCAATACCAAGATGA 516
 Qy 272 AGACAGCAACCAATTTATATTTAACTGCTTGGCAGATGCTTTAGTTACTACA 331
 Db 517 AGACTGCAACCAATTTATATTTAACTGCTTGGCAGATGCTTTAGTTACTACA 576
 Qy 332 CCATGCTTTTGAAGTAGGTCTTACTGATGATTAATTCCTGGCTTTGGGAGATGCTGT 391
 Db 577 CCTGCTTTCAGAGTAGTGAATTTACTTAATGGAACATGGCCATTTGGAAACCATCTTT 636

QY 392 GCAAGATAGTAATTCATTTGATGATCTACTACACATGTCACAGACTCTTCACTTGACCA 451
 Db 637 GCAAGATAGTATCTCCATAGTATTAATTAACATGTTACCCAGCATATTCACCTCTGCA 696
 QY 452 TGATGAGCGTGGACCGCTACATTTGCGGTGGCCACCCCGTGAAGGCTTTGACCTCCGA 511
 Db 697 CCATGAGTGTGATGATGATACATGCAAGTCTGCAACCTCTGTCAGAGGCTTAAGATTTCCGA 756
 QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGGCTGTGTCGTATCTGTTGGCA 571
 Db 757 CTCGCCGAAGTCCCAAAATTATCAATGTCGCACTGGATCTCTCTTCAGCCATTTGGTC 816
 QY 572 TCTGTCAATAGTCTTGTGAGGACCAAGTACAGGGAAGACGTGATGATCTGATGCT 631
 Db 817 TTCCTGTATGTTTCAATGCTCTACACAAAATACAGGCAAG-----TTCATATGATTTGA 870
 QY 632 CTTTGACAGTCTCCAGATGATGATCTATCTCTGCTGGAGACCTCTTCAATGAAGATCTGCT 691
 Db 871 CACTMAATGCTCTCATCCAACTGTGTACTGGAAACCTCG---TGAAGATCTGTGTT 927
 QY 692 TCATCTTTGCTTGTGATCCCTGTCTCATCATATGCTCTGCTACACCTGATGATCC 751
 Db 928 TCATCTTGTGCTTCAATTAATGCAAGTCTCATATTAACGCTGTGCTATGAGCATGATCT 987
 QY 752 TGGCTCTAAGAGCGTCCGGCTCTTTCGGCTCCCGAGAGAAAGATGSCAACCTGGCTA 811
 Db 988 TGGCTCTAAGAGTGTCCGACATGCTCTCTGAGCTCCAAAGAAAGACAGGAATCTTCGA 1047
 QY 812 GGATCACCAGATGCTGCTGT 871
 Db 1048 GGATCACCAGATGCTGCTGT 1107
 QY 872 ACATATTCATCTGCTGTGAGGCTCTGGGAGACACTCCCAACGACAGCTGCTCTCTCA 931
 Db 1108 ACATATTCATCTGCTGTGAGGCTCTGGGAGACACTCCCAACGAGCTGCTCTCTCA 1167
 QY 932 GCTATTCATCTGCTGTGAGGCTCTGCTATACCAAGATGAGCTGATCCATCTCTACG 991
 Db 1168 CTGGCCTCTGCTGTGAGGCTCTGCTATACCAAGATGAGCTGCTGATCCATCTCTTATG 1227
 QY 992 CTTTCTGTGATGAAATCTTCAACGCGGTCTTCCGGAGACTTCTGCTTTCACATGAAGATGA 1051
 Db 1228 CATTTCTGATGAAATCTTCAACAGATGCTTCAAGAGATGCTGATCCCAACCTCTTCA 1287
 QY 1052 GGATGAGCGGACAGCACTAGCAAGTCCGAATA 1087
 Db 1288 ACATGAGCAACAAATCTCCTCGAATTCGTGCA 1323

RESULT 37
 ACAS6781
 ID ACAS6781 standard; cDNA; 2162 BP.

ACAS6781;
 06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1379.

Human; probe; ss; array element; Parkinson's disease;
 signalling pathway population; cancer; adenocarcinoma; leukaemia;
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

OS Homo sapiens.
 XX US6500938-B1.
 XX 31-DEC-2002.
 XX 30-JAN-1998; 98US-00016434.
 XX 30-JAN-1998; 98US-00016434.
 XX

PA (INCY-) INCYTE GENOMICS INC.
 PI Au-Young J, Seilhamer JI;
 DR WPI; 2003-352189/33.
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides.
 PS Claim 1; SEQ ID NO 1379; 65bp; English.
 XX
 CC The invention relates to a combination which, comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signalling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
 CC
 SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 0 U; 2 Other;
 Query Match 37.7%; Score 434.8; DB 7; Length 2162;
 Best Local Similarity 66.3%; Pred.No. 14e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGGCTCGAGAGACGCGCAGCTGGAGC 151
 Db 337 CCGAGCCATGCGGCTCCGAACCGCACCAACTGTGGGGAGAGACAGCCGTGCTCCGA 396
 QY 152 CCGGACATCTCCCGGCGCATCCGGTCAATCAACGCGGCTCTACTCTGATGTTGG 211
 Db 397 CCGGAGTCCCTCCATGATCAACGGCCATCAACGATGAGCCCTTATCTCATCTGCTGG 456
 QY 212 TGTGGGCTGTGGGCAACTGCTGTGATGTTGTATCATCTCCGATACAAAGATGA 271
 Db 457 TGTGGGCTGTGGGCAACTGCTGTGATGTTGTATCATCTCCGATACAAAGATGA 516
 QY 272 AGACAGCAACCAACTTATACATATTTAACTGCTTTGGCAGATGCTTATGTTACTACA 331
 Db 517 AGACTGCCAACCAACTTATACATATTTAACTGCTTTGGCAGATGCTTATGTTACTACA 576
 QY 332 CCATGCGCTTTCAGAGTCCGCTTACTGATGATTTCTGAGCTTTTGGGAGTGTCTGT 391
 Db 577 CCCTGCGCTTTCAGAGTCCGCTTACTGATGATTTCTGAGCTTTTGGGAGTGTCTGT 636
 QY 392 GCAAGATAGTATTTCCATGATTTTACTACAAATGTTTACCCAGCATCTTACCTTGACCA 451
 Db 637 GCAAGATAGTATTTCCATGATTTTACTACAAATGTTTACCCAGCATCTTACCTTGACCA 696
 QY 452 TGATGAGCGTGGACCGCTACATTTGCGGTGGCAACCCGCTGAAGGCTTTGACTCCGA 511
 Db 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
 QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGTGTCGTATCTGTTGGCA 571
 Db 757 CTCGCCGAAGTCCCAAAATTATCAATGTCGCACTGGATCTCTCTTCAGCCATTTGGTC 816


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OS Synthetic.
XX Key location/Qualifiers
FH CDS 213..2040
FT /*tag= a
FT /product= "mu-opioid receptor"
FT misc_feature 502..503
FT /*tag= b
FT /note= "Site of intron 1"
FT mutation 666
FT /*tag= e
FT /note= "Wild type A is replaced by G"
FT misc_feature 855..856
FT /*tag= c
FT /note= "Site of intron 2"
FT misc_feature 1376..1377
FT /*tag= d
FT /note= "Site of intron 3"
XX MO9833937-A2.
XX 06-AUG-1998.
XX 02-FEB-1998; 98WO-DE000382.
XX 03-FEB-1997; 97DE-01003925.
XX (DEIB-) DEIBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Hoehe M, Wendel B;
XX WPI: 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor - XX
XX e.g. to predict pre-disposition to addiction and for development of XX
XX analgesics, anaesthetics and anti-addiction agents.
XX
XX Claim 8; Page; 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX nucleotide at position 666 of the wild-type sequence represented in
XX AAV61994 is replaced by a G. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmaceutical agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug. Particular
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism. Note: This sequence is not
XX represented in the specification and has been constructed from the wild-
XX type sequence represented in AAV61984 in accordance with the
XX specification
XX
XX Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 0 U; 2 Other:
XX
Query Match 37.5%; Score 433.2; DB 2; Length 2162;
Best Local Similarity 66.2%; Pred. No. 3.5e-96;
Matches 659; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

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QY 272 AGACAGCAACCAACATTTACATATTTACCTGGCTTTGGACAGATCTTTAGTTACTACAA 331
DB 517 AGACTGCCACCAACATCTACATTTTCAACCTTGGCTCTGGACAGATCTTTAGCCACAGTA 576
QY 332 CCATGCCCCCTTTCAGAGTACGGCTCTATGATGAAATTCCTGGCTTTGGGGATGCTGT 391
DB 577 CCTGCCCTTCCAGAGTGTGATTAATTAACATAGGGAACATGGCCATTTGGAACATCTT 636
QY 392 GCAAGATGTAATTTCCATTTGATTTACTACAAATGTTTCAACAGCATCTTCACTTGACCA 451
DB 637 GCAAGATGTAATCTCCATTAATTAATTAATGATGATGATGATGATGATGATGATGATG 696
QY 452 TGATGAGGCTGGAACCGGACATTCGCGGTGCAACCCCGTGAAGCTTTGACCTCCGCA 511
DB 697 CCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
QY 512 CACCCTTGAGGCAAAAGATCATATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571
DB 757 CTCCCGGAAATGCCAAATTTATCAATGCTGCAACTGATCTCTCTTCAAGCATTTGGTC 816
QY 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGAGCTGATGATGATGCT 631
DB 817 TTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 870
QY 632 CCTTGACATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 871 CACTAACATTTCTTCATCCAACTGGTACTGGGAAACCTGG--TGAAGATCTGTGTT 927
QY 692 TCATCTTGGCTTGCATGATCCCTGTCTCATATCATCATGCTGCTGCTGCTGCTGCTGCT 751
DB 928 TCATCTTGGCTTGCATGATCCATGATGATGATGATGATGATGATGATGATGATGATGATG 987
QY 752 TGCCTTCAAGAGCTCCGCTCTTCTGCTCCGAGAGAAAGATGCAACTGCTGCTA 811
DB 988 TGCGCTCAAGAGTGTCCGATGCTCTGCTCCAAAGAAAGAGACAGAAATCTTCCAA 1047
QY 812 GGATCAGCAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
DB 1048 GGATCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1107
QY 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
DB 1108 ACATTTAGTATCATTTAAAGCTTTGTTTAAATCCAGAAACATGATGATGATGATG 1167
QY 932 GCTATTTACTTGTGATGCTCTTGAAGCTTATACCAAGATGATGATGATGATGATG 991
DB 1168 CTGGCACTTCTGATGCTCTTGAAGCTTATACCAAGATGATGATGATGATGATG 1227
QY 992 CCTTTCTGATGAAATCTTCAAGGCTTTCCGGGACTTCTGCTTTCACATGAAAGTGA 1051
DB 1228 CATTTCTGATGAAATCTTCAAGGCTTTCCGGGACTTCTGCTTTCACATGAAAGTGA 1287
QY 1052 GGATGAGCGGACAGACACTAGACAGATGCCAATA 1087
DB 1288 ACATTTAGCAGCAAAATCTCACTGCAATTCGTGCA 1323

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RESULT 44
 AAV61992
 ID AAV61992 standard; cDNA; 2162 BP.

AAV61992;

11-JAN-1999 (first entry)

Human mu-opioid receptor cDNA variant 8.

Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 predisposition; addiction; analgesic; anaesthetic; anti-addictive;
 psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 cocaine; inherited alcoholism; human; ss.

OS	Homo sapiens.	
XX	Synthetic.	
PH	Key	Location/Qualifiers
FT	CDS	213..2040
FT		/tag= a
FT		/product= "mu-opioid receptor"
FT	misc_feature	502..503
FT		/tag= b
FT	misc_feature	/note= "Site of Intron 1"
FT		855..856
FT		/tag= c
FT	mutation	/note= "Site of Intron 2"
FT		1006
FT		/tag= e
FT	misc_feature	/note= "Wild type G is replaced by A"
FT		1376..1377
FT		/tag= d
FT		/note= "Site of Intron 3"
XX	WO9833937-A2.	
PN		
XX		
PD	06-AUG-1998.	
XX		
PF	02-FEB-1998;	98WO-DE000382.
PR	03-FEB-1997;	97DE-01003925.
XX		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
PI	Hoehne M, Wendel B;	
XX		
DR	WPI; 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g. to predict pre-disposition to addiction and for development of	
PT	analgesics, anaesthetics and anti-addiction agents.	
XX		
PS	Claim 8; Page; 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor in which a G	
CC	nucleotide at position 1006 of the wild-type sequence represented in	
CC	AAV61984 is replaced by an A. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism. Note: This sequence is not	
CC	represented in the specification and has been constructed from the wild-	
CC	type sequence represented in AAV61984 in accordance with the	
CC	specification	
XX		
SQ	Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 0 U; 2 Other;	
XX		
Query Match	37.5%; Score 433.2; DB 2; Length 2162;	
Best Local Similarity	66.2%; Pred. No. 3.5e-96;	
Matches 659; Conservative	0; Mismatches 328; Indels 9; Gaps 2;	
0Y	92 CCGGCTGGGCGAGCCGACAGCAACGGGAGCGCGCTCGGAGGACGGCGACGTGGAGC	151
Db	337 CCGACCCATGCGGTCCGAACCGCAACCTGGGCGGAGAGACAGCTGGCCCTCCGA	396
0Y	152 CCGGCGACATCTCCCCGGGCAATCCCGGATCATCATCAACGCGGCTCACTCCGATGATTGCG	211
Db	397 CCGGAGATCCCTCCATGATCAACGGGCAATCAAGATATATGGCCCTTAATCATTCGTGGG	456
0Y	212 TCGTGGCTTGGTGGGCAACTGCTGTGTCATGTTGTGATCATCCGATPACAAAGATGA	271

Db	457	TGATGAGGGGCTCTTCGGAAACTTCCTGGTCACTGATGATGATTTGTACAGATACACCAAGATGA	516
Qy	272	AGACGCAACCAACACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAA	331
Db	517	AGACTGCCACCAACATCTACATTTTCAACCTTGCTGTGGCAGATGCTTTAGCCACAGTA	576
Qy	332	CCATGCCCTTTCAAGTACGGCTCTACTGATGTAATTCCTGGCTTTTGGGGATGTCCTGT	391
Db	577	CCCTGCCCTTCCAGATGTGAATTCCTAAATGGGAACATGGCCATTTGGAACCATCTCTTT	636
Qy	392	GCAAGATAGTAATTTCCATTTGATTACTACATGTTCAACAGTGTCAACAGATCTTCACTTGACCA	451
Db	637	GCAAGATAGTATCTTCCATAGATTTCTAAACATGTTTCAACAGATTTTCAACCTCTGTGA	696
Qy	452	TGATGAGCGTGAACCGCTACATTTGGCGTGTGCCACCCCGTGAAGCTTTTGACTTCCGA	511
Db	697	CCATGATGTTGATGATACATATGGACAGTGTGCCACCTGTCAAGGCCATTAGATTTCCGTA	756
Qy	512	CACCTTTAAGGCAAAAGTCAATCAATATCTGATCTGGCTGTCTGTCTATCTTTTGGCA	571
Db	757	CTCCCGCAAAAGCCAAATTAATCAATATCTGTGCACTGATCTCTCTTTCAGCACTATGGTC	816
Qy	572	TCTCGCAATATGCTCCTTGGAGGCAACCAAGTCAAGGAAGAAGTCGATGATTTAGTGCT	631
Db	817	TTCCGTATATGTTATATGGCTACAAACAAATACAGGCAAG-----TTCCATAGATTGTA	870
Qy	632	CCTTGCAATTTCCAGATGATGATCTACTCTGGTGGGACCTCTTTCATGAAAGATCTGCT	691
Db	871	CACATAACTTCTCTCATCCAAACCTGTACTGGGAAACCTGG---TGAAGATCTGTGTTT	927
Qy	692	TCATCTTTGGCTTGTGATCCCTGTCTCTCATCATCATGCTGTCTCTACACCTGATATCC	751
Db	928	TCATCTTTCGCTTCAATTAATGCAAGTCAATCAATTAACGTGTGCTATGGAATGATGATCT	987
Qy	752	TGGCTTCAAGGCGTCCGCGCTCTCTTCTGTGCTCCCGAGAGAAATGGCAACCTGGCTGA	811
Db	988	TGCGCTTCAAGAGTGTCCACATGCTCTGTGCTCCAAAGAAAGACAGAAATCTTTCGA	1047
Qy	812	GGATCACCAGACTGGTCTGTGTGTGTGTGGCAGTCTTGTGCTGTGCTGACTCCCATTC	871
Db	1048	GGATCACCAGATGGT	1107
Qy	872	ACATATTTCACTCTGGTGGAGGCTCTGTGGGAGCACTCCCAACAGCAGCTGCTCTTCCA	931
Db	1108	ACATTTACGTATCATTTAAACCTTGTGTTAACATCCCAAGAACTACGTTCCAGACTGTTT	1167
Qy	932	GCATATTTCTTGTGATGATGCGCTTAAAGGCTTAAACAGTAAAGCTGAATCCCATCTTACG	991
Db	1168	CTTGGCACTTCTGTGATGTGCTTAAGTATCAACAAACAGTGTCTTCAACCGAGTCTTTATG	1227
Qy	992	CCTTTCTTGTATGATAAACTTCAAGGCGTGTCTCCGGGACTTCTGTCTTCCACTGAAGATGA	1051
Db	1228	CATTTCTGTGATGATAAACTTCAAGAGTGTCTTCAAGAGATTTCTGTATCCCAACCTCTTCCA	1287
Qy	1052	GGATGAGCGGCAAGACCTAAGCAGAGTCCGAAATA	1087
Db	1288	ACATTTGAGCAACAAACTCCACTGGAATTCGTCTGA	1323
RESULT 45			
AAV61993			
ID AAV61993 standard; cDNA, 2162 BP.			
XX AAV61993;			
AC AAV61993;			
XX AAV61993;			
DT 11-JAN-1999 (first entry)			
XX Human mu-opioid receptor cDNA variant 9.			
DE Human mu-opioid receptor cDNA variant 9.			
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;			
KW prediction; addition; analgesic; anaesthetic; anti-addictive;			
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;			
KW cocaine; inherited alcoholism; human; ss.			

KW autonomic nervous system; peristalsis regulator; body weight;
KW neuroendocrine disorder; MOR-1D; ss.

OS Mus sp.

FH	Key	Location/Qualifiers

FT / *tag= a

```
FT /product= "MOR-1D"  
FT /note= "no termination codon given"
```

PN WO200004046-A2.

PD 27-JAN-2000.

PF 15-JUL-1999; 99WO-US015974.

PR 16-JUL-1998; 98US-0092980P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;

DR WPI; 2000-182402/16.

XX

PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight.

PS Claim 32; Fig 2B; 83pp; English.

The present sequence encodes a murine mu-opioid receptor (MOR-1) splice variant MOR-1D. The specification describes 11 new exons for the MOR-1 gene, which combine to yield 15 novel splice variants of the MOR-1 gene. These splice variants are potential targets for modulating morphine analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide is used to screen compounds for opioid activity. Such compounds are potential analgesics or more generally agents that affect gastrointestinal motility, respiration or the immune, endocrine or autonomic nervous systems, e.g. regulators of peristalsis. Antagonists, agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids, are used to regulate morphine analgesia and body weight. The level of MOR-1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1 related pharmacological abnormalities or neuroendocrine disorders, particularly inherited disorders. Transgenic animals with extra copies of the MOR-1 gene, or with endogenous alleles deleted, are used to study loss or gain of function phenotypes

Sequence 1334 BP; 320 A; 397 C; 297 G; 320 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1334;

Matches 663; Conservative 0; Mismatches 336

92 CCGGCTGGGCCGAGCCCGACAGCAACGGCAGCCCGGCTCGGAGGACCGGCAGCTGGAGC 151

Db	185	CCGACCCAGACGGGTCTCTAACCGCAGCGGGGCTTGGCGGGAGCCAGACGGCTGTGGCTTCAGA	244
QY	152	CCGCGCAACATCTCCCGCGGATCTCCCGGATCATACGAGCGGGTCTACTCTCCGTAGTGTTCG	211
Db	245	CCGGACGCCCTTCTCATATGTCACAGGCATTCACCATCATGGCCCTCTATTCTATACGTGTGTG	304
QY	212	TCTGTGGGCTTGGTGGGCAACTCGCTGTGCATCTTTCGTATCATCGATACGATACCAAAAGATGA	271
Db	305	TAGTGGGCTCTTTGGAAACTTCTCGTGTCATGTATGTATTTGTAAATATATCCAAATATGA	364
QY	272	AGACAGCAACCAACTTATACATATTTAACTCTGGCTTGGCGAGATCTTATGTTACTACAA	331
Db	365	AGACTGTCCACCAACATCTACATTTTCAACCTTTGCTCTGGCAGATGCTCTTAGCCACTRACA	424
QY	332	CCATGCCCTTTTACAGATACGATCTTACTGTATGAAATTCCTGGCCCTTTTGGGAGATGTGCTGT	391

[illegible]

PT selective analgesic and for regulating morphine analgesia or body weight.

XX Claim 30; Fig 2A; 83bp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
CC variant MOR-1C. The specification describes 11 new exons for the MOR-1
CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
CC These splice variants are potential targets for modulating morphine
CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
CC is used to screen compounds for opioid activity. Such compounds are
CC potential analgesics or more generally agents that affect
CC gastrointestinal motility, respiration or the immune, endocrine or
CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
CC are used to regulate morphine analgesia and body weight. The level of MOR
CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
CC related pharmacological abnormalities or neuroendocrine disorders,
CC particularly inherited disorders. Transgenic animals with extra copies of
CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
CC loss or gain of function phenotypes

XX Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1423;

Best Local Similarity 65.8%; Pred. No. 4,7e-96;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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OY 92 CCGGCTGGGCGGAGCGGAGCAGCAGCGCGGCTGGAGAGCGCGAGCTGAGAC 151
DB 185 CCGAGCCATGCGGCTCTTAACCGGACGGGCTTGGGGAGCCAGCCTGTGCTCGA 244
OY 152 CCGGCGACATCTCCCGGCGCATCCGGTATCATGACGGCGGCTACTCTCGTGTTCG 211
DB 245 CCGGAGAGCTTCCATGATGACAGGACATCACCATCATGGCCCTATTCTATCGTGTG 304
OY 212 TCGTGGGCTGTGGGGCAATCGCTGTCATGTTGTATCATCCGATACACAAAGATGA 271
DB 305 TAGTGGGCTCTTGGAAATCTCGTGTATGTATGTATGTATGAATACAAATGA 364
OY 272 AGACAGCAACCAACATTACATTTAATCTGCTTGGAGAGCTTTAGTTACTACAA 331
DB 365 AGACGCGCAACCAACCTTACATTTTCAACCTTGTCTGTGGAGATGCTTAGCCATGACA 424
OY 332 CCAATGCCCTTTAGAGTACGGTCTTACTTGTATGAAATTCCTGGCTTTGGGAGTGTCT 391
DB 425 CGTGCCTTTAGAGTGTAACTACGTATGGAACGTGGCCCTTGGAAACATCTCT 484
OY 392 GCAAGATGTAAATTTCCATTGATTTACTACAAATGTTTCAACGACATTTTCACTTGACCA 451
DB 485 GCAAGATGTATCTCAATGACTACTACAAACATGTTTCAACGATCCCTGTGCA 544
OY 452 TGATGAGCGTGGAGCGGTACATTTGCGTGTGCAACCCGATGAAGGCTTTGAGACTTCGCA 511
DB 545 CCAATGAGTGTAGACCGCTACATTTGCGTGTGCAACCCGATGAAGGCTTTGAGACTTCGCA 604
OY 512 CACCTTGAAGCAAAATGATCATATATCTGATCTGCTGTGCTGATCTGTGCA 571
DB 605 CCCCCGAAATGCCAAATTTGTCATGCTGCAATGAGTCTCTCTTCTGCGCAATGTGTC 664
OY 572 TCTGTCAATAGTCTTGTGAGGCAACCAAGTCAAGGAAAGAGCTGCATGCTAGTGTCT 631
DB 665 TGCCCGTATATGTTCTGCAACCAACCAAAATACAGCAGAGGTC-----CATGATTTCA 718
OY 632 CTTTCAGTTCCTCAATGATGACTCTCTGCTGGAGACCTTTTCATGAAGATCTGCTCT 691
DB 719 CCTTACGTTCTCTATCCCATGCTACTGAGGAACCTGCTC---AAATCTGTGCT 775
OY 692 TCATCTTTCCTTGTGATCCCTGTCTCATCATCATGCTGTGCTACACCTGATGATCC 751
DB 776 TCATCTTTCCTTGTGATCCCTGTCTCATCATCATGCTGTGCTACACCTGATGATCT 835

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OY 752 TGGCTCTCAAGAGCGTCCGCTCTTTGTGGCTCCCGAGAGAAAGATGCAACCTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
OY 812 GGATCACCAGACTGTGCTGTGGTGTGGAGAGTCTTGTGCTGTGACATCCCATTC 871
DB 896 GGATCACCAGAGTGTGCTGTGGTGTGGAGAGTCTTGTGCTGTGACATCCCATTC 955
OY 872 ACATTTATCTGTGTGAGGCTCTGGGAGACCTCCCAACAGCAGACTGCTCTCTCA 931
DB 956 ACATCTATGTATCATCAACACATGATTCAGAAACCACTTTCAGACTGTCTT 1015
OY 932 GCTATTACTTTCGATGCGCTTGAAGCTTATACCAAGTACAGTCTGATTCCTGACG 991
DB 1016 CTTGCACTTTTGTGATTTGCTTGGTTACAAACAGCTGCTGAACTTCTTTATG 1075
OY 992 CTTTCTTGATGAAATCTTCAAGGCTTTCCGGACTTGTGCTTTCACATGAAGATGA 1051
DB 1076 GCTTCTGTGATGAAATCTTCAAGGCTTTTGAAGAGTCTGATCCCACTTCTCTCA 1135
OY 1052 GGAATGAGCGGCAAGACACTAGCAGATCCGAATACATTCAGATC 1099
DB 1136 CAATCGAACAGCAAAATCTGCTGAAATCGTCAAAACACTAGGGAAC 1183

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RESULT 50

AAZ60741
ID AAZ60741 standard; cDNA; 1610 BP.

AAZ60741;

16-MAY-2000 (first entry)

DE cDNA encoding murine mu-opioid receptor splice variant MOR-1.

KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioid-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system; endocrine system;
KM autonomic nervous system; peristalsis regulator; body weight;
KM neuroendocrine disorder; MOR-1; ss.

OS Mus sp.

FN Key Location/Qualifiers

FT CDS 283..1479

FT /tag= a

FT /transl_except= (pos: 916..918, aa: G1Y)

FT /product= "MOR-1"

PD WO200004046-A2.

PD 27-JAN-2000.

PF 15-JUL-1999; 99WO-US015974.

PR 16-JUL-1998; 98US-0092980P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;

DR WPI; 2000-182402/16.

DR P-PSDB; AAY68889.

PS Claim 29; Fig 2N; 83bp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
CC variant MOR-1. The specification describes 11 new exons for the MOR-1
CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.

CC These splice variants are potential targets for modulating morphine
 CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
 CC is used to screen compounds for opioid activity. Such compounds are
 CC potential analgesics or more generally agents that affect
 CC gastrointestinal motility, respiration or the immune, endocrine or
 CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
 CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
 CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
 CC are used to regulate morphine analgesia and body weight. The level of MOR
 CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
 CC related pharmacological abnormalities or neuroendocrine disorders,
 CC particularly inherited disorders. Transgenic animals with extra copies of
 CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
 CC loss or gain of function phenotypes

XX Sequence 1610 BP, 373 A, 476 C, 368 G, 393 T, 0 U, 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1610;

Best Local Similarity 65.8%; Pred. No. 5e-96;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGAGCTGAGC 151
 DB 401 CCGACCCATGGGCTCTTAACCGCACGCGGCTTGGGCGAGACACAGCTGTGCCCTCAGA 460
 QY 152 CCGGACATCTCCCGGCGCANTCCCGTCATCATCAAGCGGCTGCTCCGTAAGTTG 211
 DB 461 CCGGACCCCTTCCATGGTCAAGCAATCACCATCATATGCCCCCTATTTATCGTGTG 520
 QY 212 TCGTGGGCTTGGGCAACTCGTGTGATGTTGATGATCATCGATACCAAAAGATGA 271
 DB 521 TAGTGGGCTCTTTGGAACTTCCTGTGATGATGATGATGATGATGATGATGATGATGAT 580
 QY 272 AGACAGCAACCAATTATTAATTTAACTGCTTGGCGAGATGCTTACTACTACAA 331
 DB 581 AGACTGCGACCAACATCTTCACTTCAACTTGTGCTGCGAGATGCTTACCACTAGCA 640
 QY 332 CCATGCCCCCTTCAAGAGTCACTTGAATTAATTCCTGCGCTTTGGGAGATGCTGT 391
 DB 641 CGCTGCCCTTCAAGAGTCACTTGAATTAATTCCTGCGCTTTGGGAGATGCTGT 700
 QY 392 GCAAGATAGTAAATTTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 451
 DB 701 GCAAGATAGTAAATTTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 760
 QY 452 TGAATGAGGTGACCGCTTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 511
 DB 761 CCATGAGAGTGTAGACCGCTTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 820
 QY 512 CACCTTGAAGCAAAAGTATCATCAATATCTGATCTGCTGTGCTGATCTGTGCA 571
 DB 821 CCCCCCAAAATGCCAAATTTCTCAATGCTGTGCAATGATCTCTCTTCTTCCCATTTGCTC 880
 QY 572 TCTGTGCAATAGTCTTGTGAGGACCAAAAGTCAAGGAAAGAGTGTGATGATGATGCT 631
 DB 881 TGCCCGTAATGTTTATGAGCAACCAAAATATAGGAGGGGTC-----CATAGATTGCA 934
 QY 632 CTTTGCAGTTCCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 DB 935 CCCCACAGTTCTCTCATCTCCACATGATGATGATGATGATGATGATGATGATGATGATGAT 991
 QY 692 TCATCTTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 DB 992 TCATCTTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
 QY 752 TGCCTTCAAGAGGCTCGGCTCTTCTTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
 DB 1052 TAGACCTCAAGAGGCTCGGCTCTTCTTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 1111
 QY 812 GGATTCACCAAGCTGTCTGT 871
 DB 1112 GGATTCACCAAGCTGT 1171

QY 872 ACATATTCATCTGTGAGGCTGTGGGAGACCTCCACAGACAGCTGTCTTCCA 931
 DB 1172 ACATATTCATCTGTGAGGCTGTGGGAGACCTCCACAGACAGCTGTCTTCCA 1231
 QY 932 GCTATTAATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
 DB 1232 CTTGCACTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
 QY 992 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
 DB 1292 GCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1351
 QY 1052 GGATGAGCGGCGAGAGCATGAGATGCGGAATATAGTTCAAGGATC 1099
 DB 1352 CAATGAAACAGCAAACTTGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1399

RESULT 51

AAZ60734
 ID AAZ60734 standard; cDNA: 1729 BP.

AAZ60734;

16-MAY-2000 (first entry)

cDNA encoding murine mu-opioid receptor splice variant MOR-1F.

Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

opioid-mediated ingestive response; opioid activity; analgesic;

gastrointestinal motility; respiration; immune system; endocrine system;

autonomous nervous system; peristalsis regulator; body weight;

neuroendocrine disorder; MOR-1F; ss.

Mus sp.

Key Location/Qualifiers

67..1401

15-JUL-1999; 99MO-US015974.

16-JUL-1998; 98US-0092980P.

(SLOK) SLOAN KETTERING INST CANCER RES.

Pasternak G, Pan Y;

WPI; 2000-182402/16.

P-PSDB; AAY68888.

New splice variants of the mu-opioid receptor, useful in screening for

selective analgesics and for regulating morphine analgesia or body

weight.

Claim 36; Fig 2F; 83bp; English.

The present sequence encodes a murine mu-opioid receptor (MOR-1) splice

variant MOR-1F. The specification describes 11 new exons for the MOR-1

gene, which combine to yield 15 novel splice variants of the MOR-1 gene.

These splice variants are potential targets for modulating morphine

analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide

is used to screen compounds for opioid activity. Such compounds are

potential analgesics or more generally agents that affect

gastrointestinal motility, respiration or the immune, endocrine or

autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,

agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-

encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,

are used to regulate morphine analgesia and body weight. The level of MOR

-1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1 related pharmacological abnormalities or neuroendocrine disorders. CC particularly inherited disorders. Transgenic animals with extra copies of the MOR-1 gene, or with endogenous alleles deleted, are used to study CC loss or gain of function phenotypes

Sequence 1729 BP; 417 A; 505 C; 395 G; 412 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1729;

Best Local Similarity 65.8%; Pred. No. 5.1e-96; Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

QY 92 CCGGCTGGGCGAGCCGACAGCAACGAGCGCGGCTCGGAGAGCGGCGAGCTGAGAC 151
DB 185 CCGAGCCATGCGGTCTTAACCGGAGGGGCTGGGGAGGCGACGCTGTGCTCAGCA 244
QY 152 CCGGCGACATCTCCCGGCGATCCGGTGCATGACGCGGCTTACTCCGTAGTGTG 211
DB 245 CCGGAGCGCTTCCATGATGACAGGCGATCAGCATATGCGCTTATCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTATGTGTATCATCCGATACAAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCCTGTCATGTATGTATGTATGATACCAAAATGA 364
QY 272 AGACAGCAACCAACTTATCATATTTAACTGCGCTTGGCAGATGCTTACTACAA 331
DB 365 AGACTGCGCAACCACTTACATTTTCACTTGTCTGCGCAATGCTTACCGCATGCA 424
QY 332 CCATGCGCTTGGAGATGCGTCTTATGATGATGATGATGATGATGATGATGATG 391
DB 425 CGCTGCGCTTGGAGATGCGTCTTATGATGATGATGATGATGATGATGATGATG 484
QY 392 GCAAGATGATATTTTCCATGATGATGATGATGATGATGATGATGATGATGATG 451
DB 485 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
QY 452 TGATGAGCGTGGAGCGCTTATGCGGTGTCACCGCGTGAAGGCTTGGACCTTCCGA 511
DB 545 CCATGAGTGTGAGCGGCTTACATGCTGCTGCGCACCGGCTCAAGGCGCTTGGATTC 604
QY 512 CACCGTTGAGGCAAGATCATCAATATGTCATGTCGTCGTCGTCATGTCATGTCGA 571
DB 605 CCGCGGAAATGCAAAATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 664
QY 572 TCTGTCGAATGATCCTTGGAGGCAACCAAGTCAAGGAGAGCGTCGATGATGATG 631
DB 665 TGCCGATGATGTCATGCGCACCAAAATACAGGAGGAGTCTCTCTCTCTCTCTCT 718
QY 632 CCTTGAGTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 719 CCTTACGTTCTCTCATGCGCATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 692 TCATCTTGGCTTGGTGTATCCTGTCCTCATGATGATGATGATGATGATGATGATG 751
DB 776 TCATCTTGGCTTGGTGTATGCGGCTCTCATGATGATGATGATGATGATGATGATG 835
QY 752 TCGCTGTCAGAGCGCTCGGCTCTCTTGTGCTCCGAGAGAAAGATGCAAGCTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGATGCTGCGGCTCCAAAGAAAGAGAGCAAGAACTGCGCA 895
QY 812 GGATACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
DB 896 GGATACACCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
QY 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
DB 956 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1015
QY 932 GCTATTTACTTGTGATGCTGCTTGAAGCTATACCAAGATGATGATGATGATGATG 991
DB 1016 CTTGACACTTCTGATGCTGCTTGGGTTACAAAGAGCTGCTGAAGCAAGTCTTATG 1075
QY 992 CTTTCTTGTGAAAGATTTCAAGGAGTGTTCGCGGAGCTTCTGCTTCCACTGAAGATGA 1051

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DB 1076 CTTTCTTGTGAAAGATTTCAAGGAGTGTTCGCGGAGCTTCTGCTTCCACTTCTCA 1135
QY 1052 GGATGAGCGGAGAGCACTAGCAGATGTCGGAATATACATTGAGATC 1099
DB 1136 CAATGGAACAGCAAACTCTGCTCGAATCCGCAAAACACTAGGAGAC 1183

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RESULT 52

AB198013 standard; cDNA; 1182 BP.

AB198013;

18-FEB-2002 (first entry)

Non-endogenous human GPCR cDNA, SEQ ID NO: 546.

Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;

constitutively activated GPCR; agonist; disease; ss.

Homoe sapiens.

Synthetic.

MO200177172-A2.

18-OCT-2001.

05-APR-2001; 2001MO-US011098.

07-APR-2000; 2000US-0195747P.

(ARENA) ARENA PHARM INC.

Lehmann-Bruhlma K, Llaw CW, Lin I;

WPI: 2001-648759/74.

P-PSDB; ABB56377.

Identifying agonists of G protein-coupled receptors (GPCRs) for use in

disease treatment, comprises contacting candidate compounds with versions

of GPCRs.

Example 2; Page 347-348; 394pp; English.

The invention relates to G protein-coupled receptors (GPCRs) for which

the endogenous ligand has been identified. Non-endogenous constitutively

activated versions of known GPCRs are used in the invention for the

direct identification of candidate compounds as receptor agonists,

inverse agonists or partial agonists. Such agonists are useful as

therapeutic agents for diseases or disorders associated with GPCRs. The

present sequence encodes a non-endogenous version of a known human GPCR

Sequence 1182 BP; 292 A; 343 C; 241 G; 306 T; 0 U; 0 Other;

Query Match 37.4%; Score 431.6; DB 5; Length 1182;

Best Local Similarity 66.1%; Pred. No. 7e-96; Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGAGCCGACAGCAACGAGCGCGGCTCGGAGAGCGGCGAGCTGAGAC 151
DB 125 CCGAGCCATGCGGTCTTAACCGGAGGGGCTGGGGAGAGAGCGCTGTGCTCCGA 184
QY 152 CCGGCGACATCTCCCGGCGATCCGGTGCATGATGATGATGATGATGATGATGATG 211
DB 185 CCGGAGTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 244
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTATGTGTATGTATGTATGTATGTATGTATG 271
DB 245 TCGTGGGCTTGGTGGGCACTTCTGTCATGATGATGATGATGATGATGATGATGATG 304
QY 272 AGACAGCAACCAACTTATCATATTTAACTGCGCTTGGCAGATGCTTACTACAA 331

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Db 305 AGACTGCCACCAACATCTACATTTTCAACCTTGCTGTGAGACAGATGCTTAGCCACCAAGTA 364
Qy 332 CCATGCCCCCTTTCAGAGTACGGCTCTGATGAAATTCCTGGCCTTTTGGGATGTCGT 391
Db 365 CCGTCCCCCTTCAGAGTGTGAATTAATTAATGGAACATGGCATTGGAACCAATCCTTT 424
Qy 392 GCAAGATGTAATTTCCATTGATTACTACAACATGTTACACGACATCTTCACTTGAACCA 451
Db 425 GCAAGATGTAATTTCCATTGATTACTACAACATGTTACACGACATCTTCACTTGAACCA 484
Qy 452 TGATGAGGTGAGACCGCTACATTCGCGTGGCCACCCCGTGAAGCTTTGAACCTTCCGA 511
Db 485 CCATGAGGTGATGATGATACATTTGACATGCTGCCACCTGTCAAGGCTTAGATTTCCGTA 544
Qy 512 CACCTTGAAGGCAAGATCATCAATATCTGATGTGCTGTGTCGTCATCTGTGGCA 571
Db 545 CTCGCCGAATGCCAAATTAATCATGTCGACATGATCCTCTTCCAGCATTTGCTC 604
Qy 572 TCTCTGCAATGATGCTTGTGAGGACCAAAAGTCAGGGAAGACGTGATGCTAGTGTGCT 631
Db 605 TTCCTGTATGTTTCTATGCTACACAAATACAGGCAAG-----TTCATAGATTGTA 658
Qy 632 CTTTGACAGTCCAGATGATGATGATGCTGCTGCTGAGACCTTTCATGAAGATCTGCT 691
Db 659 CACTAACATTTCTCTCATCCAACTGTGTAAGTGGAAACCTCG--TGAAGATCTGTGTT 715
Qy 692 TCATCTTGGCTTGTGATCCCTGTCTCATCATATGTCGTCTACACCTTGATGATCC 751
Db 716 TCATCTTGGCTTGTGATCCCTGTCTCATCATATGTCGTCTACACCTTGATGATGATCT 775
Qy 752 TGGCTCTGAAGAGCTCCGCGCTCTTTCGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
Db 776 TGGCTCTGAAGAGTCTCCGCGCTCTTTCGTGCTCCGAGAGAAAGATGCAACCTGCGTA 835
Qy 812 GGATCACCAGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 836 GGATCACCAGACGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
Qy 872 ACATTTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 896 ACATTTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
Qy 932 GCTATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 956 CTTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
Qy 992 CTTTCTTGTGATGAATACTTCAAGCGGTGCTTCCGGAACCTTCTGCTTCCACTGAAGATGA 1051
Db 1016 CATTTCTGATGAAAACTTCAAAACGATGCTTCAGAGAGTCTGATCCCAACCTTCTCA 1075
Qy 1052 GGATGAGCGGACAGACCTAGACAGAGTCCGAAATA 1087
Db 1076 ACATTGAGCAACAAATCTCACTGCAATTCGTGACA 1111

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RESULT 53
ABI98012
ID ABI98012 standard; cDNA, 1203 BP.

ABI98012;
18-FEB-2002 (first entry)
Non-endogenous human GPCR cDNA, SEQ ID NO: 544.
Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
constitutively activated GPCR; agonist; disease; ss.
Homo sapiens.
Synthetic.
MO200177172-A2.

```

PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011098.
XX
PR 07-APR-2000; 2000US-0195747P.
XX
PA (ABEN-) ARENA PHARM INC.
XX
PI Lehmann-Brulisma K, Llaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
XX
DR P-PSDB; ABB56376.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
PS Example 2; Page 345-346; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence encodes a non-endogenous version of a known human GPCR
SQ
Sequence 1203 BP; 301 A; 348 C; 245 G; 309 T; 0 U; 0 Other;
Query Match 37.4%; Score 431.6; DB 5; Length 1203;
Best Local Similarity 66.1%; Pred. No. 7e-96;
Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;
Qy 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGCTGAGAGAGCGGAGCTGAGC 151
Db 125 CCGAGCCATGCGGTCGCAACCGACCAACTGGGCGGAGAGACAGCTGTGCTCCGA 184
Qy 152 CCGGCAATCTCCCGGCAATCCGGTCATCATCAGCGGCTGCTACTCCGTAGTGTG 211
Db 185 CCGGCAATCTCCCGGCAATCCGGTCATCATCAGCGGTCATCATCAGCGGCTGCTACTCCGTAGTGTG 244
Qy 212 TCGTGGGCTTGGGAGCACTCGCTGTCATGTCGATCATCCGATACCAAAAGATGA 271
Db 245 TGGTGGGCTTGGGAGCACTCGCTGTCATGTCGATCATCCGATACCAAAAGATGA 304
Qy 272 AGACAGCAACCAATTTACATTTTAACCTGGCTTTGGAGATGCTTACTACTACA 331
Db 305 AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGCGAGATGCTTAGCCACAGTA 364
Qy 332 CCATGCCCTTCAAGATGAGGTCTACTGATGATTCCTGGCTTTTGGGATGTCGT 391
Db 365 CCGTCCCCCTTTCAGAGTGTGAATTAATTAATGGAACATGGCATTGGAACCAATCCTTT 424
Qy 452 TGATGAGGTGAGACCGCTACATTCGCGTGGCCACCCCGTGAAGCTTTGAACCTTCCGA 511
Db 485 CCATGAGGTGATGATGATACATTTGACATGCTGCCACCTGTCAAGGCTTAGATTTCCGTA 544
Qy 512 CACCTTGAAGGCAAGATCATCAATATCTGATGTGCTGTGTCGTCATCTGTGGCA 571
Db 545 CTCGCCGAATGCCAAATTAATCATGTCGACATGATCCTCTTCCAGCATTTGCTC 604
Qy 572 TCTCTGCAATGATGCTTGTGAGGACCAAAAGTCAGGGAAGACGTGATGCTAGTGTGCT 631
Db 605 TTCCTGTATGTTTCTATGCTACACAAATACAGGCAAG-----TTCATAGATTGTA 658
Qy 632 CTTTGACAGTCCAGATGATGATGATGCTGCTGCTGAGACCTTTCATGAAGATCTGCT 691
Db 659 CACTAACATTTCTCTCATCCAACTGTGTAAGTGGAAACCTCG--TGAAGATCTGTGTT 715

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QY 812 GGATCACCAGACGTGGTCTGTGGTGGTGGGAGCTTGTGCTGTGAGCTCCCATTC 871
 DB 896 GGATCACCAGACGTGGTCTGTGGTGGTGGGAGCTTGTGCTGTGAGCTCCCATTC 955
 QY 872 ACATATTCATCTCTGTGGAGCTCTGGAGACCTCCACAGACAGACGTCTCTTCCA 931
 DB 956 ACATCTATGTATCATCAAGACACTGATCAGATTCAGAAACACTTTCAGACTGT 1015
 QY 932 GCTATTACTTGTGATCGCTTGAAGCTATACCAACAGTACCTGATTCATTCACG 991
 DB 1016 CTTGCACTTCTGTGATCGCTTGAAGCTATACCAACAGTACCTGATTCATTCACG 1075
 QY 992 CTTTCTTGTGATGAACCTTCAAGGAGTCTTCCGGAGCTTCTGCTTCCACCTGAAGTGA 1051
 DB 1076 CTTTCTTGTGATGAACCTTCAAGGAGTCTTCCGGAGCTTCTGCTTCCACCTGAAGTGA 1135
 QY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATACAGTTCAAGATC 1099
 DB 1136 CAATCGAAGCAGCAAAACCTCTGCTGAAATCCGTCAAAACACTAGGGAAC 1183
 RESULT 55
 AAV49252 standard; DNA; 2229 BP.
 ID AAV49252;
 AC AAV49252;
 DT 28-OCT-1998 (first entry)
 DE Mouse mu opiate receptor gene.
 XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;
 KM exon; nervous tissue; pain; drug addiction; transplant rejection;
 KM immunosuppressant; analgesic; morphine; side effect; ds.
 OS Mus sp.
 FH Key location/Qualifiers
 FT CDS 256..1452
 FT /*tag= a
 FT /product= "mu opiate receptor"
 PN MO9802534-A2.
 XX 22-JAN-1998.
 PD 11-JUL-1997; 97WO-FR001282.
 XX 15-JUL-1996; 96FR-00008810.
 PR (CNRS) CENT NAT RECH SCI.
 PA Kieffer BL, Matthes HWD, Simonin F, Dierich A, Lemeur M;
 PI WPI; 1998-110582/10.
 DR P-PSDB; AAM44937.
 XX Transgenic animals defective in one type of opioid receptor - used to
 PT identify agents for treatment of pain, drug addiction and transplant
 PT rejection, lacking side effects of known opiate(s).
 PS Disclosure; Fig 11; 58pp; French.
 This sequence represents the gene encoding the mouse mu opiate receptor
 protein. The sequence is used to generate a transgenic non-human mammal
 for identifying agents for treating disorders associated with opiate
 receptors. In the mammal, the expression of the gene encoding the opiate
 receptor is modified, particularly by the deletion of an exon and/or
 insertion of a marker gene, e.g. the neomycin resistance gene, into the
 sequence. Especially the expression of the gene is altered in nervous
 tissue. The agents are potentially useful for treating severe pain
 (chronic or acute), drug addiction and/or prevention or treatment of
 transplant rejection (as immunosuppressants). The method may isolate and

CC identify powerful analgesics that lack morphine-like side effects
 XX Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 U; 0 Other;
 SQ Query Match 37.3%; Score 430.8; DB 2; Length 2229;
 Best Local Similarity 65.7%; Pred. No. 1.4e-95;
 Matches 662; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
 QY 92 CCGGCTGGGCGGAGCCGAGACAGCAGCAGCGCCGCTGGAGAGACCGCAGCTGGAGC 151
 DB 374 CCGGACCATGCGGCTCTTACCGCAGCGGCTTGGCGGAGCAGCGCTGGCCCTGAGA 433
 QY 152 CCGGACCATGCGGCTCTTACCGCAGCGGCTTGGCGGAGCAGCGCTGGCCCTGAGA 433
 DB 434 CCGGAGCCCTTCCATGATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 493
 QY 212 TCGTGGCTTGGTGGGCACTCGTGTGATGTTGATGATCATCCGATACCAAAAGTGA 271
 DB 494 TAGTGGGCTCTTGGAAACCTTCTGATGATGATGATGATGATGATGATGATGATGATG 553
 QY 272 AGACAGCAACCAATTTACATTTAATCTGCTGGAGATGCTTTAGTTACTACAA 331
 DB 554 AGACTGCGACCAACATCTACATTTTCAACCTTGGAGAGATGCTTTAGCCACTGCA 613
 QY 332 CCATGCCCTTTCAAGATACGGTCTACTTGAATGAAATTCCTGACCTTTTGGGAGTGGCTGT 391
 DB 614 CGTGGCTTTTCAAGATGATTTAATCTGATGATGATGATGATGATGATGATGATGATG 673
 QY 392 GCAAGATGATTAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 451
 DB 674 GCAAGATGATGATTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 733
 QY 452 TGATGAGCGTGGAGCCGCTTACATTTCCGTTGCCACCCCGTGAAGCTTTGAGACTTCCGCA 511
 DB 734 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793
 QY 512 CACCTTGAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 571
 DB 794 CCCCCGAAATGCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 853
 QY 572 TCTTGCATTAATGCTTTGAGAGCAACCAAGTCAGAGAAAGCTGATGATGATGATGATG 631
 DB 854 TGCCGTAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
 QY 632 CTTTGCAGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 DB 908 CCCCACCTTCTTCATCCACATGATGATGATGATGATGATGATGATGATGATGATGATG 964
 QY 692 TCATCTTGGCTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 DB 965 TCATCTTGGCTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1024
 QY 752 TCGGTCTCAAGAGCGTCCGCTCTTCTGAGCTCCGAGAGAAAGATGCAACTGGCTGA 811
 DB 1025 TAGACTCAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGAGACAGGAACTGGGCA 1084
 QY 812 GGATCACCAGACGTGGTCTGTGGTGGTGGGAGCTTGTGCTGTGAGCTCCCATTC 871
 DB 1085 GGATCACCAGACGTGGTCTGTGGTGGTGGGAGCTTGTGCTGTGAGCTCCCATTC 1144
 QY 872 ACATATTCATCTCTGTGGAGCTCTGGAGACCTCCACAGACAGACGTCTCTTCCA 931
 DB 1145 ACATCTATGTATCATCAAGACACTGATCAGATTCAGAAACACTTTCAGACTGT 1204
 QY 932 GCTATTACTTGTGATCGCTTGAAGCTATACCAACAGTACCTGATTCATTCACG 991
 DB 1205 CTTGCACTTCTGTGATCGCTTGAAGCTATACCAACAGTACCTGATTCATTCACG 1264
 QY 992 CTTTCTTGTGATGAACCTTCAAGGAGTCTTCCGGAGCTTCTGCTTCCACCTGAAGTGA 1051
 DB 1265 CTTTCTTGTGATGAACCTTCAAGGAGTCTTCCGGAGCTTCTGCTTCCACCTGAAGTGA 1324
 QY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATACAGTTCAAGATC 1099

Db 1325 CAATGACACGCAAAACTGCTCGAATCCGCAAAACATAGGGAAC 1372

RESULT 56

ABX13057

ID ABX13057 standard; DNA; 1149 BP.

AC ABX13057;

DT 29-AUG-2003 (revised)

DT 28-MAY-2003 (first entry)

DE Human MOR-V2R DNA.

Human; G-protein coupled receptor; gene; ds; GPCR; palmitoylation site; phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis; atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain; rheumatoid arthritis; obesity; Parkinson's disease; MOR; V2R; vasopressin V2R receptor; mu opioid receptor.

XX Homo sapiens.

OS Chimeric.

FH Key Location/Qualifiers

FT CDS 1..1149

FT /tag= a

FT /product= "Human MOR-V2R"

XX US2002106739-A1.

XX PD 08-AUG-2002.

XX PF 05-NOV-2001; 2001US-00993844.

XX PR 03-NOV-2000; 2000US-0245772P.

XX PR 08-JAN-2001; 2001US-0260363P.

XX PA (OAKL/) OAKLEY R. H.

XX PA (BARA/) BARAK L. S.

XX PA (LAPO/) LAPORTE S. A.

XX PA (CARO/) CARON M. G.

XX PI Oakley RH, Barak LS, Laporte SA, Caron MG;

XX DR WPI; 2002-690758/74.

XX DR P-PSDB; ABG75675.

PT Modified G-protein coupled receptor useful for identifying an agonist,
PT inverse agonist or antagonist of the receptor, comprises a carboxyl
PT terminal having one or more clusters of phosphorylation.

XX PS Disclosure; Fig 11; 57pp; English.

XX The invention relates to a modified G-protein coupled receptor (GPCR)
CC comprising an NPXXY motif, and a carboxyl terminal tail which comprises a
CC putative site of palmitoylation and clusters of phosphorylation, and a
CC retained portion of a carboxyl terminal region of a GPCR portion fused to
CC a portion of the carboxyl terminal from a second GPCR, that comprises
CC phosphorylation clusters and a putative palmitoylation site 10-25 amino
CC acid residues downstream of a second NPXXY motif. The modified GPCR is
CC useful for screening compounds for GPCR activity which comprises
CC providing a cell that expresses at least one modified GPCR, where the
CC cell further comprises arrestin conjugated to a detectable molecule,
CC exposing the cell to the compound, detecting the location of the arrestin
CC within the cell, comparing the location of the arrestin within the cell
CC in the presence of the compound to the location of the arrestin within
CC the cell in the absence of the compound and correlating a difference
CC between the location of arrestin within the cell in the presence of the
CC compound and the presence of the location of the arrestin in the cell
CC in the absence of the compound. Preferably, the arrestin is detected in
CC endosomes. The GPCR and a nucleic acid encoding the modified GPCR are
CC useful for preventing and/or treating a disease associated with GPCR in

CC mammals, such as angina pectoris, atherosclerosis, asthma, emphysema,
CC rhinitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain,
CC obesity or Parkinson's disease, by modulating GPCR activity and affinity
CC for arrestin. This sequence represents DNA encoding a chimeric receptor
CC polypeptide used in the scope of the invention. (Updated on 29-AUG-2003
CC to standardise OS field)

XX SQ Sequence 1149 BP; 261 A; 366 C; 252 G; 270 T; 0 U; 0 Other;

Query Match 37.3%; Score 430.4; DB 6; Length 1149;

Best Local Similarity 68.1%; Pred. No. 1.4e-95;

Matches 631; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 110 ACAGCAAGCAGCGCCGCTCGAGAGCAGCGGCAAGCTGAGCCCGGACATCTCCCGG 169
Db 137 ACCGCAACGGGCTTGCGGGAAACAGACACCTGTGCCCCACAGCGGACCCCTTCATAG 196
QY 170 CCATCCCGGTCATCATCAGCGCGGTCTACCTCGTAGTGTGTCGTGGGCTTGGAGCA 229
Db 197 TCACAGCCATTACATCATGAGCCCTCTACTCATCTGTGTGTGTGTGGGCTTCCGAA 256
QY 220 ACTGCGTGTATGTCTGTATCATCCGATACAAAATGAAAGACAGCAACCAATTT 289
Db 257 ACTTCCTGTATGATGTGATTTGTAAGATACACCAATGAAAGCTGCACCAACATCT 316
QY 290 ACATTTTACCTGGCTTGGCAAGTCTTAGTTACTTACAAACCATGCGCTTTCAGAGTA 349
Db 317 ACATTTTACCTGGCTTGGCAAGTCTTAGAGCAGCAAGTACACTGCCCTTTCAGAGTG 376
QY 350 CGGTCTACTTATGATATCTTGGCTTTTGGGAGATGTGCTGTGCAAGATAGTATTTCA 409
Db 377 TCAACTACCTGATGGAAACATGCGCCCTTGGAAACATCCTCTGCAAGATCGATCTCA 436
QY 410 TTGATTTACAAACATGTTACACAGATCTTCACTTACATGATGTAGCGGTGACCGCT 469
Db 437 TAGATTACTTAAACATGTTACACAGATTTACCTCTGACCAAGTACGAGCGGTGACCGCT 496
QY 470 ACATTCGCGTGGGACCCCGTGAAGCTTTTGAATTTCCGACACACCTTGAAGCAAGA 529
Db 497 ACATTCGCTGTGCGACCCCAAGTCAAGCCCTGATTTCCGTACCCCGGAATGCGCAAA 556
QY 530 TCATCAATATGTGATCTGTGCTGTGTGTGATCTGTGTGGAATCTTCAATATGTCTTG 589
Db 557 TCGTAAAGTGTGCAAGTGAATCTCTTGTGCGCATGGTCTGTGCTGTGAATGTTCATGG 616
QY 590 GAGGCACCAAGTCAAGGAAGAGTGTGATTTGATGAGTCTCTTGCAGTTCCAGATG 649
Db 617 CAACCACAAAATACAGGCA-----GGGCTCATGATTTGACCTTCAAGCTTCCAC 670
QY 650 ATGACTACTCTGTGGGAGCCCTTTTATGAAATCTGAGTCTTCACTTTGCTTCGTA 709
Db 671 CAACCTGTACTGGAGAACCTGCTC---AAATGTGTGTGTATTTCTTCCGTTTCATCA 727
QY 710 TCCCTGTCTCATATCATGTCTGTCTACACCTGATGATCTGTGCTTCAAGAGCTGC 769
Db 728 TGGCATATCTCATATCATCTGTGTGTGAGGCTGATATCTTACAGATCAAGAGAGCTTC 787
QY 770 GAGTCTCTTGTGCTCCGAGAGAAAGATCGCAACTGTGTGATCAACAGACTGTGTC 829
Db 788 GCATCTATTCGGGGCTCCAAAGAAAGACAGGAATCTCGCGAGATCAACCCGAGTGTGC 847
QY 830 TGTGTGTGTGTGAGCTTCTGCTGTGTGTGTGAGTCCCATTCATCATATTCCTGTGG 889
Db 848 TGTGTGTGTGTGTATTTATGCTGTGTGTGTGAGTCCCATTCATCATATTCCTGTGG 907
QY 890 AGGCTCTGGAGAGCACTTCCACAGACAGAGTGTCTTCCAGCTATTTACTTTCATG 949
Db 908 AAGGCTATATCATCATTTCCAGAAACATTTACAGACGTTTCTGGGACCTTGTGATTTG 967
QY 950 CTTAGGCTATATCAAGATGAGTGAATCCATTTCTTACGCTTTTGTGAAACT 1009
Db 968 CTTTGGGTTTACAGAAAGCTGCTGATTCATGATTTTACGCTTCTGTGATGAAACT 1027

QY	1010	TCAGCGGTGTTCCGGACTTCTGC	1035
Db	1028	TCAGCGATGCTTCAGAGAGTTCTGC	1053

RESULT 57
AAZ60729
ID AAZ60729 standard; cDNA; 1542 BP.

AC AAZ60729;

DT 16-MAY-2000 (first entry)

DE cDNA encoding murine mu-opioid receptor splice variant MOR-1E.

KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
 KW opioid-mediated ingestive response; opioid activity; analgesic;
 KW gastrointestinal motility; respiration; immune system; endocrine system;
 KW autonomic nervous system; peptidals; regulator; body weight;
 KW neuroendocrine disorder; MOR-1E; ss.

OS Mus sp.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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100	100	100

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FT      /*tag= a
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ET

PN WO200004046-

PD 27-JAN-2000.

PF 15-JUL-1999; 99WO-US015974.

PR 16-JUL-1998; 98US-0092980P.

PA (SLOK) SLOAN KETTER

PI Pasternak G, Pan Y;

DR WPI; 2000-182402/

XX

PT selecti

XX

SQ Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 U; 0 Other;

Query Match	37.2%	Score 429.2;	DB 3;	Length 1542;
Best Local Similarity	65.6%;	Pred. No. 3e-85;		
Matches 661; Conservative	0;	Mismatches 338;	Indels 9;	Gaps 2;

QY	92	CCGGCTGGGGCCGAGCCGACAGCAACGGACAGCCGCTCGAGAGACGCCAGCTGGAGC	151
Db	185	CCGACCCCATGCGGCTCTTAACCGCACGGGGCTTGGCCGGAGGCACAAGCCTGGGCCCTCAGA	244
QY	152	CCGGGCAATCTCCCGGGCCATCCCGGTCATCATCAGGGCGGTCTACTCCGTAGTGTTCG	211
Db	245	CCGGCAGCCCTTCAATGCTCACAGCCATCAACCATATAGGCCCTCTATTCTATCGTGTGTC	304
QY	212	TCTGGGGCTTGGTGGGCACTCGTGTGCATGTTCTGTATCATCCGATACCAAAAGATGA	271
Db	305	TAGTGGGCGCTTTGGAAACTTCTGGGCATGATATGATATGTAAGATATACCAAAATGA	364
QY	272	AGACAGCAACCAACATTATTAATTTAACCTGGCTTTGGCAGATGCTTTACTACTACA	331
Db	365	AGACTGCGACCAACAATCTACATTTTCAACTTGTGCTGGCGAGATGCCCTTACCCACTGACA	424
QY	332	CCATGCCCTTTCAGAGTACGGTCTACTTGTATGAATTCCTGGACCTTTTGGGATGTGCTGT	391
Db	425	CGCTGCCCTTTCAGAGTGTTAATCTACTGATGGAAAGTGGCCCTTTGGAAACATCCTCT	484
QY	392	GCAAGATATGTAATTTCCATTGATTACTACAAATGTTCCACGACATCTTCCCTTTGACCA	451
Db	485	GCAAGATGTGATCTCAATATAGACTACTACAAACATGTTCCACGACATCTTCCCTCTGACA	544
QY	452	TGATGAGGTGGACCGCTACCTTCCCGTGGCCACCCCGTGAAGGCTTTGGACCTTCCGA	511
Db	545	CCATGAGTGAAGACCGCTACCTTCCCGTGGCCACCCCGTGAAGGCTTTGGACCTTCCGA	604
QY	512	CACCCCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTGCTGCATCTGTTGGCA	571
Db	605	CCCCCGGAAATGCCAAATTTGTCAATGTCTGGCACTGGATCTCTCTTCTGCGCATTTGGTC	664
QY	572	TCTCTGCATATGTCCTTGGAGGCAACCAAGTCAGGGAAAGACTGGAATGTCAATTGATGCT	631
Db	665	TGCCCTATGTTTATGGCAACCAAAATTCAGGCAAGGGTCT-----CATTAATTTGCA	718
QY	632	CCTTGAGATTCACAGATGATGACATACCTCTGGTGGGACCTTTCATGAAATCTGGCGTCT	691
Db	719	CCCTCAGCTTCTTCATCTCCACATGTAATCTGGGAAACCTGCTC---AAATATCTGTTGCT	775
QY	692	TCATCTTGTGCTTCGTGATCCCTGTCTCTCATCATCATCTGCTGTGTACACCTGTATGATCC	751
Db	776	TCATCTTGTGCTTCATCATGCGGATCTCATCATCATCTGTGTGTTATGSACTGATGATCT	835
QY	752	TGCGTTCGAAGGGGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCCGAAACCTGGGTA	811
Db	836	TACACATCTMAAGTGTCCGATGTCTGTGGGCTCCAAAGAAAGACAGGAACCTGGCGCA	895
QY	812	GGATCACCAAGCTGATCCTGGTGTGTGAGGAGCTTCGTGCTGTGTCGACTCCCATTC	871
Db	896	GGATCACCCGGATGT	955
QY	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACCTTCCACAGACAGCTGCTCTTCCA	931
Db	956	ACATCTATGTATCATCAAAAGCACTGATACAGATTCAGAGAAACCACTTCCAGACTGTTT	1015
QY	932	GCTATTAATCTTGATAGCCTTTAGGCTATACCAACATGAGCTGAATCCCATCTCTACG	991
Db	1016	CTTGGCACTTGTGATGTGCTTGGGTTTACAAACACCTGTCTBAACCCAGCTTCTTATG	1075
QY	992	CCTTTCTTGTATGAATACTTCAAGGGGTGTTCCGGGACTTCTGCTTTCACCTGAAGATGA	1051
Db	1076	CGTTCCTGTGATGAATACTTCAAAAGATGTTTAAAGAGTTCTGATCCCAACTTCTCCA	1135
QY	1052	GGATGAGCGGCAAGCACTAGCAGAGTCCGAAATPACAGTTCCAGATTC	1099
Db	1136	CAATTCGAACAGCAAACTGTGCTGAATCCCTCAAAAACATAGGGAAC	1183

RESULT 58	
AAD11041	
ID	AAD11041 standard; cDNA; 1981 BP.

XX AC AAD1041;
 XX DT 24-SEP-2001 (first entry)
 XX DE Murine delta opioid receptor (DOR-2) partial cDNA.
 XX DE Mouse; delta opioid receptor; DOR-2; analgesic; enkephalin;
 XX KM opioid addiction; anti-addictive; 88.
 XX OS Mus sp.
 XX PN US626563-B1.
 XX PD 24-JUL-2001.
 XX PF 13-FEB-1995; 95US-00387707.
 XX PR 13-AUG-1992; 92US-00929200.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Evans CJ, Keith DE, Edwards RH, Kaufman D;
 XX DR MPI; 2001-463944/50.
 XX PT Nucleic acids encoding mammalian kappa and mu opioid receptors, useful
 XX PR e.g. to identify substances for treating opioid addiction and/or useful
 XX PT as analgesics.
 XX PS Claim 7; Fig 9; 46pp; English.

CC The invention relates to recombinant nucleic acid molecules which encode
 CC the murine delta opioid receptor, as well as recombinant nucleic acid
 CC molecules which can be retrieved using low-stringency hybridisation to
 CC this disclosed DNA. The invention provides genes encoding delta, kappa,
 CC and mu receptors of any species containing genes encoding such receptors
 CC sufficiently homologous to hybridise under low-stringency conditions. The
 CC nucleic acids may be used to recombinantly express kappa and mu opioid
 CC receptors in host cells. These cells may then be used in assays to
 CC identify modulators of the receptors activity that may be used, for
 CC example as analgesics or to combat the effects of opioid addiction. The
 CC nucleic acids and their complements may also be used as probe sequences
 CC to identify and characterise opioid receptor nucleic acids. The present
 CC sequence is murine delta opioid receptor (DOR-2) partial cDNA, mOR-1
 XX XX

Sequence 1981 BP; 499 A; 550 C; 436 G; 495 T; 0 U; 1 Other;

Query Match 37.2%; Score 429.2; DB 5; Length 1981;
 Best Local Similarity 65.6%; Pred. No. 3.3e-95;
 Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGAGCCGACAGCAAGCGAGCGCGCTCGAGAGACGCGAGCTGAGAC 151
 DB 374 CCGAGCCATGCGGTCTTAACCCGAGCGGCTTGGCGGAGACAGACCTGTGCCCTGAGA 433
 QY 152 CCGGCAACATCTCCCGGCGATCCGGTATCATCGGCGGTCTAATCCGTAGTGTG 211
 DB 434 CCGGAGCGCTTCCATGTGTACAGAGCCATCATGAGCCCTTATCTATCGTGTG 493
 QY 212 TCGTGGGCTTGGTGGCACTCGCTGTGTATGTTGTATCATCCGATACAAAGATGA 271
 DB 494 TAGTGGGCTCTTGGAACTTCCTGTGTATGTATGTATTAAGATTAACCAAAATGA 553
 QY 272 AGACAGCAACAAATTTACATATTTAACTGAGCTTTGGAGATGTTAGTTACTACA 331
 DB 554 AAGCTGCCCAACATCTTACATTTTCAACTTGTCTGTGCAATGCTTACGCACTAGCA 613
 QY 332 CGATGCCCTTTAGAGTACGCTTACTTATGATGATTTCTGGCTTTTGGGAGTGTGCT 391
 DB 614 CGCTGCCCTTTAGAGTGTATTAACCTGATGGAACGTGGCCCTTTGGAACATCTCT 673
 QY 392 GCAAGATAGTAAATTTCAATTGATTAACAACATGTTCAACAGATCTTCACTTGACCA 451

DB 674 GCAAGATGATGATCTCAATAGACTACTCAACATGTTCAACGATATCTTCACTTCGCA 733
 QY 452 TGATAGCGTGGACCGCTTACATTTGCCGTGTGCGACCCCGTGAAGCTTTGACTTCGCA 511
 DB 734 CCATAGTGTAGACCGCTTACATTTGCCGTGTGCGACCCCGTGAAGCTTTGACTTCGCA 793
 QY 512 CACCGTTGAAGCAAAAGATCAATATCTGATCTGCTGTGCTGTGATCTGTTGGA 571
 DB 794 CCCCCGAAATGCCAAATTTGTCATGTCTGCAATGATCTTCTTGTGCAATTTGCT 853
 QY 572 TCTTCGAATAGTCTTGGAGGACCAAAAGTCAGGAAGACGTGATGATGATGCT 631
 DB 854 TGCCGCTATGTTTACATGCAACCAAAATACAGCAAGGCTC-----CATAGATTGCA 907
 QY 632 CTTGCAAGTCCCAATGATGATGATCTCTGCTGAGACCTTTCAATGAAGATCTGCT 691
 DB 908 CCTCAGCTTCTCTCATCCACATGATGATGATGATGATGATGATGATGATGATGAT 964
 QY 692 TCATCTTGGCTTGGATCCCTGTGCTCATGATGATGATGATGATGATGATGATGATGAT 751
 DB 965 TCATCTTGGCTTGGATCCCTGTGCTCATGATGATGATGATGATGATGATGATGATGAT 1024
 QY 752 TGCGTCTCAAGAGCTGCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
 DB 1025 TACAGCTCAAGAGTGTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
 QY 812 GGATGACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 DB 1085 GGATGACCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
 QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
 DB 1145 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
 QY 932 GCTATTACTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
 DB 1205 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
 QY 992 CTTTCTTGTGAAATCTTCAAGCGGTGCTTCCGGAATCTTCTGCTTCTGCTGCTGCT 1051
 DB 1265 GCTTCTGATGAAATCTTCAAGCGGTGCTTCCGGAATCTTCTGCTTCTGCTGCTGCT 1324
 QY 1052 GGATGACCGGCAAGCACTAGCAAGTCCGAAATACACTTCAAGATC 1099
 DB 1325 CAATGAAACGCAAAATCTGCTGATCCGTCGAAACATAGGAAC 1372

RESULT 59
 ABS53445
 ID ABS53445 standard; DNA, 1981 BP.
 XX
 XX ABS53445;
 XX
 DE 19-NOV-2002 (first entry)
 XX
 DE DNA sequence of murine mu-receptor clone DOR-2.
 XX
 DE Enkephalin; opioid receptor; poisoning; addiction; morphine; codeine; ds;
 XX mouse; DOR-2.
 XX
 OS Mus sp.
 XX
 PN US6432652-B1.
 XX
 PD 13-AUG-2002.
 XX
 PF 14-MAR-1995; 95US-00405271.
 XX
 PR 13-AUG-1992; 92US-00929200.
 PR 13-AUG-1993; 93WO-US007665.
 PR 13-FEB-1995; 95US-00387707.
 PR 13-MAR-1995; 95US-00403260.

XX (RBCG) UNIV CALIFORNIA.
 PA
 XX Evans CJ, Keith DE, Edwards RH, Kaufman D;
 XX WPI; 2002-681194/73.
 XX
 PT Mammalian DOR-1 opioid receptors, useful for screening for compounds
 PT useful in the treatment of opioid addiction and poisoning.
 XX
 PS Example 9; Fig 9; 61pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel
 CC mammalian opioid receptor (DOR-1) displayed at the surface of recombinant
 CC host cells. The invention also comprises a method for screening a
 CC candidate substance for opioid agonist activity and a method for
 CC detecting the amount of activation of the opioid receptor in the presence
 CC as compared to the absence of the candidate substance. The methods and
 CC compounds of the invention may have anti-addictive agents and may be used
 CC to modulate opioid receptor activity. The mammalian opioid receptor of
 CC the invention may be used to screen for agonists and antagonists of its
 CC expression and activity which may be used to treat e.g. poisoning by, and
 CC addiction to, opioids (such as morphine, codeine, and many semi-synthetic
 CC congeners of morphine). The present sequence represents the DNA sequence
 CC of the mouse mu opioid receptor DOR-2 of the invention
 CC
 XX Sequence 1981 BP; 499 A; 550 C; 436 G; 495 T; 0 U; 1 Other;

Query Match 37.2%; Score 429.2; DB 6; Length 1981;
 Best Local Similarity 65.6%; Pred. No. 3.3e-95;
 Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGCGGCTCGAGAGACCGGACGTGAGC 151
 DB 374 CCGACCCATGGGCTCTTAACCCGACGCGCTTGGGAGAACACGACCTGTGCCCTGAGA 433
 QY 152 CCGGACATCATCTCCCGGCGCATCCGGTCTATCATCAGCGGCTTACTCCGAGTTCG 211
 DB 434 CCGGAGCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
 QY 212 TCGTGGGCTTGGTGGGCACTGCTGTGATGATGATGATGATGATGATGATGATGATGATG 271
 DB 494 TAGTGGGCTCTTGGAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 553
 QY 272 AGACGCAACCAACATTTACATTTAATCTGCTTGGGAGATGCTTATGATGATGATGATG 331
 DB 554 AGACTGCCACCAACATTTAATTTTCACTTGTCTGAGATGCTTATGATGATGATGATG 613
 QY 332 CCATGCGCTTTCAGAGTACGCTCTACTGATGATGATGATGATGATGATGATGATGATGATG 391
 DB 614 CGCTGCGCTTTCAGAGTCTTAACTTCTGATGATGATGATGATGATGATGATGATGATGATG 673
 QY 392 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
 DB 674 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 733
 QY 452 TGATGAGGCTGAGCCGCTACATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
 DB 734 CCATGAGTGTGAGCCGCTACATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
 QY 512 CACGCTTGAAGCAAAAGATCATCAATATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
 DB 794 CCCCCGAAATGCCAAATTTGTCAATGTCTGCAATGATCTCTCTTCTGCGATTTGCTC 853
 QY 572 TCTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAGACGTGATGATGATGATGATGATG 631
 DB 854 TGCCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
 QY 632 CCTTGCACTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
 DB 908 CCCCACGCTTCTCTCATCCACATGATGATGATGATGATGATGATGATGATGATGATGATG 964
 QY 692 TCATCTTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751

DB 965 TCATCTTGGCTTATCATATGCGGCGCTCATCATCATCTGTGTATGATGATGATGATCT 1024
 QY 752 TGGCTTCAAGAGCGTCCGCTCTTCTTGGCTCCGAGAGAAAGATGCAACTGCGTA 811
 DB 1025 TACAGCTCAAGAGTCCGCAATGCTGTGCGGCTCCAAAGAAAGACAGAAACCTGCGCA 1084
 QY 812 GGATCACCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
 DB 1085 GGATCACCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
 QY 872 ACATATTCATCTCTGAGGCTCTGAGGACCTCCACAGACAGACAGCTGCTCTTCCA 931
 DB 1145 ACATCTATGATCATATCAAAACATGATCAGATTCAGAAACACCTTCCAGCTGTTT 1204
 QY 932 GCTATTTACTTGTGATGCTCTTACGCTTATACCAACAGTACGCTGATATCTTCTACG 991
 DB 1205 CTTGGCACTTCTGATGCTCTTGGGTTACACAAACAGCTGCTGAAACCACTTCTTATG 1264
 QY 992 CTTTCTTGTGATGAAACTTCAAGGCTGTTCCGGAAGCTTCTGCTTCCACTGAAGATGA 1051
 DB 1265 GCTTCTGATGAAACTTCAAGGCTGTTCCGGAAGCTTCTGCTTCCACTGAAGATGA 1324
 QY 1052 GGATGAGCGGCGAGACATGACAGATCCGAATTAACAGTTCAAGATC 1099
 DB 1325 CAATGGAACAGCAAAACCTGCTCGAATCCGTCAAAACACTAGGAGAC 1372

RESULT 60
 AA056705
 ID AA056705 standard; cDNA; 1981 BP.

XX AC AA056705;
 XX 25-MAR-2003 (revised)
 XX 15-SBP-1994 (first entry)
 DE Partial sequence of the murine mu-receptor clone DOR-2 (MOR-1, MOR-1a1pha).
 XX
 KW Opioid receptor; morphine; opiate; ss.
 XX
 OS Mus musculus.
 XX
 PN W09404552-A1.
 PD 03-MAR-1994.
 PF 13-AUG-1993; 93WO-US007665.
 XX
 PR 13-AUG-1992; 92US-00929200.
 XX
 PA (RBCG) UNIV CALIFORNIA.
 PI Evans CJ, Keith DE, Edwards RH, Kaufman D;
 XX WPI; 1994-083099/10.
 XX
 DR DNA encoding opioid receptors and antibodies against this receptor - used
 PT to express and locate these receptors, and screen cpls. for opioid
 PT (ant) agonist activity.
 XX
 PS Example; Fig 9; 74pp; English.
 XX
 CC A cDNA library prep'd. from mouse brain was probed using DOR-1 (see
 CC CC AA056704) as a probe. One clone was recovered and sequenced. This clone,
 CC designated DOR-2, represented a new gene. DOR-2 hybridised to a different
 CC pattern of bands than did DOR-1 and showed greater labeling of the
 CC striatum. The identity of DOR-2 (mOR-1) as that of a mu receptor was
 CC confirmed. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T; 0 U; 1 Other;

Query Match 37.1%; Score 427.6; DB 2; Length 1981;
 Best Local Similarity 65.5%; Pred. No. 8.1e-95;
 Matches 660; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

```

QY 92 CCGGCTGGGCGCCAGCCGACAGCAACGAGCGCGGCTCGAGAGGACGGCGACGCTGAGGC 151
DB 374 CCGACCCATGCGGCTCTTAACCCGACGGGCTTGGCGGAGACAGACGCCGTGCCCCACAA 433
QY 152 CCGGCAACATCTCCCGGCGCATCCGGTATCATCACGGCGGCTACTCCGTAGTTTGG 211
DB 434 CCGGACGCCCTTCCATGTCACAGCCATCAACATCAAGCCCTCTATTCTTATCGTGTG 493
QY 212 TCGTGGGCTTGGGCAACTCGCTGTCATGTTCTGATCATCCGATACAGAAAGATGA 271
DB 494 TAGTGGGCTCTTGGAAACTTCGTGTCATGATGATGATGATGATGATGATGATGATG 553
QY 272 AGACGCAACCAACATTTACATTTTAACTTGGCTTTGGCAGATGCTTTACTACAA 331
DB 554 AGACTGGCCACCAACATTTTCACTTTTCACTTGTGCTGTCAGATGCTTGGCAGCAGCA 613
QY 332 CCATGCCCTTTAGAGTACGCTCTGATGATGATTTCCGTGCTTTGGGAGATGTCGT 391
DB 614 CGCTCCCTTTAGAGTGTAACTACCTGATGAGAACTGCGCCCTTTGAAACATCTCT 673
QY 392 GCAAGATAGTAAATTTCCATTTGATTTACTACACATGTTCCAGACATCTTCACTTGA 451
DB 674 GCAAGATGCTGATCTCAATAGACTACTACACATGTTCCAGATCTTCACTTCTGCA 733
QY 452 TGATGAGCGTGAGCCGCTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTT 511
DB 734 CCATGAGTGTAGACCGCTACATTTGCGTGTGCGACCCCGTGAAGGCTTGAATTTCC 793
QY 512 CACCTTTGAAGGCAAGATCATCATATCTGATCTGCTGTCTGATCTGTTGGA 571
DB 794 CCCCCGAATGTCGCAAAATTTGTCATGTCGCACTGATTCCTCTTCTTGGCATTGTC 853
QY 572 TCTTGCAATAGCTCTTGGAGGACCAAGATGAGGAAACGTCATGATCTTGAATGCT 631
DB 854 TGCCCTGATGTTTCATGCGACCAAAATACAGGAGGGGTC-----CATAGATTGCA 907
QY 632 CTTTCAGTTCACAGATGATGATCTACTCTGCTGAGGACCTCTTCAATGAGATCTGCT 691
DB 908 CCCTCAGCTTCTCTATCCACATGATGATGAGGAACTGCTC---AAATCTGTGCT 964
QY 692 TCATCTTTGCTTCTGATGATCTGCTCTATCATCATCTGCTGCTACACCTGATGAT 751
DB 965 TCATCTTGGCTTCTATCATGCTGCGGCTCTCATCATCTGTGTTATGATGATGATGAT 1024
QY 752 TGCGTCTCAAGAGCGCTCGGCTCTTTCGCTCCGAGAGAAAGTGGCACTGCGCTA 811
DB 1025 TACAGCTCAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAGAACTGCGCA 1084
QY 812 GGATCAGCAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 1085 GGATCAGCAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
QY 872 ACAATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 1145 ACATCTATGTCATCATCAAGACATGATCAGATTCAGAAACCACTTTCCAGACTGTTT 1204
QY 992 GGTATTTACTTTCATGCTGCTGATGCTGATACCAAGATGCTGATGCTGATGCTGATG 991
DB 1205 CTTGCACTTCTGCAATGCTTGGGTGTACAAACAGCTGTCTGAACCCAGTTCTTTAG 1264
QY 992 CTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCATGGAAGATGA 1051
DB 1265 CGTTCTGATGAAAACTTCAACAGATGTTTATGAGAGTGTCTGCACTCCAACTTCTCTCA 1324
QY 1052 GGATGAGCGGAGACACTACAGATGCTCGAAATTCAGTTCAAGATC 1099
DB 1325 CAATGAGACGAAAACTGCTGCTGATCCGTCAAAAACTAGGGAC 1372

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RESULT 61
 AAQ56700
 ID AAQ56700 standard; cDNA; 1821 BP.
 XX
 AC AAQ56700;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-SEP-1994 (first entry)
 XX
 DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
 XX
 KW Opioid receptor; morphine; opiate; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 29..1139
 FT /*tag= a
 PN
 PN MO9404552-A1.
 PD 03-MAR-1994.
 XX
 PF 13-AUG-1993; 93WO-US007665.
 XX
 PR 13-AUG-1992; 92US-00929200.
 XX
 PA (REBC) UNIV CALIFORNIA.
 PI Evans CJ, Keith DE, Edwards RH, Kaufman D,
 DR MPI: 1994-081099/10.
 DR P-PSDB; AAR48629.
 XX
 PT DNA encoding opioid receptors and antibodies against this receptor - used
 PT to express and locate these receptors, and screen cpds. for opioid
 PT (ant)agonist activity.
 XX
 PS Claim 1; Fig 5; 74pp; English.
 XX
 CC A cDNA library was constructed using mRNA isolated from the NG109-15 cell
 CC line. A single clone, named the DOR-1 clone was isolated. Comparisons
 CC with known sequences in Genbank showed highest homology between DOR-1 and
 CC the G-protein-coupled somatostatin receptor. Other features of the DOR-1
 CC clone AA sequence deduced from the cDNA sequence include 3 consensus
 CC glycosylation sites at residues 18 and 33 (predicted to be in the
 CC extracellular N-terminal domain), and at residue 310 (close to the C-
 CC terminus and predicted to be intracellular). Phosphokinase C consensus
 CC sites are present within predicted intracellular domains, at residues
 CC 242,255, 344 & 352. Seven putative membrane-spanning regions were
 CC identified. The DOR-1 clone produces a delta receptor with a predicted
 CC mol. wt. of 40,558 kDa prior to post-translational modifications.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SO Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T; 0 U; 0 Other;

Query Match 36.6%; Score 422.6; DB 2; Length 1821;
 Best Local Similarity 67.1%; Pred. No. 1.3e-93;
 Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

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QY 93 CCGGCTGGGCGCCAGCCGACAGCAACGAGCGCGGCTCGAGAGGACGGCGACGCTGAGGC 152
DB 91 CGCTTTCCCAAGCGCTTTCCCAAGCGCGGCGCCAAATGCTGTGGGATGCGCGGAGCCG 150
QY 153 CCGGCAACATCTCCCGGCGCATCCGGTATCATCAAGGCGGTCTACTCCGTAGTTTGGT 212
DB 151 TAGTGGGCTCTTGGAAACTTCGTGTCATGATGATGATGATGATGATGATGATGATG 210
QY 212 CTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCATGGAAGATGA 272
DB 211 AGTGGGCTTCTGCAATGCTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 270
QY 272 GACGACCAACCAATTTACATTTTAACTTGGCTTTGGCAGATGCTTTAGTACTACAAAC 332

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Db 271 GACCGCCACCAACATCTACATCTTCAATGTGGCTTTGGCTGATGGCGTGGCCACGAC 330
Oy 333 CATGCCCTTTCAAGATAGCGTCTACTTGATGATGTAATTCCTGGCCCTTTTGGGATGTGCTG 392
Db 331 GCTGCCCTTCCAGACGCGCAAGTACTGTATGAGAAAGTGGCCGTTTGGCGAAGCTGCTG 390
Oy 393 CAAGATAGTAATTTCCATTGATTACTACAAAGTTCACAGATCTTCACCTTACCAT 452
Db 391 CAAGGCTGTGCTCTCCATTGACTACACAAAGTTCATACATCTTCACCTTCACCAT 450
Oy 453 GATGAGCGTGAACCGCTACATTCACCGTGTGGCAACCCCGTGAAGGCTTTGGAATTCGAC 512
Db 451 GATGAGCGTGAACCGCTACATTCGCTGTGCGCATCTGTCAAGCCCTTGAATTCGAGAC 510
Oy 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGCTGTGTCTCTGTGGCAT 572
Db 511 ACCAGCCAAAGGCCAAGCTGATCAATATATGATCTGGGCTTTCAGGTGTGGGGT 570
Oy 573 CTCTGCAATAGTCTTTGGAGGACCAAAAGTCAGGGAAGCGTTCGATTTGAGTGTCTC 632
Db 571 CCCCATCATAGTGCATAGGACGATGACCCACCCGGAGTGTGCAGTGTATGATGCTCCA 630
Oy 633 CTTCGAGTTCCCAATGATGATGACTACTCTGTGTGGAGCTCTTCATGAGATCTGGCTTT 692
Db 631 GTTCCCAAGTCC-----CAGCTGTACTGGGACACTGTGACCAAGATCTGGGTGT 681
Oy 693 CATCTTTGGCTTGTGATCCCTGTCTCTCATCATCATCTGTCTGTACACCTTATGATCTT 752
Db 682 CCTCTTTGGCTTGTGTGTGCTCCATCTCATCATCAAGGTGTCTATGTGCTCATCTACT 741
Oy 753 GCGTCCAAAGAGCGTCCGGCTCTTCTGTGCTCCGAGAAAGATCGCAACCTGCGTGTG 812
Db 742 GCGCTTGGCGACGTCGCTCTGTCTGTCTCCGTTTCAAGGAAAGAGACCGAGCTGTGGG 801
Oy 813 GATCAACAGACTGTCTGTGTGTGTGTGAGCACTTTCGTGTGTGTGACTTCCATTC 872
Db 802 CATCAACGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
Oy 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929
Db 862 CATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 921
Oy 930 CAGCTATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db 922 CGCACTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 981
Oy 990 CGCCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
Db 982 CGCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026

RESULT 62
AAd11035
ID AAd11035 standard; cDNA; 1829 BP.
XX
XX AAd11035;
XX
XX 24-SEP-2001 (first entry)
XX
XX Murine delta opioid receptor (DOR-1) cDNA.
XX
XX Mouse; delta opioid receptor; DOR-1; analgesic; enkephalin;
XX
XX opioid addiction; anti-addictive; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 29. 1147
XX FT //tag= a
XX FT /product= "Murine DOR-1"
XX
XX US6265563-B1.
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XX
PD 24-JUL-2001.
XX
XX 13-FEB-1995; 95US-00387707.
XX
XX 13-AUG-1992; 92US-00929200.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Evans CJ, Keith DE, Edwards RH, Kaufman D;
XX
XX WPI; 2001-463944/50.
XX
XX P-PSDB; AAE05742.
XX
XX Nucleic acids encoding mammalian kappa and mu opioid receptors, useful
XX
XX e.g. to identify substances for treating opioid addiction and/or useful
XX
XX as analgesics.
XX
XX Example 5; Fig 5; 46pp; English.
XX
XX The invention relates to recombinant nucleic acid molecules which encode
XX
XX the murine delta opioid receptor, as well as recombinant nucleic acid
XX
XX molecules which can be retrieved using low-stringency hybridisation to
XX
XX this disclosed DNA. The invention provides genes encoding delta, kappa,
XX
XX and mu receptors of any species containing genes encoding such receptors
XX
XX sufficiently homologous to hybridise under low-stringency conditions. The
XX
XX nucleic acids may be used to recombinantly express kappa and mu opioid
XX
XX receptors in host cells. These cells may then be used in assays to
XX
XX identify modulators of the receptors activity that may be used, for
XX
XX example as analgesics or to combat the effects of opioid addiction. The
XX
XX nucleic acids and their complements may also be used as probe sequences
XX
XX to identify and characterise opioid receptor nucleic acids. The present
XX
XX sequence is murine delta opioid receptor (DOR-1) cDNA
XX
XX
SQ Sequence 1829 BP; 340 A; 562 C; 543 G; 384 T; 0 U; 0 Other;
Query Match 36.6%; Score 422.6; DB 5; Length 1829;
Best Local Similarity 67.1%; Pred. No. 1.3e-93;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
Oy 93 GCGCTGGGCGGAGCCGACAGCAAGCGAGCGCGCTTCGAGAGACGCGAGCTGGAACC 152
Db 91 CGCCTTCCAGCGCTTCCGAGCGCGGCGCCATGCTGGGGTGGCGCGAGCCG 150
Oy 153 GCGGACATCTCCCGGCGATCCGGTATCATCAAGCGGCTCTACTCCGTATGTTGAT 212
Db 151 TAGTCCCTGTCTCGGCTAGCCATGCGCATCAACGCGCTCTACTGGCTGTGTGCG 210
Oy 213 CGTGGCTTGTGTGCAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
Db 211 AGTGGGGCTTGTGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 270
Oy 273 GACAGCAACCAATTTATATTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
Db 271 GACCGCACCAACATCTATCTTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330
Oy 333 CATGCCCTTTCAAGATAGCGTCTACTTGATGATGTAATTCCTGGCCCTTTTGGGATGTGCTG 392
Db 331 GCTGCCCTTCCAGACGCGCAAGTACTGTATGAGAAAGTGGCCGTTTGGCGAAGCTGCTG 390
Oy 393 CAAGATAGTAATTTCCATTGATTACTACAAAGTTCACAGATCTTCACCTTACCAT 452
Db 391 CAAGGCTGTGCTCTCCATTGACTACACAAAGTTCATACATCTTCACCTTCACCAT 450
Oy 453 GATGAGCGTGAACCGCTACATTCACCGTGTGGCAACCCCGTGAAGGCTTTGGAATTCGAC 512
Db 451 GATGAGCGTGAACCGCTACATTCGCTGTGCGCATCTGTCAAGCCCTTGAATTCGAGAC 510
Oy 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGCTGTGTCTCTGTGGCAT 572
Db 511 ACCAGCCAAAGGCCAAGCTGATCAATATATGATCTGGGCTTTCAGGTGTGGGGT 570
Oy 573 CTCTGCAATAGTCTTTGGAGGACCAAAAGTCAGGGAAGCGTTCGATTTGAGTGTCTC 632
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Db      571 CCCCATCATGATGAGGAGTGAACCCCGGGATGGTGAAGTATGATGCTCA 630
Qy      633 CTTCGAGTTCCAGATGATGACTCTCTGTGGGAGCTTCTTATGAGATCTGGCTTT 692
Db      631 GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAGATCTGGCTGTT 681
Qy      693 CATCTTTGCTTGTGATCCCTGCTCTCATTCATTCGCTGTACACCTGATATCTCT 752
Db      692 CTTCTTTGCTTGTGATCCCTGCTCTCATTCATTCGCTGTATGGCTCATGCTACT 741
Qy      753 GCGTCTCAAGAGCGTCCGGCTCTTTCTGGCTCCGAGAGAAAGATCGCACTGCGTAG 812
Db      742 GCGCTTGGCGACGTCGCTGTCTGTCCGGTTCCAGAGAAAGAACCGAGCTGGGGG 801
Qy      813 GATCACAGACTGTGCTCTGTGGTGGTGGAGCTTCTGTCTGTGTGACTCCATTCA 872
Db      802 CATCACGGCGCATGTGCTGTGGTGGGCGCTTCTGTGTGTGTGGGCGCCATCCA 861
Qy      873 CATATTCAATCCGTGTGAGAGCTGTGGG---AGCACTCCCAAGACAGCTGTCTCTC 929
Db      862 CATCTTCGTCATGCTGTGACGCTGTGTGACATCAATCGGCGACCCCTTGTGTGGC 921
Qy      930 CAGCTATTACTTCTGCTATGCTAGAGCTATACCAAGTAGAGCTGAATCCCATTTCTTA 989
Db      922 CGCACTGACACTGTGCTATGCGCTGCGGTGAGCGCAAGACAGACCTCAACCCGCTTCTTA 981
Qy      990 CGCCTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTG 1034
Db      982 CGCCTTCTGTGAGAGAACTTCAAGCGCTGTTCGCGCAGCTCTG 1026

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RESULT 63

ABSS53439 ID ABS53439 standard; cDNA; 1829 BP.

ABSS53439;

19-NOV-2002 (first entry)

CDNA encoding human delta opioid receptor protein (DOR-1).

Enkephalin; opioid receptor; poisoning; addiction; morphine; codeine; ss; gene; DOR-1; human.

Homo sapiens.

Key Location/Qualifiers

FT CDS 29..1147

FT CDS 29..1147

US6432652-B1.

13-AUG-2002.

14-MAR-1995; 95US-00405271.

13-AUG-1992; 92US-00929200.

13-AUG-1993; 93WO-US007665.

13-FEB-1995; 95US-00387707.

13-MAR-1995; 95US-00403260.

(REBC) UNIV CALIFORNIA.

Evans CJ, Keith DE, Edwards RH, Kaufman D;

WPI; 2002-681194/73.

P-PSDB; ABG33029.

Mammalian DOR-1 opioid receptors, useful for screening for compounds useful in the treatment of opioid addiction and poisoning.

PS Claim 3; Fig 5; 61pp; English.

CC This invention relates to the DNA and protein sequences of novel
 CC mammalian opioid receptor (DOR-1) displayed at the surface of recombinant
 CC host cells. The invention also comprises a method for screening a
 CC candidate substance for opioid agonist activity and a method for
 CC detecting the amount of activation of the opioid receptor in the presence
 CC of a compared to the absence of the candidate substance. The methods and
 CC compounds of the invention may have anti-addictive agents and may be used
 CC to modulate opioid receptor activity. The mammalian opioid receptor of
 CC the invention may be used to screen for agonists and antagonists of its
 CC expression and activity which may be used to treat e.g. poisoning by, and
 CC addiction to, opioids (such as morphine, codeine, and many semi-synthetic
 CC congeners of morphine). The present sequence represents the cDNA sequence
 CC encoding the human delta opioid receptor (DOR-1) protein of the invention
 XX

Sequence 1829 BP; 340 A; 562 C; 543 G; 384 T; 0 U; 0 Other;

Query Match 36.6%; Score 422.6; DB 6; Length 1829;

Best Local Similarity 67.1%; Pred. No. 1.3e-93;

Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

```

Qy      93 CGGCTGGGCGGAGCCCGACAGCAACGCGCGCGCTCGAGAGACGCGAGCTGGAGCC 152
Db      91 CGCCTTCCAGAGCGCTTCCAGAGCGGCGCGCAATGCTGGGGGTGCGCGGAGCCCG 150
Qy      153 CGGCAATCTTCCCGGCGCATCCGGGTATATCAACGCGGTCTACTCCGTAAGTTCGT 212
Db      151 TAGTCTCTGTCCTCGCGCTGAGCCATCGCATCAACGCGGCTCTACTCGCTGTGGCC 210
Qy      213 CGTGGGCTTGGTGGGCACTGCTGTGATCTGTCGATCATCCGATACAAAGATGAA 272
Db      211 AGTGGAGCTTCTGGGCACTGTCTGTATGTTTGACATGTCGATGACCAATTTGAA 270
Qy      273 GACAGCAACCAATTTACATATTAACCTGCTTTGGAGATGCTTTAGTTACTACAAC 332
Db      271 GACGCGCAACCAATCTACATCTTCAATCTGCTTTGGTGTATGGCTGGCCACAGCAC 330
Qy      333 CATGCCCTTTCAAGATGAGCTTACTTGATTAATTCCTGGCTTTGGGAGATGTCTG 392
Db      331 GCTGCCCTTCCAGAGCGCGCAATGATGAAAGTGGCGGCTTGGGAGACTGCTG 390
Qy      393 CAAGATGATTAATTCATGATTACTATCAACAATGTCACCAATCTTACCTGACAT 452
Db      391 CAAGCTGTGCTCTCATTTGACTACTACAAATGTTCACTATCACTTACCTACCAT 450
Qy      453 GATGAGCGTGAACCGCTACATGCGGTGACCAACCGCGTAAGAGCTTTGAGATTCGCGAC 512
Db      451 GATGAGCGTGAACCGCTACATGCTGTCTGACATCTGTCAAGACCGCTTGGAGCTTCCGAGC 510
Qy      513 ACCCTTGAAGGCAAGATCATATATCTGATCTGCTGTCTGTCTATCTGTGGCAT 572
Db      511 ACCAGCAAGGCAAGTGAATATATGATCTGCGGTCTTGGCTTACAGTGTCCGAGGT 570
Qy      573 CTTCGATTAATCTTGAAGGACCAAGATCGGGAAGACGTCGATTAATGAGTGC 632
Db      571 CCCCATCATGATGAGGAGTGAACCCCGGGATGGTGAAGTATGATGCTCA 630
Qy      633 CTTCGAGTTCCAGATGATGACTCTCTGTGGGAGCTTCTTATGAGATCTGGCTTT 692
Db      631 GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAGATCTGGCTGTT 681
Qy      693 CATCTTTGCTTGTGATCCCTGCTCTCATTCATTCGCTGTATGGCTCATGCTACT 752
Db      692 CTTCTTTGCTTGTGATCCCTGCTCTCATTCATTCGCTGTATGGCTCATGCTACT 741
Qy      753 GCGTCTCAAGAGCGTCCGGCTCTTTCTGGCTCCGAGAGAAAGATCGCACTGCGTAG 812
Db      742 GCGCTTGGCGACGTCGCTGTCTGTCCGGTTCCAGAGAAAGAACCGAGCTGGGGG 801
Qy      813 GATCACAGACTGTGCTCTGTGGTGGTGGAGCTTCTGTCTGTGTGACTCCATTCA 872
Db      802 CATCACGGCGCATGTGCTGTGGTGGGCGCTTCTGTGTGTGTGGGCGCCATCCA 861

```

Query Match	36.6%	Score 422.6	DB 2	Length 2218
Best Local Similarity	67.1%	Pred. No. 1,4e-93		
Matches 634	Conservative 0	Mismatches 299	Indels 12	Gaps 2

OY	93	CGCGTGGGCGAGGCCCGACACGACACGGCAGCGCCGGCTCGAAGGACCGCGACGCTGGAGCC	152
Db	120	CGCCTTTTCCAGCGCCTTTCCCGACCGGGGGCCAAATGCGTGGGGGTGCGCGGGAGCCCG	179
OY	153	CGCGCACTCTCCCCCGGCGCATCCGGGTATCATCAGCGCGAGTACTCCGTAGTGTGCT	212
Db	180	TAGTGCTCTGCTCCCTCGCCCTAGGCATCGGCATCACCGCCCTTACTCTCGGTGTGTGCG	239
OY	213	CGTGGGCTTGTTGGGGCAACTCGCTGTCATGTTCTGTATCATCCGATACACAAAGATGA	272
Db	240	AGTGGGGCTTCTGGGGCAACGTGCTGTCATGTTTGGCATGTCGGGTACACCAATTTGAA	299
OY	273	GACAGCAACCAACATTTACATATTTAACTGGGCTTTGGCAGATGCTTTAGTTACTAAC	332
Db	300	GACCGCACCAACACTACATCTTCAATCTGGCTTTGGCTGATGCGCTGGCCACACAC	359
OY	333	CATGCCCTTTCAGATGACGGTCTACTGTATGATATTCCTGGCTTTTGGGAGTGTGCTG	392
Db	360	GCTGCCCTTCCAGAGGCCCAAGTACTTGATGGAAACGTGGCCGTTTGGCGAGCTGCTGTG	419
OY	393	CAAGATAGTAAATTTCCATTGATTACTAACAATGTTCACACAGCATCTTTCACCTTGACAT	452
Db	420	CAAGGCTGTGCTCTCAATGACTCTAACACATGTTCACTAGCATCTTCAACCTCCACAT	479
OY	453	GATAGGGGTGAGCGGCTACATTTGGCGATGGCAACCGGTGAAGCTTTGGACTTCGCGAC	512
Db	480	GATAGGGGTGAGCGGCTACATTTGGCTGTCTGTCATCTGTCAAAAGCCTTGACTTCGCGAC	539
OY	513	ACCCTTGAAGGCAAGAATCATCAATATCTGATCTGGCTGCTGTGATCTGTGGCAT	572
Db	540	ACCAGCCAAAGGCCAAGCTGATCATATATATGATCTGGGATCTTGGCTTCAGGTGCGGGGT	599
OY	573	CTCTGCATATAGTCTTTGGAGGCAACCAAGTCAAGGGAAGAGGTGATGTCAATAGTGTCTC	632
Db	600	CCCCATCATGTGTCATGGCAGTGAACCAACCCCGGAGTGTGCATGTGATGATGATGCTCA	659
OY	633	CTTGCAGTTCACAGATGATGACTACTCCTGGTGGGACCTCTTCAATGAAGATCTGCGCTT	692
Db	660	GTTCCCGAGTCC-----CACTGGTACTGGGACACTGTGACCAAGATCTGCGTGT	710
OY	693	CATCTTGGCTTGGTATTCCTGTCTCTCATCATCTGTCTGTCTACACCTGATGATCTT	752
Db	711	CCTCTTGGCTTGGTGGCCGATCTCATCATCACGGTGTGCTTATGACCTCATGCTACT	770
OY	753	GCGTCTCAAGAGCGTCCGGCTCTTTCGTGGCTCCCGAGAGAAATGCGAACCTGCGTAG	812
Db	771	GCGCTTGGCGACGGTGGTCTGCTGTCCGGTTCAGAGAGAGGACCGCACGCTGCGGGC	830
OY	813	GATCACAGAGATGTCCTGT	872
Db	831	CATCACGGGATGATGT	890
OY	873	CATATATCATCTGT	925
Db	891	CATCTGTGTATCTGT	950
OY	930	CAGCATATTAATCTGT	989
Db	951	CGACATGCACTGT	1010
OY	990	CGCCTTCTTGT	1034
Db	1011	CGCCTTCTTGT	1055
RESULT 65			
ABV75085			
ID	ABV75085 standard; DNA; 2219 BP.		
XX	ABV75085;		
DT	19-FEB-2003 (first entry)		

XX XX Murine delta-opioid receptor encoding DNA.
XX XX Delta-opioid receptor; transgenic; anticonvulsant; epilepsy; mouse; gene;
KM ds.
XX Mus sp.
OS Mus sp.
XX Key Location/Qualifiers
FH CDS 59..1177
FT /*tag= a
FT /product= "delta-opioid receptor"
PN WO200279423-A2.
XX 10-OCT-2002.
XX PD
XX PF 29-MAR-2002; 2002WO-US009715.
XX PR 29-MAR-2001; 2001US-0280513P.
XX (DELT-) DELTAGEN INC.
XX Allen KD;
PI WPI; 2003-067441/06.
XX DR P-P8DB; ABB82650.
XX New transgenic mouse comprising a disruption in a delta-opioid receptor gene, useful for preparing a pharmaceutical composition for treating epilepsy.
XX PT
XX Discloure; Fig 1, 61pp; English.
XX The invention relates to a transgenic mouse comprising a disruption in a delta-opioid receptor gene. There is no native expression of endogenous delta-opioid receptor gene. The transgenic mouse comprising a disruption in a delta-opioid receptor gene is useful for preparing a pharmaceutical composition for treating epilepsy. The present sequence represents a mouse delta-opioid receptor encoding DNA
CC mouse delta-opioid receptor encoding DNA
CC
XX Sequence 2219 BP; 460 A; 649 C; 650 G; 460 T; 0 U; 0 Other;
SQ

Query Match 36.6%; Score 422.6; DB 7; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1.4e-93;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

QY 93 CGGCTGGGCGGAGCCGAGCAGCAAGCGAGCGCGGCTGGAGAGCGCGAGCTGGAGCC 152
DB 121 CGCCTTCCGACGCGCTTCCGAGCGGCGGCGCAATGCGTGGGGTCCGCGGAGCCGG 180
QY 153 CGCGCATCTCCCGGCGCATCCCGTCAATCAACGCGGCTCTACTCCGTAAGTTCGT 212
DB 181 TAGTCCCTGCTCCGCGCTAGCCATCGCATACCGGCTCTACTCCGCTGTGTGCGC 240
QY 213 CGTGGCTTGGTGGGGAATCCGCTGCTATGTTTCGATCAACCAATACAAATGA 272
DB 241 AGTGGGCTTGGGCAAGTCTGTCATGTTTGGCATGTCGCGTACACCAAAATTGA 300
QY 273 GACAGCAACCAATTTATATATTTAACTGGCTTGGAGATGCTTAGTTACTACAC 332
DB 301 GACCGGCAACCAATCTATATCTTCAATCTGGCTTGGATGCGCTGGACCAACGAC 360
QY 333 CATGCCCTTTCAGAGTACGCTACTTGAATGATTCCTGCGCTTGGGAATGTGCTGTG 392
DB 361 GCTGCCCTTTCAGAGGCGCAAGTACTTGAATGAAGTGGCGATTGGGAGCTGCTGTG 420
QY 393 CAAGATAGTAATTTCCATGATTAATCAAGCAATGTTCAACACACTTCACTTACCAT 452
DB 421 CAAGGCTGTGCTCTCATTAATGACTACAAAGTTCATCACTTCACTTCACTCAT 480
QY 453 GATGAGCGTGAACGCTATACGCTGTGACACCGCGGAAGGCTTTGACTTCGCGAC 512
|||||

DB 481 GATGAGCGTGAACCGCTATACCTGCTGTGCCATCCTGTCAAAAGCCGTGAGCTCCGAC 540
QY 513 ACCCTTGAAGGAAGATATCATATCTGCATCTGGCGCTGTGTCTATCTGTGGCAT 572
DB 541 ACCAGCCAAAGCCAGCTGATATATATGCAATCTGGGCTTGGCTTCAAGTGTCCGGGT 600
QY 573 CTTCGAATAGTCTTGGAGGACCAAGTCAAGGAGAGAGTGTATGATGAGTGTCTC 632
DB 601 CCCCATCATGCTATGAGGAGTACCAACCCCGGAGTGTGACAGTGTATGATGTCTCA 660
QY 633 CTTCGAGTTCCAGATGATGACTACTCTGTGTGGGACTTCTTATGAAATCTGCGTCT 692
DB 661 GTTCCCAAGTCC-----CAGCTGTGATCTGGGACACTGTGACCAAGATCTGCGTGT 711
QY 693 CATCTTGGCTTGTGATATCCCTGTCTCAATCATCTGTCTCAACCTGATATCTCT 752
DB 712 CCTCTTGGCTTGTGTGTCGATCTCTCATATCAAGGTGTGCTTATGAGCTTCAATGCTACT 771
QY 753 GCGTCTCAAGAGCGTCCGCGCTCTTCTGTGGCTCCGAGAGAAAGATCGCACTGCGTAG 812
DB 772 GCGCTGGCGAGCGTCCGCTCTGTCTGTCCGAGTTCMAAGAGAGAGACCGAGCTGGGGG 831
QY 813 GATCAACAGACTGTCTGT 872
DB 832 CATCAAGCGCATGT 891
QY 873 CATATTCATCTGT 929
DB 892 CATCTTGTGATCTGT 951
QY 930 CAGTATTACTTCTGCATGCGCTTGGGCTATTCACAAAGTACCTGATCCATTCTCTA 989
DB 952 CCGACTGCACTGT 1011
QY 990 CGCCTTCTTGTATGAATTTCAAGCGGTGTTTCGGGACTTCTG 1034
DB 1012 CGCCTTCTGAGCAAGAACTTCAAGCGGTGTTTCGGGACTTCTG 1056
|||||

RESULT 66
AAQ75927
ID AAQ75927 strand; DNA; 2272 BP.
XX
AC AAQ75927;
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
DE Mouse delta opioid receptor MOR1 cDNA.
XX
KM Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeraic; assay; probe; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FH CDS 12..1130
FT /*tag= a
FT /product= "mouse delta opioid receptor"
PN WO9428132-A2.
XX
XX PD 08-DEC-1994.
XX PF 20-MAY-1994; 94WO-US005747.
XX
XX PR 20-MAY-1993; 93US-00066286.
XX PR 30-JUL-1993; 93US-00100694.
XX PR 05-NOV-1993; 93US-00147592.
XX
XX (ARCH-) ARCH DEV CORP.
XX

PI Bell GI, Reisine T, Yasuda K;
 XX WPI; 1995-022804/03.
 DR P-PSDB; AAR67670.
 XX Polynucleotides and peptides derived from opioid receptor polypeptides -
 PT for use in therapeutic compositions and in screening assays for useful
 XX drug substances.
 PS
 XX
 XX

Claim 6; Page 215-221; 300pp; English.

The nucleotide sequence of the novel mouse delta opioid receptor gene MOR1. The gene was isolated from a mouse brain cDNA library using a fragment (amplified from the cDNA library with primers AAQ7529-30) as a probe. The primers are based on the conserved sequences present in the second and third transmembrane domains of somatostatin (SRII) receptor subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the mouse delta opioid receptor clone, lambda ms1-2, was subcloned into the CMV promoter-based expression vector pCMV-6c. The resultant construct pCMV-ms1-2 was transfected into COS-1 cells for protein production. The gene encoding the opioid receptor can be used to produce complete, truncated or chimeric opioid receptor proteins. The opioid receptors thus produced are useful for the development of novel assays designed to select or improve substances, capable of interacting with the opioid receptor proteins, for use in diagnosis, drug design and therapeutic applications. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T; 0 U; 0 Other;

Query Match 36.6%; Score 422.6; DB 2; Length 2272;
 Best Local Similarity 67.1%; Pred. No. 1.4e-93;

Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

QY 93 CGGCTGGGCGGACCGGACGAGCAACGCGCGGCTTGAGAGACGCGACCTGAGGCC 152
 DB 74 CGCCTTTCCAGAGCGCTTCCCGACGCGGCGGCGCAATGCGGGGTGCGCGGAGCCG 133
 QY 153 CGCGCACTCTCCCGCGCATCCCGGTATCATCAGCGGGGTCTACTCCGTAGTTCGT 212
 DB 134 TAGTGCCTGCTCCCTCGCCCTTACGCAATCGCAATCGCGGCTCTACTCCGCTGTGTGCGC 193
 QY 213 CGTGGGCTTGATGGGCACTCGGTGTCATGTTGATCATCCGATACCAAAAGATGAA 272
 DB 194 AGTGGGCTTCTGGGCAACGTCTGTCATGTTTGGCATGTCGCGTACCAAAATGAA 253
 QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTTAGTTAATAAC 332
 DB 254 GACCGCAACCAATCTATCATCTTCAATCTGGCTTTGGCTGATGCGCTGGCACAC 313
 QY 333 CATGCCCTTTAGAGTACGCTCTACTGTATGAATTCCTGGCCCTTTGGGAGATGTGTG 392
 DB 314 GCTGCCCTTCCAGAGGCGCAAGTACTGATGAAAGTGCGCGCTTTGGGAGTGTGTG 373
 QY 393 CAAGATAGTAATTTTCATGATTACTACAAAGTTCACACAGCATCTTACCTTGACAT 452
 DB 374 CAAGGCTGTGCTCTCATGATGACTACCAACATGTTCACTAGCATTTACCTTACCAT 433
 QY 453 GATGACGTGACCGCTTACATTCGCTGTGCAACCCCGTGAAGGCTTTGACTTCGAC 512
 DB 434 GATGACGTGACCGCTTACATTCGCTGTGCAACCCCGTGAAGGCTTTGACTTCGAC 493
 QY 513 ACCCTTGAAGGCAAGATATCATATCTGCACTTGGCTGCTGTCTCATCTTTGGCAT 572
 DB 494 ACCAGCAAGGCGCAAGCTATCAATATATGACATCTGGCTTGGCTTGGGTGCGGGT 553
 QY 573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAGAGAGCTGATGATGAGTCTC 632
 DB 554 CCCCATCATGCTATGAGTACCAACCCCGGAGATGATGAGTATGATGATGATGATG 613
 QY 633 CTTCGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
 DB 614 GTTCCCAAGTCC-----CAGCTGTGATGAGGACATGATGACCAAGATGCGCTGTT 664

QY 693 CATCTTGCCTTCGATCCGCTGCTCATCATCATGCTGCTGACACCTGATGATCCT 752
 DB 665 CCTCTTGCCTTCGATCCGCTGCTCATCATCATGCTGCTGACACCTGATGATCCT 724
 QY 753 GCGTCTCAAGAGCGCTCCGCTCTCTTCTGCGCTCCGAGAGAAAGATCCCACTGAG 812
 DB 725 GCGCTTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784
 QY 813 GATCAACCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 DB 785 CATCAAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
 QY 873 CATATTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929
 DB 845 CATCTTGCCTTCGATCCGCTGCTCATCATCATGCTGCTGCTGCTGCTGCTGCTGCT 904
 QY 930 CAGCTATTATCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
 DB 905 CGCACTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
 QY 990 CGCCTTTCTGATGAAAACTTCAAGCGGTGTTTCCGGACCTTCTG 1034
 DB 965 CGCCTTCTGAGAGAACTTCAAGCGGTGTTTCCGGACCTTCTG 1009

RESULT 67

AAD50856
 ID AAD50856 standard; DNA, 1176 BP.

XX AAD50856;
 AC 27-OCT-2003 (revised)
 XX 02-APR-2003 (first entry)

DT 02-APR-2003 (first entry)

XX Human modified mu opioid receptor DNA #1.

KW Human; membrane-spanning signal-transducing protein; MSST protein;

OS mu opioid receptor; receptor; gene; mutant; mutein; de.

OS Homo sapiens.

OS Tobacco etch virus.

OS Chimeric.

XX Key

FT CDS

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

FT misc_feature

Location/Qualifiers
 1..1176
 /*tag= a
 /*product= "Mu opioid receptor modified protein"
 /*note= "No stop codon"
 /partial
 529..549
 /*tag= b
 /*note= "TEV protease cleavage site"
 WO200286507-A1.
 31-OCT-2002.
 24-APR-2002; 2002WO-US013250.
 24-APR-2001; 2001US-0286250P.
 21-AUG-2001; 2001US-00935061.
 (STRD) UNIV LELAND STANFORD JUNIOR.
 Koblika BK, Ghanouni P, Lee TW;
 WPI; 2003-103418/09.
 P-PSDB; AAE33276.
 Identifying an agent that modulates activity of a membrane-spanning,
 signal-transducing (MSST) protein, by detecting a conformational change
 in a MSST protein upon interaction with a ligand.

PS Example 12; Page 96-98; 104pp; English.

CC The present invention relates to methods and compositions for identifying
CC agents that modulate activity of a membrane-spanning, signal-transducing
CC (MSRT) protein. The method involves detecting a conformational change in
CC a MSRT protein upon interaction with a ligand. The method is useful for
CC identifying agents that modulate (e.g. agonists or antagonists) activity
CC of MSRT protein. The present sequence is a human modified mu opiod
CC receptor DNA. This sequence is modified to contain a Tobacco etch virus
CC (TEV) protease cleavage site in the second intracellular loop. This
CC sequence is used to illustrate the method of the invention. (Updated on
CC 27-OCT-2003 to standardise OS field)

XX Sequence 1176 BP; 292 A; 342 C; 241 G; 301 T; 0 U; 0 Other;

Query Match 36.0%; Score 415.6; DB 7; Length 1176;
Best Local Similarity 65.1%; Pred. No. 5,99-92;
Matches 648; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGCTCCGAGAGCGGCGAGCTGGAGC 151
DB 125 CCGACCCATCGGCTCCGAACCGACCGACCTGGCGGAGAGACGCTGTGCTCCAA 184
QY 152 CCGCGACATCTCCCGGCGCATCCGCTCATCATCAGCGCGGTCTACTCCGATGTTGG 211
DB 185 CCGGAGATCCCTCCATGATCAGCGGCATCAGCATATGCGCTCTACTCCATCGTGTGG 244
QY 212 TGTGGGCTGTGGGCAACGCTGTGTATGTTGCTGATCCGATACCAAGATGA 271
DB 245 TGGTGGGCTCTTCGGAACCTTCGTGTATGATGATTCATCATACCAAGATGA 304
QY 272 AGACAGCAACCAACATTTACATATTACCTGGCTTTGGCAGATGTTAGTTACAGAA 331
DB 305 AACCTGCAACCAACATTTACATTTTACCTGTGCTGGCAGATGCTTACCGACAGTA 364
QY 332 CCATGCGCTTTGAGAGTACGCTTACTTATGATGAATTCCTGGCTTTGGGAGATGCTGT 391
DB 365 CCGTCCCTTCAGAGTGTGAATTAATCTAATGGGAACATGGCATTTGGAACCATCTTT 424
QY 392 GCAAGATGATTAATTTCCATTGATTAACAAATGTTCAACAGCATCTTCACTTGACCA 451
DB 425 GCAAGATGATTAATTTCCATTGATTAACAAATGTTCAACAGCATCTTCACTTGACCA 484
QY 452 TGATAGAGTGTGACGCTACATTTGCGGTGCGCAACCGCGTGAAGCTTTGAGCTTCGGA 511
DB 485 CCATAGAGTGTGATGATACATTCAGTGTGCGACCTGTGCAAGGAAACCTTACTTTC 544
QY 512 CACCTTGAAGCAAGATCATCATATATCTGATCTGCTGTGCTGATCTGTGGCA 571
DB 545 AGGGGGAATGCAAAATTAATCAATGTCTGCAACGATGATCTCTTCAAGCATTTGTC 604
QY 572 TCTTGCAATAGTCTTTGGAGGCAACCAAGTCAAGGAGAGCTGCATTTAGTGTCT 631
DB 605 TTCTGTATATGTTATAGCTACAAACAAATACAGGCAAG-----TTCCATATGATTGA 658
QY 632 CTTTGAGTTCCTCAATGATGACTACTCTGTGTGGGAACTCTTCAATGAAGATCTGGTCT 691
DB 659 CACTAATCTCTCTCATCCAACTGTGTAATGGGAAACCTGCG---TGAAGATCTGTGTT 715
QY 692 TCATCTTTGCTGCGATCGCTGTCTCATCATCATCTGCTGCTACACCTGATATCG 751
DB 716 TCAATCTGCTTCAATTAATGCAAGCTCTATCATTAACCTGTGCTATGATGATATCT 775
QY 752 TCGCTTCAAGAGCTCGGCTCTCTTCTTGGCTCCGAGAGAAAGATCGCAACTGCTGA 811
DB 776 TCGGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAGAAAGACAGAAATCTTCGAA 835
QY 812 GGATACCAAGATGCTGT 871
DB 836 GGATACCAAGAGT 895
QY 872 ACATATTTCTCTGT 931

DB 896 ACATTTACGTCATCTTAAAGCTTGTTCATACATCCAGAAATCACTGTCCAGCTGTT 955
QY 932 GCTATTACTTGTGATCGCTTGAAGCTATACCAAGATGAGCTGATCCATTTCTAGC 991
DB 956 CTGGGACCTTGTGATTTGCTCTAGGTTACAAACAGCTGCTTCAACCAATCTTATG 1015
QY 992 CTTTCTTGATGAAACCTTCAAGCGGTGTTTCCGGGACTTGTCTTTCATGGAATGA 1051
DB 1016 CATTTCTGATGAAACCTTCAACGATGCTTCAAGAGATTTGTATCCCAACTTTCGA 1075
QY 1052 GGATGAGCGGCAAGCACTTACAGATCCGAATN 1087
DB 1076 ACATTTGAGCAACAAATCTCACTCGAATTCGACGA 1111

RESULT 68

AA06656
AA06656 standard; cDNA; 2216 BP.

AC AA06656;

DT 25-MAR-2003 (revised)

DT 19-JAN-1995 (first entry)

DE Murine delta opiod receptor coding sequence.

XX delta opiod; enkephalin; receptor; mouse; murine; analgesic; pain;

KW drug addiction; neurological disorder; psychiatric; disorder;

KW cardiovascular disorder; de.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 59..1174

FT FT /*tag= a /product= "opiod_receptor"

PN FR2697850-A1.

PD 13-MAY-1994.

PF 10-NOV-1992; 92PR-00013526.

PR 10-NOV-1992; 92PR-00013526.

PA (U957-) UNIT PASTEUR STRASBOURG LOUIS.

PI Kieffer B;

DR WPI; 1994-178255/22.

DR P-PSDB; AAR6503.

PT New nucleic acid encoding opiod receptor - and related polypeptide,

PT antisense nucleic acid, probes, recombinant cells and ligands, useful in

PT diagnosis and treatment of e.g. neurological disorders.

PS Claim 3; Page 16-18; 29pp; French.

XX A cDNA bank constructed from hybridoma NG108-15, was used to transfect

CC COS-1 cells. The cells were tested for ability to bind tritium-labelled

CC Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or absence of the opiod

CC antagonist naloxone. Clone K56 was isolated from a positive colony and

CC found to contain a 2216bp insert. This cDNA encodes a delta opiod

CC (enkephalin) receptor with apparent dissociation constant 1.4nM and Bmax

CC 3.9-6.4 pmole/mg protein. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T; 0 U; 0 Other;

Query Match 35.6%; Score 411.4; DB 2; Length 2216;

Best Local Similarity 67.1%; Pred. No. 8,1e-91;

Matches 634; Conservative 0; Mismatches 296; Indels 15; Gaps 3;

QY 93 CCGGCTGGGCGGAGCCGACAGCAACGCGCGCTCGAGAGACGCGCAGCTGTGAGCC 152

Db 121 |C|C|C|T|T|C|C|C|A|G|C|G|C|T|T|C|C|C|A|G|C|G|C|C|C|C|A|T|G|T|G|G|G|G|C|C|C|G|G|A|G|C|C|G| 180
Qy 153 |G|C|G|G|C|A|C|T|T|C|C|C|G|G|C|C|A|T|C|C|G|G|T|C|A|T|C|A|G|G|G|G|T|C|T|A|C|T|C|G|A|G|T|T|G|T| 212
Db 181 |T|A|G|T|G|C|T|G|T|C|C|C|T|G|C|C|C|T|A|G|C|C|A|T|G|C|C|G|C|T|A|C|T|G|G|G|T|G|G|C|G|C| 240
Qy 213 |C|G|T|G|G|C|T|T|G|G|G|G|C|A|C|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 272
Db 241 |A|G|T|G|G|G|C|T|T|G|G|G|G|C|A|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 300
Qy 273 |G|A|C|A|G|C|A|C|A|C|A|T|T|A|C|A|T|T|A|C|T|G|G|C|T|T|G|G|A|T|G|T|T|A|G|T|A|T|A|C| 332
Db 301 |G|A|C|G|G|C|A|C|A|C|A|C|A|T|T|A|C|A|T|T|A|C|A|T|T|A|C|A|T|T|A|C|A|T|T|A|C|A|T|T|A|C| 360
Qy 333 |C|A|T|G|C|C|T|T|C|C|A|G|G|G|C|C|A|G|T|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 392
Db 361 |G|C|T|G|C|C|T|T|C|C|A|G|G|G|C|C|A|G|T|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 420
Qy 393 |C|A|G|A|T|A|T|A|T|T|T|C|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T|T|A|T| 452
Db 421 |C|A|G|G|C|T|G|C|T|C|C|A|T|T|G|A|C|T|A|C|A|A|G|T|T|C|A|C|A|T|T|C|C|C|T|C|A|C|A|C|A|T| 480
Qy 453 |G|A|T|G|A|G|G|G|A|C|C|G|T|A|C|T|G|C|G|T|G|C|C|A|C|C|C|G|T|G|A|G|G|C|T|T|G|A|C|T|T|G|C|G|A|C| 512
Db 481 |G|A|T|G|A|G|G|G|A|C|C|G|T|A|C|T|G|C|G|T|G|C|C|A|C|C|C|G|T|G|A|G|G|C|T|T|G|A|C|T|T|G|C|G|A|C| 540
Qy 513 |A|C|C|T|T|G|A|A|G|G|C|A|A|G|A|T|C|A|T|A|T|T|G|A|T|T|G|A|T|T|G|A|T|T|G|A|T|T|G|A|T|T|G|A|T| 572
Db 541 |A|C|C|A|G|C|A|A|G|G|C|A|A|G|C|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T|A|T| 600
Qy 573 |C|T|T|G|C|A|T|A|T|G|T|T|G|A|G|G|A|C|C|A|A|G|T|C|A|T|G|T|C|A|T|G|T|C|A|T|G|T|C|A|T|G|T|C|A|T| 632
Db 601 |C|C|C|A|T|A|T|G|T|C|A|T|G|A|G|G|A|C|C|C|C|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 653
Qy 633 |C|T|T|G|A|G|T|T|C|C|C|A|G|A|T|G|A|T|A|C|T|C|G|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 692
Db 654 |G|C|T|C|A|G|T|T|C|C|C|A|G|T|C|C|G|C|G|T|G|T|A|C|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 708
Qy 693 |C|A|T|T|T|G|C|T|T|G|T|G|T|G|T|C|C|G|T|C|T|C|A|T|C|A|T|G|T|G|T|C|T|A|C|C|C|T|G|A|T|G|T|C|T| 752
Db 709 |C|C|T|T|T|G|C|T|T|G|T|G|T|G|T|C|C|G|T|C|T|C|A|T|C|A|T|G|T|G|T|C|T|A|C|C|C|T|G|A|T|G|T|C|T| 768
Qy 753 |G|G|T|T|C|A|A|G|A|G|C|C|G|C|T|C|T|T|G|T|G|G|C|C|C|G|A|G|A|A|G|A|T|G|C|A|C|C|T|G|G|T|A|G| 812
Db 769 |G|G|G|C|T|G|C|G|A|C|G|G|C|G|T|C|T|G|T|C|C|G|T|T|C|C|A|G|A|G|A|G|A|C|C|G|A|C|C|T|G|G|G|G| 828
Qy 813 |G|A|T|C|A|C|A|G|A|C|G|T|C|T|G|T|G|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 872
Db 829 |C|A|T|C|A|C|G|G|G|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G| 888
Qy 873 |C|A|T|A|T|T|C|A|T|C|T|G|T|G|A|G|G|C|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 929
Db 889 |C|A|T|T|T|G|C|A|T|G|T|G|A|C|G|T|G|T|G|A|C|A|T|C|A|T|C|G|G|C|C|G|A|C|C|C|A|C|C|T|G|T|G|T|G|G| 948
Qy 930 |C|A|G|C|A|T|A|T|A|T|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G| 989
Db 949 |C|G|C|A|T|G|A|C|C|T|G|T|G|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G| 1008
Qy 990 |G|C|C|T|T|T|C|T|G|A|T|G|A|A|A|C|T|T|C|A|G|G|G|G|T|T|T|C|C|G|G|A|C|T|T|G| 1034
Db 1009 |G|C|C|T|T|C|C|T|G|A|G|A|A|C|T|T|C|A|G|G|G|C|T|G|T|T|C|C|G|C|A|G|C|T|G| 1053

RESULT 69
ACAS6807
ID ACAS6807 standard; cDNA; 1773 BP.
XX ACAS6807;
AC ACAS6807;
XX 06-JUN-2003 (first entry)
DT
XX Human signalling pathway polynucleotide probe SEQ ID NO 1405.

XX Human; probe; ss; array element; Parkinson's disease;
KM signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
OS Homo sapiens.
PN US6500938-B1.
PD 31-DEC-2002.
PF 30-JAN-1998; 98US-00016434.
PR 30-JAN-1998; 98US-00016434.
PA (INCY-) INCYTE GENOMICS INC.
PI Au-Young J, Seilhamer JJ;
DR WPI; 2003-352189/33.
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
PS Claim 1; SEQ ID NO 1405; 65bp; English.
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX for monitoring progression of diseases and for developing sophisticated
XX profiles for the effects of currently available therapeutic drugs. The
XX combination is also useful for purifying a subpopulation of mRNAs. CDNA
XX and genomic fragments and in research and diagnostic applications. The
XX array can detect changes in expression in a large number of genes coding
XX for different signalling pathway populations which can be used to diagnose
XX various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX and Parkinson's disease. The present sequence represents a polynucleotide
XX probe of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX segdata.uspto.gov/sequence.html?docID=06500938B1
SQ Sequence 1773 BP; 263 A; 602 C; 591 G; 317 T; 0 U; 0 Other;
Query Match 35.4%; Score 408.6; DB 7; Length 1773;
Best Local Similarity 64.7%; Pred. No. 3.6e-90;
Matches 644; Conservative 0; Mismatches 339; Indels 12; Gaps 2;
Qy 44 |C|T|T|G|C|C|C|C|A|G|C|C|T|G|C|T|G|C|C|C|C|C|C|A|C|A|G|A|G|C|C|T|G|T|T|C|C|G|G|C|T|G|G|C|G| 103
Db 247 |C|C|T|C|G|C|C|G|G|C|C|C|A|G|T|G|A|G|C|C|C|C|C|C|T|T|T|G|C|C|A|A|G|C|C|T|G|A|C|G|C|T|A|C|C|T|A| 306
Qy 104 |A|G|C|C|G|A|C|A|G|A|C|G|G|C|C|G|G|C|C|G|G|A|G|A|C|G|C|C|A|G|C|C|G|G|A|G|C|C|G|G|A|C|A|T|T| 163
Db 307 |G|G|G|C|T|T|C|C|A|G|C|C|T|G|G|C|C|A|T|G|G|T|G|G|G|G|C|C|C|G|A|G|A|C|C|G|G|A|G|C|C|T|G|T| 366
Qy 164 |C|C|C|G|G|C|A|T|C|C|G|G|T|C|A|T|C|A|C|A|G|G|G|G|T|T|A|C|T|C|C|G|A|G|T|T|G|T|G|T|G|G|C|T|T|G| 223
Db 367 |C|C|T|G|C|C|C|T|G|G|C|A|T|G|C|A|T|C|A|C|G|G|C|T|T|A|T|C|G|G|C|C|G|T|G|G|C|C|G|G|G|G|G|G|G|G| 426
Qy 224 |T|G|G|G|A|A|C|T|G|T|G|T|A|T|T|T|G|T|G|A|T|C|C|A|T|A|C|A|A|A|G|T|G|A|A|G|A|G|A|C|A|C|A| 283
Db 427 |T|G|G|G|A|A|C|T|G|T|T|A|T|G|T|T|G|G|C|A|T|G|T|C|C|G|G|A|C|T|T|A|A|G|A|T|G|A|A|G|G|G|C|A|C|A| 486
Qy 284 |A|C|A|T|T|A|C|A|T|T|T|A|A|C|T|G|G|C|T|T|G|G|A|G|A|T|G|T|T|A|G|T|T|A|C|T|A|C|A|C|A|T|G|C|C|T|T|C| 343

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DB 487 ACATCTACATCTTCAACCTGGCTTAGCCGATGCGCTGGCCACGACGAGCTGCTTCC 546
QY 344 AGAGTACCGCTTACTTGTATGAATTCCTGGCTTTTGGGATGCTGTGCAAGATATGA 403
DB 547 AGAGTGCACAGTATGATGAGACGCTGGCCCTTGGCGACGCTGTCTTCAAGGCTGTGC 606
QY 404 TTTCCATTGATTACTACAAATGTTTCAACGAGATCTTTCACCTTGAACGATGAGAGTGG 463
DB 607 TCTCATGACTACTACAAATATGTTTACACGACATCTTTCACGCTCACCAATGATGAGTGG 666
QY 464 ACCGCTACATTCCTGGTSCCAACCCCGTAGAGCTTTGACTTCGCAACACCTTGAAG 523
DB 667 ACCGCTACATTCCTGGTSCCAACCCCGTAGAGCTTTGACTTCGCAACGCTTGAAG 726
QY 524 CAAAGATCAATATCTGATCTGGCTGTCTGTCTATCTGTGGCATCTCTGCAATAG 583
DB 727 CCAAGCTGATCAACATCTGTATCTGGGCTCTGGCCCTCAGGCGTGGCGTGCATCATG 786
QY 584 TCCTTGGAGGACCAAAAGTCAGGGAAGAGCTGATGTCAATGAGTCTCTTGCAGTTCC 643
DB 787 TCATGCTGTGACCCGCTCCCGGAGCGTGCAGTGTGTGTCATGTCTCCAGTCCCGAGCC 846
QY 644 CAGATGATGACTACTCTCTGGTGGAGACCTTTCATGTAAGATCTGCGCTTCTTGTGCT 703
DB 847 C-----CAGCTGTACTGGGACACGCTGACCAAGATCTGCGCTTCTTGTGCT 897
QY 704 TCGATGTCCTGTCTCATCATCATCATGTCTGTCTACACCTGTATGATCTGCGCTTCAGA 763
DB 899 TGTGTGTGTCATCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 957
QY 764 GCGTCCGCTCTCTTCTGTGCTCCGAGAGAAAGATGCAACTGCTGAGATCAACGAC 823
DB 958 GTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1017
QY 824 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 883
DB 1018 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
QY 884 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 940
DB 1078 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1137
QY 941 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1000
DB 1138 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1197
QY 1001 ATGAAACTTCAAGCGGTGTTCGCGGAGCTTCTGC 1035
DB 1198 ACGAGAACTTCAAGCGGTGTTCGCGGAGCTTCTGC 1232

RESULT 70
ABT34217
ID ABT34217 standard; DNA; 1773 BP.
XX
XX ABT34217;
AC
XX
XX
XX
XX 12-JUN-2003 (first entry)
DT
XX
DE Human delta-opioid receptor gene SEQ ID No 3.
XX
XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;
XX serotonn receptor 1p; delta-opioid receptor; dopamine receptor D2;
XX anorexia nervosa; bulimia nervosa; human; de.
OS
XX Homo sapiens.
XX
XX WO2003012143-A1.
XX
XX 13-FEB-2003.
XX
XX 16-JUL-2002; 2002WO-US022555.
PF
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XX
PR 16-JUL-2001; 2001US-0305153P.
PR 20-JUL-2001; 2001US-0306440P.
PR 13-NOV-2001; 2001US-0331285P.
PR 19-DEC-2001; 2001US-0340843P.
PR 19-DEC-2001; 2001US-0340844P.
XX
PA (PRIC-) PRICE FOUND LTD.
XX
XX Bergen AW, Yeager M;
PI
XX
XX WPI; 2003-268122/26.
XX
XX New nucleic acid molecule having polymorphisms in the serotonn receptor
PT ID, delta-opioid receptor, or dopamine receptor D2, useful in diagnostic
PT and prognostic assays for eating disorders, such as anorexia and bulimia
PT nervosa.
XX
PS Disclosure; Page 126-127; 149pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule
XX comprising a variant gene associated with an eating disorder and selected
XX from any of 119 polymorphisms with their corresponding genotyping in
XX dataset, alleles and HGBASE identification, given in the specification.
XX The novel nucleic acid molecule has polymorphisms in the serotonn
XX receptor ID, delta-opioid receptor, or dopamine receptor D2, which is
XX useful in diagnostic and prognostic assays for eating disorders, in
XX particular anorexia nervosa and bulimia nervosa. This polynucleotide
XX sequence represents a human delta-opioid receptor gene of the invention
XX
SQ Sequence 1773 BP; 263 A; 602 C; 591 G; 317 T; 0 U; 0 Other;
XX
XX Query Match 35.4%; Score 408.6; DB 7; Length 1773;
XX Best Local Similarity 64.7%; Pred. No. 3.6e-90;
XX Matches 644; Conservative 0; Mismatches 339; Indels 12; Gaps 2;
QY 44 CCGTGGCCCGGAGCGCGCTGCGTCCGCAACAGAGCGCTGTTCGCGGTGGGCGG 103
DB 247 CCGTGGCGGCGCGCGAGCTGCGAGCCCGCTTTGCGCAACGCTGAGCGCTTACCCTA 306
QY 104 AGCCGACAGCAACGAGCGAGCGCGCTGCGAGAGAGCGCGAGCTGAGCGCGGACATCT 163
DB 307 GGGCTTCCCGACCGCTGCGCAATGCTGCGGCGCGCGAGAGCGCGGAGCGCGCTCGT 366
QY 164 CCGCGGCGATCCCGGCTATCATCAGCGCGGTCTTCTCTAGTGTCTGTGTGGCTTGG 223
DB 367 CCTCGCGCTGCGCAATCGCATCACCGCGCTTACTCGCGCGCGTGTGCGCGCGCTGC 426
QY 224 TGGGGAATCGGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 283
DB 427 TGGGGAATCGGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 486
QY 284 ACATTTCATATTTAACTGCTTGGAGATGCTTTAGTACTTACTCAACCATGCGCTTTC 343
DB 487 ACATCTACATCTTCAACCTGGCTTAGCCGATGCGCTGGCCACGACGAGCTGCTTTC 546
QY 344 AGAGTACCGCTTACTTGTATGAATTCCTGGCTTTTGGGATGCTGTGCAAGATATGA 403
DB 547 AGAGTGCACAGTATGATGAGACGCTGGCCCTTGGCGACGCTGTCTTCAAGGCTGTGC 606
QY 404 TTTCCATTGATTACTACAAATGTTTCAACGAGATCTTTCACCTTGAACGATGAGAGTGG 463
DB 607 TCTCATGACTACTACAAATATGTTTACACGACATCTTTCACGCTCACCAATGATGAGTGG 666
QY 464 ACCGCTACATTCCTGGTSCCAACCCCGTAGAGCTTTGACTTCGCAACACCTTGAAG 523
DB 667 ACCGCTACATTCCTGGTSCCAACCCCGTAGAGCTTTGACTTCGCAACGCTTGAAG 726
QY 524 CAAAGATCAATATCTGATCTGGCTGTCTGTCTATCTGTGGCATCTCTGCAATAG 583
DB 727 CCAAGCTGATCAACATCTGTATCTGGGCTCTGGCCCTCAGGCGTGGCGTGCATCATG 786
QY 584 TCCTTGGAGGACCAAAAGTCAGGGAAGAGCTGATGTCAATGAGTCTCTTGCAGTTCC 643
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OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..1197
FT /tag= a
FT /product= "Mu oploid receptor modified protein"
FT /note= "No stop codon"
FT /partial
FT 823..843
FT misc_feature
FT /tag= b
FT /note= "TEV protease cleavage site"

MO20026507-A1.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-US013250.
XX
PR 24-APR-2001; 2001US-0286250P.
PR 21-AUG-2001; 2001US-00935061.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Kobilka BK, Ghanouni P, Lee TW;
XX
PI WPI; 2003-103418/09.
XX
DR P-PSDB; AAE33277.
XX
PT Identifying an agent that modulates activity of a membrane-spanning,
PT signal-transducing (MSST) protein, by detecting a conformational change
PT in a MSST protein upon interaction with a ligand.
XX
PS Example 12; Page 99-101; 104pp; English.
XX
CC The present invention relates to methods and compositions for identifying
CC agents that modulate activity of a membrane-spanning, signal-transducing
CC (MSST) protein. The method involves detecting a conformational change in
CC a MSST protein upon interaction with a ligand. The method is useful for
CC identifying agents that modulate (e.g. agonists or antagonists) activity
CC of MSST protein. The present sequence is human modified mu oploid
CC receptor DNA. This sequence is modified to contain a Tobacco etch virus
CC (TEV) protease cleavage site in the third intracellular loop. This
CC sequence is used to illustrate the method of the invention. (Updated on
CC 27-OCT-2003 to standardise OS field)
XX
SQ Sequence 1197 BP; 295 A; 350 C; 244 G; 308 T; 0 U; 0 Other;

Query Match 34.9%; Score 402.2; DB 7; Length 1197;
Best Local Similarity 64.8%; Pred. No. 1.2e-88;
Matches 659; Conservative 0; Mismatches 328; Indels 30; Gaps 3;

QY 92 CCGGCTGGGCGGAGCCGACGACGAGCGCGGCTCGAGAGAGCGGCGAGCTGGAGC 151
DB 125 CCGACCCATGCGGTCGGAACCGACCGACCTGGGCGGAGAGACACCTGTGCTCCAA 184
QY 152 CCGGCGACATCTCCCGGCGCATCCGCTCATCATCGGCGGCTCTACTCCGATGTTGG 211
DB 185 CCGGCGAGTCCCTCCAGATCAGCGGCGCATCAGATCATGCGGCTCTACTCCATGTTGGG 244
QY 212 TGGTGGGCTTGGGGGCACTGCTGCTGATGTCGATGTCATCCGATACCAAAAGATGA 271
DB 245 TGGTGGGCTTGGGAACTTCTGCTGATGATGATGATGTCATACCAAAAGATGA 304
QY 272 AGACAGCAACAACATTTACATTTTACCTGGCTTTGGCAGATGCTTTAGTTACTACAA 331
DB 305 AGACTGGCCACCAACATCTATTTTCAACTTGTCTGTGGAGATGCTTAGCCACAGTA 364
QY 332 CCATGCCCTTTTCAAGATAGCTTACTTGAATGATTCCTGGCTTTGGGATGTCGTGT 391
DB 365 CCTGCGCTTCCAGAGTGTGAATTAATTAATGAGAAATGAGCATTTGAAACCATCTTT 424
QY 392 GCAAGATAGTAATTTCATTGATTACTACAAAGTGTCAACGATCTTCACTTGAACA 451

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DB 425 GCAAGATAGTAATTCATAGATTAATAACATGTTCAACGATATTCAACCTCTGCA 484
QY 452 TCATGAGCTGGAACGGCTATATTGCGGTGTGGCACCCTGTGAAGCTTTGGACTTCCGA 511
DB 485 CCATGATGTTGATGATACATTTGACATGTCGACCTGTCAAGGCTTAGATTTCCGA 544
QY 512 CACCTTGAAGGCAAAAGATCATCAATATCTGATCTGCTGTGCTGATCTGTTGGCA 571
DB 545 CTCCTCGAATGCAAAATTTATCATATGTCGAATGATCTCTCTTTAGCCATTGGTC 604
QY 572 TCTCTGATATAGTCTTGGAGGACCAAAAGTCAGGAGACGTCGATGATGATGCT 631
DB 605 TTCCTGATATGTTCAATAGCTACACAAATATACAGGCA-----GGTTCATGATTTGA 658
QY 632 CTTGCAAGTCCCAAGATGATGATCTCTGTTGGGACCTTTTATGAAGATCTGCTCT 691
DB 659 CACTAACATCTCTCATCCMACCTGTACTGGGAAACCTGTCT--GAAGATCTGTGTT 715
QY 692 TCATCTTGGCTTGGGATCCCTGTCTGATCATCATGCTGCTACACCTGATGATCC 751
DB 716 TCATCTTGGCTTCTATTAATGACATGCTCATCATTAACGTGTGCTATGACATGATCT 775
QY 752 TCGCTCTCAAGAGCGTCCGCTCTTCTGAGCTCCCGAGAGAAAG-----797
DB 776 TCGGCTCAAGAGTGTCCGATGCTCTGTGCTCCAAAGAGAGAGAAACCTTACT 835
QY 798 -----TCGCACTGCGTAGATACCAAGCTGCTCTGTGTGTGTGTGTGTGTG 850
DB 836 TCCAGGGAGAGATCTTCCAGAGATCACCAGATGTGTGTGTGTGTGTGTGTGTG 895
QY 851 TCGTCTGAGAGCTCCCATTCATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTG 910
DB 896 TCGTCTGAGAGCTCCCATTCATATTCATATTCATATTCATATTCATATTCATATTC 955
QY 911 ACAGACAGAGCTCTCTCTCACTATTAATTTGATCGCTTAGGCTATTAACACAGTA 970
DB 956 AATCAATGTTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1015
QY 971 GCGTGAATCCATTTCTTACGCTTTTGTGATGAAGAACTTCAAGCGGTGTTCGGGACT 1030
DB 1016 GCGTCAACCCAGATCTTTTATGATTTGTGATGAAGAACTTCAAGCGATGCTTCAGAGAGT 1075
QY 1031 TCTGCTTTCAGTGAAGATGAGAGAGGAGGAGAGCACTGAGAGTCCGAAATA 1087
DB 1076 TCTGATTCCAACTCTTCCAAATTTGAGCAACAAATCTCACTCGAATTCGACAA 1132

RESULT 75
ABX94262
ID ABX94262 standard; DNA; 1829 BP.
AC ABX94262;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human orphanin FQ/nociceptin receptor gene, coding sequence #2.
XX
XX Human; single nucleotide polymorphism; SNP; C510T; A804G;
XX orphanin FQ/nociceptin receptor; loci mapping; C1026T; C1126G;
XX addictive disease; pain; analgesic response; physiological response;
XX anxiety; stress; endogenous opiod system; neurotransmitter release;
XX learning; memory; cognition; alcohol self-administration;
XX behavioural sensitisation; cocaine; drug addiction; opiate withdrawal;
XX immune function; cardiovascular function; renal function;
XX gastrointestinal function; motor function; coding region; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH variation replace(510..T)
FT /tag= a
FT /standard name= "SNP"
FT /note= "C510T SNP specifically claimed in Claim 1"

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FT variation replace(804,A)
FT /*tag= b
FT /standard_name= "SNP"
FT /note= "A804G SNP specifically claimed in Claim 1"
FT variation replace(1026,T)
FT /*tag= c
FT /standard_name= "SNP"
FT /note= "C1026T SNP specifically claimed in Claim 1"
FT variation replace(1126,G)
FT /*tag= d
FT /standard_name= "SNP"
FT /note= "C1126G SNP specifically claimed in Claim 1"
XX US2003008289-A1.
XX
XX 09-JAN-2003.
XX
XX 09-OCT-2001; 2001US-00905186.
XX
XX 14-JUL-2000; 2000US-0218205P.
XX
XX (KREEK/) KREEK M J.
XX (LAFO/) LAFORE K S.
XX
XX Kreek MJ, Laforge KS;
XX
XX MPI; 2003-353089/33.
XX
XX New variant allele of a human orphanin FQ/nociceptin receptor gene,
XX useful for determining a subject's susceptibility to addictive diseases
XX or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
XX in its DNA sequence.
XX
XX Example: Fig 9; 29pp; English.
XX
XX The present invention relates to the identification of novel single
XX nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
XX receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
XX untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
XX (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
XX mutation located in the coding region), GIVS III 67T (located in intron
XX 3), A804G (a silent mutation located in the coding region), C1026T (a
XX silent mutation in the coding region), and C1126G (located in the 3'-
XX untranslated region). The SNPs and variant alleles of human orphanin
XX FQ/nociceptin receptor DNA are useful in mapping the locus of the human
XX orphanin FQ/nociceptin receptor gene, determining a subject's increased
XX or decreased susceptibility to addictive diseases, susceptibility to pain
XX and response to analgesics, physiological responses related to the
XX endogenous opioid system or neurotransmitter release, anxiety and stress,
XX learning, memory and cognition, alcohol self-administration, behavioural
XX sensitisation to cocaine, drug addiction, opiate withdrawal and
XX tolerance, food intake, immune function, cardiovascular function, renal
XX function, gastrointestinal function, and motor function. The present
XX sequence represents the coding region of the human orphanin FQ/nociceptin
XX receptor gene
XX
SQ Sequence 1829 BP; 296 A; 602 C; 542 G; 389 T; 0 U; 0 Other;
Query Match 34.2%; Score 395; DB 7; Length 1829;
Best Local Similarity 65.2%; Pred. No. 8.1e-87;
Matches 616; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

QY 333 CATGCCCTTTGAGAGTACGGTCTACTGTGATGTAATTCCTGGCTTTTGGGAGATGTCGTG 392
DB 342 GCTGCCCTTCCAGGGACGAGACATCTCTGGGCTTGGCCGTTTGGGAATGCGCTGG 401
QY 393 CAAGATAGTAATTTTCATTTGATTAATTAACAAGTTCACGACATCTTCACTTGACCAT 452
DB 402 CAAGACATGATGTCATTTGACTACTTAACAATGTTACGACACCTTCACTTAACCTG 461
QY 453 GATGAGCGTGAACCGCTACATTTGCCGTGTCACCCCGTGAAGGCTTTGGAATTCGAC 512
DB 462 CATGAGTGTGATCGCTATGTAGCCATCTGCACCCCATCCGTGCTCGACGTCGAC 521
QY 513 ACCCTTGAAGCAAAATCATCAATATCTGCATCTGCTGTCTGTCATCTGTTGGCAT 572
DB 522 GTCCAGCAAAAGCCAGGCTGTCAATGTGACCATCTGGGCCCTTGCTGTGTTCGTG 581
QY 573 CTCTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAGACGTGATGTCATTTAGTGTCTC 632
DB 582 TCCCGTTGCCATCATGAGGCTCGGACAGGTC-----GAGATGAAGATGAGTGCCT 635
QY 633 CTTCGAGTTCCCAATGATGACTACTCTGTGGGACCTTTTCATGAAGATCTGCGTCTT 692
DB 636 GGTGAGATCCCTACCCCTCAGATTAAC---TGGGGCCCGGTGTGTTGCCATCTGCATCTT 692
QY 693 CATCTTGGCTTCGATCCCTGTCCTGATCATGATGCTGCTACACCTGATGATCTCT 752
DB 693 CCTCTTCTCTTCATCGTCCCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 752
QY 753 GCGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATCGCAACTGCGTAG 812
DB 753 GCGGCTCGTGAAGTCCGCGCTGCTCTGTGCGGCTCCGAGAGAAAGACCGGAACCTGCGCG 812
QY 813 GATCACCAAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 813 CATCACTCGCGT 872
QY 873 CATATTCAATCCGT 932
DB 873 GGTCTTGT 932
QY 933 CTATTACTTGTGATCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 933 TGTGCGTTTGTGACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
QY 993 CTTTCTTGTATGAATTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 993 CTTCTGTATGATGAATTTCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
QY 1053 GATGAGCGGAGAGACATACAGATGTCGGAATTAAGTTGAGA 1097
DB 1053 CCGGAGCTGACGATGTGTGACCGCGTGGCAGCATTTGCCAAGAA 1097
RESULT 76
ABS53446
ID ABS53446 standard; cDNA; 1805 BP.
XX
XX ABS53446;
XX
XX 19-NOV-2002 (first entry)
XX
XX cDNA encoding human opioid receptor ORL-1.
XX
XX Enkephalin; opioid receptor; poisoning; addiction; morphine; codeine; ss;
XX gene; human; ORL-1.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 10..1176
FT /*tag= a
FT /product= "Human opioid receptor ORL-1"

XX US6432652-B1.
 XX 13-AUG-2002.
 PD 14-MAR-1995; 95US-00405271.
 XX 13-AUG-1992; 92US-00929200.
 XX 13-AUG-1993; 93WO-US007665.
 PR 13-FEB-1995; 95US-00387707.
 PR 13-MAR-1995; 95US-00403260.
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Evans CJ, Keith DE, Edwards RH, Kaufman D;
 PI WPI, 2002-681194/73.
 DR P-PSDB; ABG33031.
 XX Mammalian DOR-1 opioid receptors, useful for screening for compounds
 PT useful in the treatment of opioid addiction and poisoning.
 XX
 PS Disclosure; Fig 11; 61pp; English.
 CC This invention relates to the DNA and protein sequences of novel
 CC mammalian opioid receptor (DOR-1) displayed at the surface of recombinant
 CC host cells. The invention also comprises a method for screening a
 CC candidate substance for opioid agonist activity and a method for
 CC detecting the amount of activation of the opioid receptor in the presence
 CC as compared to the absence of the candidate substance. The methods and
 CC compounds of the invention may have anti-addictive agents and may be used
 CC to modulate opioid receptor activity. The mammalian opioid receptor of
 CC the invention may be used to screen for agonists and antagonists of its
 CC expression and activity which may be used to treat e.g. poisoning by, and
 CC addiction to, opioids (such as morphine, codeine, and many semi-synthetic
 CC congeners of morphine). The present sequence represents the cDNA encoding
 CC the human opioid receptor ORL-1 protein shown in the specification
 XX
 SQ Sequence 1805 BP; 291 A; 598 C; 533 G; 383 T; 0 U; 0 Other;

Query Match 34.1%; Score 393.4; DB 6; Length 1805;
 Best Local Similarity 65.1%; Pred. No. 2e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CCGGCACATCTCCCGGCGATCCCGGTATCATCACGGGGCTCTACTCCGTAGTGTCT 212
 DB 138 CCCCTTCCCTGCCCCCTCGGGCTCAAGGTCAACATCGGGCTCTACTCGCGGTGTGT 197
 QY 213 CGTGGGCTTGGTGGGCACTCGGTGTATGTTCCGATCATCCGATACAAAGATGAA 272
 DB 198 CGAAGGCTCTGGGGAACCTGCTGTATGATGATCTCAAGGACACCAAAATGAA 257
 QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTTAGTTACTACAAC 332
 DB 258 GACAGCAACCAATTATTAATTTAACTGGCCCTGGGCGACACATCTGTCTGTGAC 317
 QY 333 CATGCCCTTTCAAGATGAGGTCTACTGATGAATTCCTGGCTTTGGGAGATGTGTG 392
 DB 318 GCTGCCCTTCCAGGGGACGAGACATCTCTGGGCTTTGGCGTTGGAAATGCGGTG 377
 QY 393 CAAGATAGAAATTTCCATGATTAATTAACAAAGTTTCAACAGACATCTTAACCTT 452
 DB 378 CAAGACAGTATTCATTTGACTACTCAAAAGTTTCAACAGACATCTTAACCTTAATG 437
 QY 453 GATGAGCTGAGCCGCTATATTCGCTGTGCAACCCCGTGAAGGCTTTGAGATTGCGAC 512
 DB 438 CATGATGTGATTCGCTATGTAGCCATTCGCCACCCCATCGGCTTGAAGTCCGAC 497
 QY 513 ACCCTTGAAGCAAGATCATCAATATCTGCATCTGGCTGTCTGTCTATCTGTGGCAT 572
 DB 498 GTTCAGCAAAAGCCAGGCTGTCAATGTGGCCATCTGGGCTTGTGTGTGTGTGT 557
 QY 573 CTCTCAATATGCTTTGGAGGACCAAAATCAAGGAAAGCTGATGTGATTTGAGTCTC 632

DB 558 TCCCGTGCACATCAGGGGCTCGGCACAGATC-----GAGATGAAGAGATGAGTCCCT 611
 QY 633 CTTCGAGTTCCAGATGATGACTACTCCGTGGGGGACCTCTTCATGAAGATCGGCTT 692
 DB 612 GGTGAGATCCCTTACCCCTCAGAAATTA--TGGGCCCCGGGTGTTTGCATCTGCATCTT 668
 QY 693 CATCTTGGCTTCGTGATTCCTGTCTTCATCATTCGTCTGCTACACCTGATGATCT 752
 DB 669 CCTCTTCTTCATCTGATCCCGGTCTGTATCTGTCTGTCTACAGCTCATGATCCG 728
 QY 753 GCGTCTCAAGAGCGTCCGGCTCTTTCTGGCTCCGAGAAAGATCGCACTGCTG 812
 DB 729 GCGGCTCCGTGAGATCCGCTGCTCTCGGGCTCCGAGAAAGACCGGAACCTGCGCG 788
 QY 813 GATCAACAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
 DB 789 CATCACTGGGCTGGGT 848
 QY 873 CATATTCATCTGTGAGAGGCTCTGGGGAGCACTCCCAACAGAGCTCTCTCCAG 932
 DB 849 GGTCTTCTGTGCTGCCCCAAGGCTGGGGTTAGCCGAGACGAGACTGCGTGGCAT 908
 QY 933 CTATTACTTCTGATTCGCTTATAGCTATACCAAGATAGCTGAAATCCCATTTCTACGC 992
 DB 909 TCTGGGCTTCTGACGGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
 QY 993 CTTTCTTGATGAATCTTCAAGCGGTGTTTCCGGGACTTCTGCTTCTTCACTGAAGTGA 1052
 DB 969 CTTCCTGTGATGAACTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028
 QY 1053 GATGAGGCGGAGACACTAGCAGAGTCCGAATACAGTTCAAGA 1097
 DB 1029 CCGGACGTGACAGGTGTCTGACCGGTGGGACATTTGCAAGA 1073

RESULT 77
 ABX94264
 ID ABX94264 standard; DNA; 1829 BP.
 XX
 AC ABX94264;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human orphanin FQ/nociceptin receptor gene, 3'-untranslated region.
 XX
 KW Human; single nucleotide polymorphism; SNP; C1126G;
 KW orphanin FQ/nociceptin receptor; local mapping; motor function;
 KW addictive disease; pain; analgesic response; physiological response;
 KW anxiety; stress; endogenous opioid system; neurotransmitter release;
 KW learning; memory; cognition; alcohol self-administration;
 KW behavioral sensitization; cocaine; drug addiction; opiate withdrawal;
 KW immune function; cardiovascular function; renal function;
 KW gastrointestinal function; ds.
 KW
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT variation replace(1126, C)
 FT /tag= a
 FT /standard_name= "SNP"
 FT /note= "C1126G SNP specifically claimed in Claim 1"
 XX
 PN US2003008289-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 09-OCT-2001; 2001US-00905186.
 XX
 PR 14-JUL-2000; 2000US-0218205P.
 XX
 PA (KREEK/) KREEK M J.
 PA (LAFO/) LAFORE K S.

XX Kreek MJ, LaForge KS;
 XX WPI, 2003-353089/33.
 XX
 PT New variant allele of a human orphanin FQ/nociceptin receptor gene,
 PT useful for determining a subject's susceptibility to addictive diseases
 PT or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
 PT in its DNA sequence.
 XX
 XX Example; Fig 11; 29pd; English.
 CC The present invention relates to the identification of novel single
 CC nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
 CC receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
 CC untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
 CC (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
 CC mutation located in the coding region), GIVS III 67T (located in intron
 CC 3), A804G (a silent mutation located in the coding region), C1026T (a
 CC silent mutation in the coding region), and C1126G (located in the 3'-
 CC untranslated region). The SNPs and variant alleles of human orphanin
 CC FQ/nociceptin receptor DNA are useful in mapping the locus of the human
 CC orphanin FQ/nociceptin receptor gene, determining a subject's increased
 CC or decreased susceptibility to addictive diseases, susceptibility to pain
 CC and response to analgesics, physiological responses related to the
 CC endogenous opioid system or neurotransmitter release, anxiety and stress,
 CC learning, memory and cognition, alcohol self-administration, behavioural
 CC sensitisation to cocaine, drug addiction, opiate withdrawal and
 CC tolerance, food intake, immune function, cardiovascular function, renal
 CC function, gastrointestinal function, and motor function. The present
 CC sequence represents the 3'-untranslated region of the human orphanin
 CC FQ/nociceptin receptor gene
 XX
 XX Sequence 1829 BP, 297 A, 601 C, 542 G, 389 T, 0 U, 0 Other;

Query Match 34.1%; Score 393.4; DB 7; Length 1829;
 Best Local Similarity 65.1%; Pred. No. 2e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

153 GCGGCAATCTCCCGGCAATCCGGTATCATACGAGGGCTCTACTCCGATGTTGCT 212
 162 GCGCTTCTCGCCCTCGGGCTCAAGGTACACATCGGGGGCTCTACTCGCGTGTGT 221
 213 CGTGGCTTGTGGGCACTCGTGTATGTTCCGATCATCCGATACAAAGATGAA 272
 222 CGAGGGCTCCGGGGAATGCTGTATGTAACGATCTCCAGCAACCAAAATGAA 281
 273 GACAGCAACCAATTTATACATTTTAACTGGCTTGGAGATGCTTTAGTTACTACAAC 332
 282 GACAGCCACCAATTTTATACATTTTAACTGGCCCTGGCCGACACTCTGTCTGTGAC 341
 333 CATGCCCTTCAAGATACGCTTACTGTATGAAATTCCTGAGCTTTTGGGGAATGTCTGTG 392
 342 GGTGCCCTTCAAGGCAACGGAATCTCTCTGGGCTTCTGGCCGTTGGAAATGCGCTGTG 401
 393 CAAGATGTAATTTCCATGATGATTACTACAAATGTTTACACAGATTTTACCTTGACAT 452
 402 CAAGACAGTCATTCATTCATGATCTACAAACATGTTACACAGACCTTACCTTAATCTGC 461
 453 GATGACGCTGGAACGCTTACATTCGCTGTGAGCCACCCCGTGAAGGCTTTGAACTTCCGCAC 512
 462 CATGATGTGATTCGCTATGATGACATCTGACACCCCACTCCGCTCGACGTCGCGAC 521
 513 ACCCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGTCTGTCTGTTGGCAT 572
 522 GTCCAGCAAGCCCAAGCTGTGTAATGTGGCAATCTGGGCCCTTGCTGTGCGGTGT 581
 573 CTCTGCAATAGTCTTGTGAGGACCAAAATGACGGAAGAGCTGATGATGAGTGTCTC 632
 582 TCCCGTTGTCATCATGTGGCTCGGCAAGGTC-----GAGGATGAAGAGATCAAGTCCCT 635
 633 CTTGCAAGTTCCCAAGATGATGACTACTCTGTGTGGGACCTCTTCATAGAAGTCTGCGCTTT 692

DB 636 GGTGAGATCCCTACCCCTCAGATTAAC--TG66GCCCCGGTGTGGCATTCATTCATCTT 692
 QY CATCTTGGCTTTCGATATCCCTGTCTCATATATGCTGTCTACACCTGATGATCT 752
 DB 693 CCTCTTCTCCCTTCAACGCTCCCGTGTCTGTATCTGTGTCTACAGCTTCATATCCG 752
 QY GCGTCTCAAGACCGCTCCGCTCTCTTGTGCTCCCGAAGAAAGATCCCACTGCTGAG 812
 DB 753 GCGGCTCCGTGAGATCCGCTCTCTCTGCTCCGAGAGAAAGACCCGAACCTGCGCG 812
 QY GATCAACAGACTGTGCTGT 872
 DB 813 CATCACTCGGCTGT 872
 QY CATATTCATCTGT 932
 DB 873 GGTCTTCTGT 932
 QY CTATTACTTGT 992
 DB 933 TCTGCGCTTGT 992
 QY CTTTCCTGTATGAAAATTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
 DB 993 CTTCCTGTGATGAAATTCGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
 QY 1053 GATGAGGCGGACAGACATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
 DB 1053 CCGGACGCTGACAGGT 1097
 RESULT 78
 ABX94263
 ID ABX94263 standard; DNA, 1829 BP.
 XX
 XX ABX94263;
 AC 12-JUN-2003 (first entry)
 XX
 DT Human orphanin FQ/nociceptin receptor gene, coding sequence #3.
 DE
 XX Human; single nucleotide polymorphism; SNP; C510T; A804G;
 XX orphanin FQ/nociceptin receptor; loci mapping; C1026T; C1126G;
 KW addictive disease; pain; analgesic response; physiological response;
 KW anxiety; stress; endogenous opioid system; neurotransmitter release;
 KW learning; memory; cognition; alcohol self-administration;
 KW behavioural sensitisation; cocaine; drug addiction; opiate withdrawal;
 KW immune function; cardiovascular function; renal function;
 KW gastrointestinal function; motor function; coding region; de.
 XX
 OS Homo sapiens.
 XX
 XX Key location/Qualifiers
 FH replace(510,T)
 FT
 FT variation
 FT /tag= a
 FT /standard name= "SNP"
 FT /note= "C510T SNP specifically claimed in Claim 1"
 FT replace(804,G)
 FT /tag= b
 FT /standard name= "SNP"
 FT /note= "A804G SNP specifically claimed in Claim 1"
 FT variation
 FT /tag= c
 FT /standard name= "SNP"
 FT /note= "C1026T SNP specifically claimed in Claim 1"
 FT replace(1126,G)
 FT /tag= d
 FT /standard name= "SNP"
 FT /note= "C1126G SNP specifically claimed in Claim 1"
 XX
 XX US2003008289-A1.
 PN 09-JAN-2003.

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XX 09-OCT-2001; 2001US-00905186.
PF
XX
PR 14-JUL-2000; 2000US-0218205P.
XX
XX (KREEB/) KREEK M J.
XX PA (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, LaForge KS;
XX
DR MPI; 2003-353089/33.
XX
PT New variant allele of a human orphanin FQ/nociceptin receptor gene,
PT useful for determining a subject's susceptibility to addictive diseases
PT or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
PT in its DNA sequence.
XX
XX Example; Fig 10; 299p; English.
XX
XX The present invention relates to the identification of novel single
XX nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
XX receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
XX untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
XX (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
XX mutation located in the coding region), GIVS III 67T (located in intron
XX 3), A804G (a silent mutation located in the coding region), C1026T (a
XX silent mutation in the coding region), and C1126G (located in the 3'-
XX untranslated region). The SNPs and variant alleles of human orphanin
XX FQ/nociceptin receptor DNA are useful in mapping the locus of the human
XX orphanin FQ/nociceptin receptor gene, determining a subject's increased
XX or decreased susceptibility to addictive diseases, susceptibility to pain
XX and response to analgesics, physiological responses related to the
XX endogenous opioid system or neurotransmitter release, anxiety and stress,
XX learning, memory and cognition, alcohol self-administration, behavioural
XX sensitisation to cocaine, drug addiction, opiate withdrawal and
XX tolerance, food intake, immune function, cardiovascular function, renal
XX function, gastrointestinal function, and motor function. The present
XX sequence represents the coding region of the human orphanin FQ/nociceptin
XX receptor gene
XX
SQ Sequence 1829 BP; 297 A; 601 C; 541 G; 390 T; 0 U; 0 Other;

```

```

Query Match      34.1%; Score 393.4; DB 7; Length 1829;
Best Local Similarity 65.1%; Pred. No. 2e-86;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```

```

QY 153 CGCGACATCTCCCGGCCATCCGGTCATCATCAGCGCGTCTACTCCGATGTTCT 212
DB 162 GCGCTTCCGCGCCCTCGGGCTCAAGGTACATCGGGGGCTCTACCTGGCGTGTGT 221
QY 213 CGTGGCTTGTGGGCACTCCGTGTCTATGTTCCGTATCATCCATACAAAGATGAA 272
DB 222 CGAGGGGCTCTGGGGAACTGGCTGTCTATCATGTCATCTCAGGACACCAAAATGAA 281
QY 273 GACAGCAACCAATTTATTAATTAACCTGGCTTGGAGATGCTTTAGTACTACAAAC 332
DB 282 GACAGCAACCAATTTATTAATTTAACTGGCCCTGGCGAACACTCTGCTCTGCTGAC 341
QY 333 CATGCCCTTTCAAGATACGCTACTTGAATGTAATTCCTGGCCCTTTTGGAGATGCTGTG 392
DB 342 GCTGCCCTTTCAGGGGACGGAATCTCTGGGGCTTCTGGCCGTTTGGGAAATGGCGTGG 401
QY 393 CAAGATAGTAATTTCCATTGATTACTACAAATGTTTACACAGACATTTCACTTGACAT 452
DB 402 CAAGACAGTCAATGCTATGACTACTACAAATGTTTACACAGACCTTCACTTAATCTGC 461
QY 453 GATGACGCGGACCGGCTATATGCGGTGGCCACCCCGGAGGAGGCTTTGACCTCCGAC 512
DB 462 CATGAGTGTGAATCGCTATGATGACATCTGCCACCCCACTCCGCTTGAAGTCCGAC 521
QY 513 ACCCTTGAAGCAAGATCATCAATATCTGCATCTGGCTGTCTGTCTCATCTGTTGGCAT 572
DB 522 GTTCAGCAAGCCGAGCTGTCAATGTGGCACTCTGGGCCCTGGCTCTGTTGTGGGTGT 581

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QY 573 CTCTGCAATAGTCCTTGGAGGACCAAGTCAAGGAGACGTGATGTCATTTAGTGTCTC 632
DB 582 TCCCGTTGCCATCATGGGCTCGGACAGGTCTC-----GAGATGAAGATGAGTGCCT 635
QY 633 CTTCGAGTTCACCAATGATGACTACTCTGTGGAGACCTTTTCATGAAGATGTGGCTTT 692
DB 636 GGTGAGATCCCTACCCCTCAGAGATTAC---TGGGGCCCGGATGTTTGCATCTGCATCTT 692
QY 693 CATCTTGGCTTTCGTGATTCCTGTCTCATCATCATCTGTCTCTACACCTGATGATCTCT 752
DB 693 CCTCTTCTTCATCATGCTCCCGTCTGTCTCATCTGTCTCTACAGCTCATGATGATCCG 752
QY 753 GCGTCTCAAGACGCGCGGCTCTTTCTGGGCTCCGAGAGAAAGATCCGACCTGGTAG 812
DB 753 GCGGCTCCGTGAGTCCGCTGTCTCTCGGCTCTCGGATCCGAGAGAGACCGGACCTGGGCG 812
QY 813 GATCACAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 813 CATCATCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
QY 873 CATATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 873 GGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
QY 933 CATTAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 933 TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
QY 993 CTTCCTGATGAAGAACTTCAAGCGGTGTTTCCGGAGCTTGTCTTCCACTGAAGATGAG 1052
DB 993 CTTCCTGATGAAGAACTTCAAGCGGTGTTTCCGGAGCTTGTCTTCCACTGAAGATGAG 1052
QY 1053 GATGAGCGGCGAGACCATTAAGAGATGCCAAATACAGTTACGA 1097
DB 1053 CCGGATGTGACGATGTGTGACCGGCTGTGCGAGCATTTGCCAAGA 1097

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RESULT 79

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ACAS6793
ID ACAS6793 standard; cDNA; 1973 BP.
XX
AC ACAS6793;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1391.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR MPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
PS Claim 1; SEQ ID NO 1391; 65bp; English.

```

XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX

Sequence 1973 BP, 315 A; 650 C; 587 G; 421 T; 0 U; 0 Other;

Query Match 34.1%; Score 393.4; DB 7; Length 1973;

Best Local Similarity 65.1%; Pred. No. 2.1e-86; Mismatches 321; Indels 9; Gaps 2;

Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

153 CGCGACATCTCCCGGCCATCCGGTTCATCAACGGCGGCTCTACCTCCGATGTTGCT 212
DB CGCCCTTCCTGCCCCCTCGGGCTCAAGGTACATCGGGGCTCTACCTGCGCTGTGTGT 365
213 CGTGGCTTGTGTGGCACTCGCTGTGTATGTTCTGTATCATCGATACACAAAGATGA 272
DB CGAGGGGCTCCCTGGGGAACCTGCTGTATGTAAGTCACTCTCAGGCAACCAAAATGA 425
273 GACAGCAACCAATTTACATATTTAACTGAGTGTGGAAGTGTGTTAGTACTACAC 332
DB GACAGCCACCAATTTACATCTTTAACTGAGTGTGGAAGTGTGTTAGTACTACAC 485
333 CATGCGCTTTCAGATACGCTTACTGTATGTAATTCCTGGGCTTGTGGGATGTGCTGTG 392
DB GGTGCTTTCAGGGAACGACATCTCTGGGCTTGTGGGCTTGTGGGATGTGCTGTG 545
393 CAAGATGATTTTCCATTGATTACTACAAAGTTCACACGACATCTTACCTTACCAT 452
DB CAAGACAGTCAATGCTACTACTACAAAGTTCACACGACATCTTACCTTACCAT 605
453 GATGAGCGTGAACGGCTCATTCGGCTGTGACACCCCGGAAGGCTTGGACTTCCGAC 512
DB CATGAGTGTGATGCTGATGTAATGCAATGCAACCCCATCGTGCCTTGAGAGTCCGAC 665
513 ACCCTTGAAGGCAAGATCATCAATATCTGATCTGCTGTGTGTGTGTGTGTGTGTGT 572
DB GTCCGCAAAAGCCAGGCTGTCAATGTGGCCATCTGGGCTGTGTGTGTGTGTGTGTGT 725
573 CTCTGCAATAGTCTCTGAGGACCAAAAGTCAAGGAAAGCTGTGATGTGAGTGTCTC 632
DB TCCCTGTGCAATGATGAGGCTCGGCAAGGTC-----GAGGATGAAGATGAGTGTGCT 779
633 CTGAGATTTCCAGATGATGATCTCTCTGTGTGGGACCTCTTCAAGAAATGTGTGTGT 692
DB GGTGAGATTCCTTACCCCTCAGGATTTAC--TGGGGCTCCGGGCTTGTGCAATGTGATCT 836
693 CATCTTGTGCTGTGATCTCTGTCTGTATCATCTGTGTGTGTGTGTGTGTGTGTGTGT 752
DB CCTCTTCTCTTCAATGATGCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 896
753 GGTGTCAAGAGCGTCCGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
DB GCGGCTCCGTGAGTCCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956

QY 813 GATGACGAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB CATCTGCGGCTGT 1016
QY 873 CATATTCATCTGT 932
DB GGTCTTCTGT 1076
QY 933 CTATTACTTGT 992
DB TCTGCGCTTGT 1136
QY 993 CTCTTGTGATGAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB CTCTGATGATGAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1196
QY 1053 GATGAGCGGCGAGACATACAGAGTCCGAATATCAAGTTGAGGA 1097
DB CCGGAGCGTGCAGGT 1241

RESULT 80
ADCC40517
ID ADCC40517 standard; DNA; 1973 BP.

AC ADCC40517;

XX 18-DEC-2003 (first entry)

DE DNA derived from human G-protein coupled receptor (GPCR) mRNA.

KM gene expression analysis; collective quantitative analysis;

KM G protein coupled receptor; tyrosine oxidase receptor family;

KM ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

OS myocardial infarction; infarct; ischaemic disease; human; GPCR; ds.

XX Homo sapiens.

PN W02003052096-A1.

PD 26-JUN-2003.

PF 13-DEC-2002; 2002WO-JP013097.

PR 14-DEC-2001; 2001JP-00382053.

PR 21-FEB-2002; 2002JP-00045104.

PR 15-MAY-2002; 2002JP-00140111.

PR 18-NOV-2002; 2002JP-00333769.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsunura F, Kawamata Y, Ogi K;

DR WPI; 2003-533023/50.

XX Method for gene expression analysis for treatment of cancers.

XX Example 1; SEQ ID NO 1; 261pp; Japanese.

PS The invention relates to a novel method for gene expression analysis by

CC collective quantitative analysis of the expression of a number of genes

CC to identify those that are promoted or inhibited in a given cell or

CC tissue. The genes are preferably gene families such as the G protein

CC coupled receptor family, tyrosine oxidase receptor family, or ion channel

CC gene family. The methods may be used in treatment of cancers, including

CC prostate, ovarian, stomach, bladder, breast, and cancer of the

CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used

CC in the treatment and prevention of atherosclerosis, myocardial

CC infarction, infarct or ischaemic disease of the brain. This

CC polynucleotide sequence represents the DNA derived from human G-protein

CC coupled receptor (GPCR) mRNA of the invention.

XX Sequence 1973 BP; 315 A; 650 C; 587 G; 421 T; 0 U; 0 Other;
 SQ

Query Match 34.1%; Score 393.4; DB 9; Length 1973;
 Best Local Similarity 65.1%; Pred. No. 2.1e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```

OY 153 CGCGCATCTCCCGGCGCATCCGGTCATCATCAGGCGGTCTACTCCGTAGTGTCT 212
DB 306 CCGCTTCTGCGCCCTCGGGCTCAAGGTCAACATCGTGGGCTCTTACCTGGCGGTGTGT 365
OY 213 CGTGGGCTTGTGGGCACTCGGTGTCTATGTTCTGTATCATCCGATACAAAGATGA 272
DB 366 CGAGGGCTCTCGGGAACTGCTTGTCTATGTCATCTCAGGACACCAAAATGA 425
OY 273 GACAGCAACCAATTATTAATTAACCTGCTTGGAGATGCTTTAGTTAATAACAAC 332
DB 426 GACAGCAACCAATTATTAATTAATTAACCTGCTTGGAGATGCTTTAGTTAATAACAAC 485
OY 333 CATGCCCTTTCAGAGTACGCTCTACTGATGAAATTCCTGGCCCTTTGGGAGTGTGTG 392
DB 486 GCTGCCCTTTCAGAGGACGAGACATCTCTGGGCTTCTGGCCCTTTGGGAGTGTGTG 545
OY 393 CAAGATAGTAATTTCCATTGATTAATAACAAGATGTTACACAGCATCTTACCTTGACAT 452
DB 546 CAAGATAGTATTCGATGATTAATAACAAGATGTTACACAGCATCTTACCTTGACAT 605
OY 453 GATGAGCGTGACCGCTTACATGCGGTGTGCCACCCCGTGAAGCTTTGGAATCTCGGAC 512
DB 606 CATGAGTGTGATCGCTATGATGACCATGTGCCACCCCATCCGCTCGACGCTCGGAC 665
OY 513 ACCCTTGAAGCAAAAGATCATCAATCTGCACTCTGGCTGTCTCTCATCTGTGGCAT 572
DB 666 GTTCAGCAAGCCAGAGCTGTCAATGTGGCCATCTGGGCTGTCTGTGTCTGTGT 725
OY 573 CTCTGCAATAGTCTCTTGAAGCACCAAGTCAAGGAGAGAGTGTATGATGATGCTC 632
DB 726 TCCCGTTCATCATGAGGCTCGGACAGGTC-----GAGATGAAGATGAGTGTCT 779
OY 633 CTTCGATTTCCAGATGATGATCACTCTCGTGTGGAGCTTTCATGAAAGTGTGTCT 692
DB 780 GGTGAGATCCCTAACCCTCAGGATTAAC---TGGGGCCCGGTGTGTGTGTGTGTGT 836
OY 693 CATCTTGTCTCTGTATCTCTGTCTCTCATCATCTGTCTGTGTGTGTGTGTGTGTCT 752
DB 837 CCTCTTCTCTCATCTGTCTCGGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 896
OY 753 GCGTCTCAAGAGGCTCGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
DB 897 GCGGCTCCGTGAGTCCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
OY 813 GATCACAAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 957 CATCACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
OY 873 CATATTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1017 GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
OY 933 CATATTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1077 TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
OY 993 CTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1137 CTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1196
OY 1053 GATGAGCGGACAGCATTAAGCAGAGTCCGAATATACAGTTTCAGGA 1097
DB 1197 CGGAGCGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

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RESULT 81

ABX94045
 ID ABX94045 strand; cDNA; 2534 BP.

XX AC ABX94045;
 XX DT 12-JUN-2003 (first entry)
 XX DE

CDNA encoding human orphanin FQ receptor (OPQR).

XX Human; orphanin FQ receptor; OPQ; orphanin FQ; psychotropic drug;
 KW nociceptin; gastrointestinal motility; diarrhoea; nausea; fever; pain;
 KW inflammation; learning disorder; memory disorder; drug dependence;
 KW stress-related neuronal dysfunction;
 KW orphanin FR receptor-mediated disease; gene; ss.

OS Homo sapiens.
 XX US2003045696-A1.
 XX PN

PD 06-MAR-2003.

XX 01-MAR-2002; 2002US-00087345.

XX 01-MAR-2001; 2001US-0272429P.

XX (UNMI) UNIV MICHIGAN.

XX Owyang C;

XX WPI; 2003-371474/35.

PT New compositions, useful for identifying pharmaceutical agents for
 PT treating diseases mediated by orphanin FQ signaling, e.g. learning and
 PT memory disorders, comprises orphanin FQ receptor splice variants or
 PT encoding nucleic acids.

PS Disclosure; Fig 19; 65pp; English.

XX The invention describes a new composition comprising: (a) an isolated
 CC nucleic acid having one of 9 fully defined sequences with 439-1566 base
 CC pairs (bp); (b) an isolated nucleic acid 85% identical to (a) and
 CC encoding a polypeptide that binds to Orphanin FQ; or (c) an isolated
 CC polypeptide that is at least 95% identical to one of 5 fully defined
 CC sequences with 99-367 amino acids, where the polypeptide binds to
 CC Orphanin FQ. The polypeptide or nucleic acid is useful for screening or
 CC identifying pharmaceutical agents, particularly psychotropic drugs, for
 CC the treatment of a variety of disease states mediated by orphanin FQ
 CC (also called nociceptin) signalling. These disease states include
 CC gastrointestinal motility (e.g. diarrhoea), nausea, fever, pain,
 CC inflammation, learning and memory disorders, drug dependence, stress-
 CC related neuronal dysfunctions, etc. The polypeptide or nucleic acid is
 CC also useful for generating animal models of orphanin FR receptor-mediated
 CC disease state. This is the CDNA sequence of human orphanin FQ receptor
 CC (OPQR)

XX Sequence 2534 BP; 416 A; 809 C; 769 G; 540 T; 0 U; 0 Other;

Query Match 34.1%; Score 393.4; DB 7; Length 2534;
 Best Local Similarity 65.1%; Pred. No. 2.3e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```

OY 153 CGCGCATCTCCCGGCGCATCCGGTCATCATCAGGCGGTCTACTCCGTAGTGTCT 212
DB 246 CCGCTTCTGCGCCCTCGGGCTCAAGGTCAACATCGTGGGCTCTTACCTGGCGGTGTGT 305
OY 213 CGTGGGCTTGTGGGCACTCGGTGTCTATGTTCTGTGATCATCCGATACAAAGATGA 272
DB 306 CGAGGGCTCTCGGGAACTGCTTGTCTATGTCATCTCAGGACACCAAAATGA 365
OY 273 GACAGCAACCAATTATTAATTAATTAACCTGCTTGGAGATGCTTTAGTTAATAACAAC 332
DB 366 GACAGCAACCAATTATTAATTAATTAATTAACCTGCTTGGAGATGCTTTAGTTAATAACAAC 425

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QY 333 CATGCCCTTTGAGATGAGTCTACTGTAATTCCTGACCTTTTGGGATGTGCTG 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 GCTGCCCTTCCAGGCGACGGAATCTCTCTGGGCTTTCTGGCCGTTTGGAAATGCGCTGG 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 393 CAAGATAGTAATTTCCATTGATTACTACAACATGTTCCACAGCATCTTCACTTGAACAT 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 486 CAAGACAGTCAATGACCTACTACAAACATGTTCAACAGACCTTCACTTGAACATG 545
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 GATGAGCGTGAACCGCTACATTCGCGTGTGCCACCCCGGAAAGGCTTGGACTTCCGAC 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 CATGAGTGTGATGCTGTATGTAGCCATCTGCCACCCCATCCGTCCTTGAAGTCCGAC 605
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 ACCCTTGAAGCAAGATCATATATCTGATCTGAGCTGTGTGATCTTGGTGCAT 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 606 GTCCAGCAAGGCCAGGCTGTCAATGTGGCCATCTGGGCCCTGGCTCTGTGTGTGGT 665
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CTCTGCAATGATCTTGGAGGACCAAGTCCAGGGAAGAGTGTGATTTAGTGTCTC 632
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 666 TCCCGTGGCATCATGGGCTCGGACAGGTC-----GAGGATGAAGAGATCGAGTGCCT 719
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 633 CTTCGATTTCCAGATGATGACTACTCCGTGTGGGACCTTTCATGAAATCTGGCTCT 692
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 720 GGTGAGATGCTCTACCCCTCAGGATTAAC---TGAGGCGCGGTGTTCATCTGATCTT 776
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 CATCTTGGCTTCGTGATCCCTGTCTCATCATCTGCTGCTACACCCCTGATGATCCT 752
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 777 CCTCTTCTCTTCATCTGCTCCGCTGCTGCTCATCTGTCTGTCTACAGCTCATGATCCG 836
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTTCTGCTCCGAGAAAGATCCGACCTGCTAG 812
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 837 GCGGCTCGGTGAGTCCGCTGCTCTCGGGCTCCGAGAGAGACCGGAACTCTCGGCG 896
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 813 GATACACAGACTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 897 CATCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 957 GGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 933 CTATTACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1017 TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 993 CTTTCTGTATGAATCTTCAAGCGGTGTTTCCGGGACTTGTGCTTTCATGTAATAG 1052
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1077 CTTCTGTATGAATCTTCAAGCGGTGTTTCCGGGACTTGTGCTTTCATGTAATAG 1136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1053 GATGAGCGGCGACAGCAGTACAGAGTCCGAATACAGTTTCAGGA 1097
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1137 CCGGACGTCGACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 82
ABZ42709
ID ABZ42709 standard; DNA; 2534 BP.

AC ABZ42709;

DT 04-MAR-2003 (first entry)

DE Human opiate receptor-like 1 nucleotide seq ID NO:208.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor; modulator; antibody; immun-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

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KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN W020261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
DR P-PsDB; ABP81862.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 2534 BP; 416 A; 809 C; 769 G; 540 T; 0 U; 0 Other;

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Query Match 34.1%; Score 393.4; DB 7; Length 2534;
 Best Local Similarity 65.1%; Pred. No. 2.3e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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QY 153 CGCGCAATCTTCCCGGCGCATCCGGTCAATATACAGCGGCTCTACTCCGATGTTCT 212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 246 CGCCTTCTGTCCTCGGGCTCAAGGTCAACCATGTGGGGCTCTTACCTGCGCGTGTGTGT 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 213 CGTGGGCTTGTGTGGAACCTGCTGTGATGTTGTGTATCTCCGATTCACAAAGATGAA 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 CGAGAGGCTCTGTGGAACTGCTTGTATATGATGATCTTCAAGGACACCAAAATGAA 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 273 GACAGCAACCAATTTACATATTAACTGTGCTTGTGGACAGATCTTTAGTTACTACAAC 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 366 GACAGCAACCAATTTAACTTTAACTTTAACTGTGCGCTGCGACACTGTGCTGTGAC 425
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 333 CATGCCCTTTGAGATGAGTCTACTGTAATTCCTGACCTTTTGGGATGTGCTG 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 GCTGCCCTTCCAGGCGACGGAATCTCTCTGGGCTTTCTGGCCGTTTGGAAATGCGCTGG 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 393 CAAGATAGTAAATTCCTGATGATTAACAACATGTTACACAGATCTGCATGACAT 452
 DB 486 CAAGACAGTCAATGCTGATGATTAACAACATGTTACACAGATCTGCATGACAT 545
 QY 453 GATGACGCTGACCGGTACATGCTGCTGTCACACCCCGTGAAGCTTTGAGCTTCGAC 512
 DB 546 CATGAGTGTGATCGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 605
 QY 513 ACCCTTGAAGCAAGATATCATATATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 572
 DB 606 GTCCAGCAAGCCGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 665
 QY 573 CTCTGCAATATGCTCTGAGGACCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 DB 666 TCCCGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
 QY 633 CTTCGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
 DB 720 GGTGAGATCCCTACCCCTCAGGATTAAC---TGGGGCCGGGTGTTGATGATGATGAT 776
 QY 693 CATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
 DB 777 CCTCTTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
 QY 753 GGTCTCAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 DB 837 GGGGCTCGGTGAGTCCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 896
 QY 813 GATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 DB 897 CATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
 QY 873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 DB 957 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
 QY 933 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
 DB 1017 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
 QY 993 CTTCCTGATGAAATCTTCAAGCGGTGCTTCCGAGCTTCTGCTTCTCACTGAAGTGA 1052
 DB 1077 CTTCCTGATGAAATCTTCAAGCGGTGCTTCCGAGCTTCTGCTTCTCACTGAAGTGA 1136
 QY 1053 GATGAGCGGCAAGACCTAGAGAGTCCGAATATACATGTTCAAGGA 1097
 DB 1137 CCGGACGTCAGGTGTCTGACCGGCTGCGCAGCATTTGCCAAGGA 1181
 RESULT 83
 ABI98010
 ID ABI98010 standard; cDNA; 1113 BP.
 AC ABI98010;
 DE 18-FEB-2002 (first entry)
 XX Non-endogenous human GPCR cDNA, SEQ ID NO: 540.
 KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease; ss.
 OS Homo sapiens.
 XX Synthetic.
 PN WO20017172-A2.
 XX 18-OCT-2001.
 PD 05-APR-2001; 2001WO-US011098.
 XX 07-APR-2000; 2000US-0195747P.
 PR

XX (AREN-) ARENA PHARM INC.
 PA Lehmann-Brunnema K, Llaw CM, Lin I;
 PI WPI; 2001-648759/74.
 XX DR P-PSDB; ABB56374.
 XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.
 PS Example 2; Page 342; 394pp; English.
 XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence encodes a non-endogenous version of a known human GPCR
 SQ Sequence 1113 BP; 176 A; 378 C; 309 G; 250 T; 0 U; 0 Other;
 Query Match 34.0%; Score 391.8; DB 5; Length 1113;
 Best Local Similarity 65.0%; Pred. No. 4,1e-86;
 Matches 614; Conservative 0; Mismatches 322; Indels 9; Gaps 2;
 QY 153 CGCGACATCTTCCCGGCGATCCCGGATCATCAACGCGGCTTACTCCGATGTTGCT 212
 DB 129 GCGCTTCGCGCTCTCGGGCTCAAGTCAACATGCGGGGCTCTACCTGCGGTGTGT 188
 QY 213 CGTGGCTTGTGGGCACTGCTGCTGATGTTCTGATATCCGATACAAAGATGA 272
 DB 189 CGAAGGCTCTCGGGAACTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 248
 QY 273 GACAGCAACCAATTTATATTTTACCTGCTTGGAGATGCTTATGTTACTTAAAC 332
 DB 249 GACAGCAACCAATTTATATTTTACCTGCTTGGAGATGCTTATGTTACTTAAAC 308
 QY 333 CATGCCCTTTCAGATGAGTCTTACTTATGATGATGATGATGATGATGATGATGATGAT 392
 DB 309 GCTGCCCTTTCAGAGGCAAGACATCTCTGCGCTTCTGCGGTTGGAAATGCGCTGTG 368
 QY 393 CAAGATAGTAAATTCCTGATGATTAACAACATGTTACACAGATCTGCATGACAT 452
 DB 369 CAAGACAGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
 QY 453 GATGACGCTGACCGGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
 DB 429 CATGAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
 QY 513 ACCCTTGAAGCAAGATATCATATATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 DB 489 GTCCAGCAAGCCGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
 QY 573 CTCTGCAATATGCTCTGAGGACCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 DB 549 TCCCGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
 QY 633 CTTCGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
 DB 603 GGTGAGATCCCTACCCCTCAGGATTAAC---TGGGGCCGGGTGTTGATGATGATGAT 659
 QY 693 CATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
 DB 660 CCTCTTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
 QY 753 GGTCTCAAGAGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
 DB 720 GCGGCTCGGTGAGTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
 QY 813 GATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872

DT 11-DEC-2002 (first entry)
 XX DNA encoding human mu1/mu4 fusion protein.
 DE
 XX Human; mu4; opioid receptor; ss; morphine; receptor;
 KM Intracellular calcium; mu1.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200268594-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-US005452.
 XX
 PR 22-FEB-2001; 2001US-0270479P.
 PR 05-DEC-2001; 2001US-0336677P.
 XX
 PA (RESU-) RES FOUND SUNY.
 XX
 PI Cadet P, Stefano GB;
 XX
 DR WPI; 2002-706977/76.
 XX
 PT New isolated nucleic acid molecule encoding a polypeptide having mu3
 PT opiate receptor activity, useful as research tools for exploring the
 PT interactions, molecular mechanisms and relationship of morphine with the
 PT mu3 opiate receptor.
 XX
 PS Example 2; Page 37-38; 52pp; English.
 XX
 CC This invention relates to a novel nucleic acid molecule encoding a
 CC polypeptide having mu3 opiate receptor activity. Mu opioid receptors
 CC exhibit a high binding specificity for morphine. The invention also
 CC comprises a method for identifying a mu3 opiate receptor agonist or
 CC antagonist. The nucleic acids and polypeptides of the invention are
 CC useful as research tools for exploring the interactions of morphine with
 CC the mu3 opiate receptor, the molecular mechanisms by which morphine
 CC induces intracellular calcium concentration changes and the relationship
 CC of mu3 opiate receptors with other mu opioid receptors. They are also
 CC useful for identifying a mu3 opiate receptor agonist or antagonist. The
 CC present sequence represents the cDNA encoding a human mu1/mu4 opioid
 CC receptor fusion protein of the invention
 CC
 XX
 SQ Sequence 1670 BP; 490 A; 392 C; 311 G; 469 T; 0 U; 8 Other;
 Query Match 33.3%; Score 384; DB 6; Length 1670;
 Best Local Similarity 68.2%; Pred. No. 3.9e-84;
 Matches 566; Conservative 0; Mismatches 255; Indels 9; Gaps 2;
 QY 258 ATACACAAAGATGAGAGACGACCAACATTTACATATTAACTGGCTTGGCAGATGC 317
 DB 1 ATRACCAAGATGAGAGACGACCAACATTTACATATTAACTGGCTTGGCAGATGC 60
 QY 318 TTTAGTTACTACACACATGCGCTTTGAGAGTACGCTTACTTGATGAATTCTGGCCTTT 377
 DB 61 CTTAGCCACACAGTACCTGCTCCCTTCAGAGTGTGAAATTACTAATGGAAATGGCCATT 120
 QY 378 TGGGGATGCTGTGTGAGATGATGATTTCCATGTTTCTCAATGATTCACACGAGAT 437
 DB 121 TGGAAACATCTTTGAGATGATGATCTCCATAGTATCTATACATGTTTCAACGAGAT 180
 QY 438 CTTTACCTTGACCATGATGAGCGGTGACCGCTACATTTGCGTGCCACCCCGTGAAGGC 497
 DB 181 ATTCAACCTCTGTGACATAGTGTGATGATATGATGACGTGTGCAACCTGTCAAGGC 240
 QY 498 TTTGACCTTCCGACACCTTTGAAGGCAAGATCATATTTGATCTGGCTGCTGTC 557
 DB 241 CTTAGATTTCCTGATCTCCCGAAATCCAAATATATCAATGCTGTGACATGATCTCTTC 300
 QY 558 GTCATGTGTGGATCTGTGCAATAGTCTTGTGAGGACACCAAGTGAAGGAAAGCTCGA 617

DB 301 TTCACCATGTGCTTCTCCGTAAATGTTCAATAGTCAACAAATAACAGGCA-----GG 354
 QY 618 TGTCAATGAGTGTCTCTTGACAGTTCCAGATGATGACTACTGCTGGAGACTCTTCAT 677
 DB 355 TTCATTAATTTGACTAATCAATTTCTC--TCATCAACCTGTGTACTGGAAAACCTGCT 411
 QY 678 GAAGATCTGCGCTTCATCTTTGCTGGTGTATCCCTGTCTCATCATCATGCTGTGCTA 737
 DB 412 GAAGATCTGTGTTTTCATCTTGTGCTTATATGCAATGCTCATATTAACGTTGCTCA 471
 QY 738 CACCTGATGATCTGCGCTTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGA 797
 DB 472 TGGACTGATGATCTTGCGCTTCAGAGATGCTGCTCTGTGCTCCAAAAGAAAGGA 531
 QY 798 TGGCAACTGCTGTAGATCAACAGACTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTG 857
 DB 532 CAGGAATCTTGAAGAGATCACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 591
 QY 858 CTGACTCCCATTCATATTTATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 917
 DB 592 CTGACTCCCATTCATATTTATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 651
 QY 918 AGCTGCTCTTCCAGCTATTTACTTGTGATGCGCTTGAAGCTATACCAAGATGCTGAA 977
 DB 652 GTTCCAGACTGTCTTGTGCACTTCTGCAATGCTCTAGGTACAAACAGCTGCTCAA 711
 QY 978 TCCCATTTCTTACGCTTTCTTGTGATGAAACCTTCAAGCGGTCTTCCGGAATCTGTCT 1037
 DB 712 CCCAGTCTCTTATGATTTGTGATGAAACCTTCAAGCGGTCTTCAAGAGATGCTGTAT 771
 QY 1038 TCCACTGAAGATGATGAGCGGACAGACTGTGACAGTCCGAATA 1087
 DB 772 CCCAACCTTTCACATTTGAGCAACAAACCTCCACTGCAATTCGTGCA 821
 RESULT 88
 ID ABX94042
 ABX94042 standard; cDNA; 1243 BP.
 AC ABX94042;
 XX
 DX 12-JUN-2003 (first entry)
 XX
 DE Rat orphanin FQ receptor splice variant OFQR-c'.
 XX
 XX Rat; orphanin FQ receptor; OFQ; orphanin FQ; psychotropic drug;
 KM nociception; gastrointestinal motility; diarrhoea; nausea; fever; pain;
 KM inflammation; learning disorder; memory disorder; drug dependence;
 KM stress-related neuronal dysfunction;
 KM orphanin FR receptor-mediated disease; gene; ss; splice variant.
 XX
 OS Rattus norvegicus.
 XX
 PN US2003045696-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 01-MAR-2002; 2002US-00087345.
 XX
 PR 01-MAR-2001; 2001US-0272429P.
 XX
 PA (UNMI) UNITV MICHIGAN.
 XX
 PI Owyang C;
 XX
 DR WPI; 2003-371474/35.
 XX
 PT New compositions, useful for identifying pharmaceutical agents for
 PT treating diseases mediated by orphanin FQ signaling, e.g. learning and
 PT memory disorders, comprises orphanin FQ receptor splice variants or
 PT encoding nucleic acids.
 XX
 PS Claim 1; Fig 16; 65pp; English.

inflammation, learning and memory disorders, drug dependence, stress-related neuronal dysfunctions, etc. The polypeptide or nucleic acid is also useful for generating animal models of orphanin FR receptor-mediated disease state. This is the cDNA sequence of rat orphanin FQ receptor (OFQR) splice variant OFQR-c

Sequence 1387 BP; 252 A; 403 C; 356 G; 376 T; 0 U; 0 Other;

```

Query Match      32.7%; Score 377.6; DB 7; Length 1387;
Best Local Similarity 63.9%; Pred. No. 1.4e-82;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCATCATCAGGGGGTCTACTCCGTAAGTTCGT 212
DB 403 CGCCTTCCCTGCCCCCTTGGAAGTCAAGGTCAACATCGTGGGGCTTACTTGGCTGTGCAAT 462
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGATGTTGATCATCCGATACACAAAGATGAA 272
DB 463 CGGGGGGCTCTGGGGAACTGGCTGTGATGATGATGATGATGATGATGATGATGATGAT 522
QY 273 GACAGCAACCAACATTATATTTAACTGGCTTTGGGAGATGCTTTAGTTACTACAC 332
DB 523 GACAGTACCAACATTATATTTAACTGGGACATGCTGATACCTGTGCTTGTCTAAC 582
QY 333 CATGCCCTTTCAGAGTACGGTCTACTTGATGAAATTCCTGAGCTTTGGGAGATGCTGTG 392
DB 583 ACTGCCCTTTCAGAGGACAGACATCTACTGGGCTTCTGAGCAATTTGGAAATGCACTCTG 642
QY 393 CAAGATAGTAAATTTCCATGATTTACTACAAAGTTCACACAGATCTTCACTTGAACAT 452
DB 643 CAAGATGTCATTTGCTATGACTACTACAAAGTTTTACAGACATTTTACTCTGACCCG 702
QY 453 GATGAGCGTGAACCGCTATCATTTGCCGTGGCCACCCCGTGAAGGCTTTGACTCCGAC 512
DB 703 CATGAGCGTGAACCGCTATGCTGTATCTGCCACCTATCCGCTTGAATGTTGCGAGC 762
QY 513 ACCCTTGAAGGCAAGATCATCATATCTGCATCTGGCTGTGCTGATCTGTGGCAT 572
DB 763 ATCCAGCAAGCCCGAGGCTGTTATGTGCGCATATGGCCCTTGCTTCACTGTGTGTGT 822
QY 573 CTCTGCAATATGCTCTTGGAGGACCAAGTCAAGGGAAGACGTGATGATTTGAGTCTC 632
DB 823 TCCCTGTGTCATCATCGGTTTCAAGCAAGT-----GGAAGATGAAGATGAGTGCCT 876
QY 633 CTTCGACTTCCAGATGATGATCTACTCTGTGTGGGACCTTCTTCATGAAATCTGCCTTT 692
DB 877 GGTGGAGATCCCTGCCCCCTCAGGACTATTTGGGG---CCCTGTAATTCGCCATCTGCAT 933
QY 693 CATCTTTGCTCGTATCCCTGCTCTCATCATCATGCTGTGTACACCTGATATGATCTCT 752
DB 934 CATTCTTTCTTCATCATCTCTGTGTGATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
QY 753 GCGTCTCAAGAGCGTCCGGCTCTCTTCTGTGCTCCAGAGAAAGATCGAACCTGTGGTAG 812
DB 994 AAGACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
QY 813 GATCACCAAGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 1054 TATCTCTGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1113
QY 873 CATTTTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1114 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1173
QY 933 CTATTACTTCTGATCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1174 CCGGAGCTTCTGACAGCCCTGTGGGCTATGTCAACATTTGTCTCAATCCATCTCTATATG 1233
QY 993 CTTTCTTGATGAATTTCAAGCGGTGTTCGGGACCTTGTCTTGTCTTCACTGAAGATGAG 1052
DB 1234 TTTCTCGATGAGAACTTCAAGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1293
QY 1053 GATGAGCGGCGAGAGACATGAGAGTCCGAAATATAGTTTCAAGGATCTCTG 1102

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DB 1294 CGGGAGATGACAGGTTTCTGATCGTGTGTGGAGCATTTGCCAAGATGTTG 1343

RESULT 90

AA089233

AA089233 standard; cDNA; 1567 BP.

AC AA089233;

DT 25-MAR-2003 (revised)

DT 20-OCT-1995 (first entry)

DE Rat oploid receptor cDNA.

KW Opioid receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

FH Key location/Qualifiers

FT CDS 173..1276

PN MO9507983-A1.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US010358.

PR 13-SEP-1993; 93US-00120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

DR MPI; 1995-131351/17.

PT P-PSDB; AAR71968.

PT New nucleic acid encoding new human mu opioid receptor - and related

PT vectors, transformed cells, antibodies etc., useful in diagnosis,

PT treatment and drug screening.

PS Example 9; Page 218-222; 266pp; English.

CC The cDNA given in AA089233 was isolated from a rat brain library by low

CC stringency hybridization with rat mu opioid receptor cDNA (AA089222). The

CC clone encoded a 367-amino acid protein (AAR71968) that showed high

CC homology with mu, kappa and delta opioid receptors but lacked affinity

CC for their ligands, suggesting it to be a novel member of the oploid

CC receptor family. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 U; 0 Other;

XX Query Match 32.7%; Score 377.6; DB 2; Length 1567;

XX Best Local Similarity 63.9%; Pred. No. 1.4e-82;

XX Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCATCATCAGGGGGTCTACTCCGTAAGTTCGT 212

DB 229 CGCCTTCTGCCCCCTTGGAAGTCAAGGTCAACATCGTGGGGCTTACTTGGCTGTGCAAT 351

QY 213 CGTGGGCTTGTGGGCACTCGCTGTGATGTTTGTGATCATCCGATACACAAAGATGAA 272

DB 352 CGGGGGGCTCTGGGGAACTGGCTGTGATGATGATGATGATGATGATGATGATGATGAT 411

QY 273 GACAGCAACCAACATTATATTTAACTGGCTTTGGGAGATGCTTTAGTTACTACAC 332

DB 412 GACAGTACCAACATTATATTTAACTGGGACATGCTGATACCTGTGCTTGTCTAAC 471

QY 333 CATGCCCTTTCAGAGTACGGTCTACTTGATGAAATTCCTGAGCTTTGGGAGATGCTGTG 392

DB 472 ACTGCCCTTTCAGAGGACAGACATCTACTGGGCTTGTGCCATTTGGAAATGCACTCTG 531

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QY 393 CAAGATAGTAAATTCATGATTACTACAAAGTTCACACAGATCTTCACCTTGACAT 452
DB 532 CAAGACTGTGATCTGATCTGATCTACACATGTTTACAGACCTTTACTCTGACCGC 591
QY 453 GATGACGCTGACCCGCTACATTCGCTGTGCAACCCCGTGAAGGCTTTGACCTCGCAC 512
DB 592 CATGAGCGTAGAACCGCTATGTGGCTATCTGCAACCTTACCGGCTTGATGATTTGAGAC 651
QY 513 ACCCTTGAAGGCAAAAGATCATATATCTGCAATCTGGCTGTGTGCTCATCTGTTGGCAT 572
DB 652 ATCCAGCAAGGCCAGGCTGTAAATGTGCAATATGGGCCCTTGAGCTTCAGTGGTGTGT 711
QY 573 CTCTGCAATAGTCTCTTGAGAGCAACCAAGTCAAGGGAAGCTGATGTGATTAAGAGTCTC 632
DB 712 TCCTGTGGCATCATAGGTTTCAGACACAACT-----GGAAGATGAAGATGAAGTGCCT 765
QY 633 CTTCGAGTTCCCAATGATGACTACTCTCTGTGGGACCTTTCAATGAAGATCTGGCTTT 692
DB 766 GGTGAGATCCCTGCCCCCTCAGAGACTATTGGGG---CCCTGATATCGCATCTGCATCTT 822
QY 693 CATCTTGGCTTCGTGATCCCTGTCTCTCATATCATCTGTCTGTACACCTTGATATCTCT 752
DB 823 CTTTTTTTCTTCATCATCTCTGTGTATCATCTCTGTCTGTACAGCTCATATGATTCG 882
QY 753 GCGCTCAAGAGACGTCGGGCTCCTTTCTGCTCCGAGAGAAAGATCGCAACCTGGGTAG 812
DB 883 AGGACTCTGTGTGTCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 942
QY 813 GATCAACAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 943 TATCACTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1002
QY 873 CATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1003 GGTGTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062
QY 933 CTATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1063 CCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1122
QY 993 CTTTCTTGATGAAAATTCAAGCGGTGTTTCCGGGACTTTGCTTTTCACTGAAGATGAG 1052
DB 1123 TTTCTGTGATGAACTTCAAGGCTGCTTTAGAAAGTTCTGTGTGTGTGTGTGTGTGT 1182
QY 1053 GATGAGCGGCGAGACACTAGACAGTCCGAATATACAGTTGATCCG 1102
DB 1183 CCGGAGATGACGGTTTCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232

```

RESULT 91
AAA59510
ID AAA59510 standard; cDNA; 1567 BP.

AAA59510;
14-NOV-2000 (first entry)
cDNA encoding a rat mu opioid receptor polypeptide.
mu opioid receptor; transcription regulatory polypeptide;
opioid receptor-like polypeptide; ss.
Rattus sp.
Key Location/Qualifiers
FT 173..1276
FT /tag= a
FT /product= "mu opioid receptor"

US6103492-A.
15-AUG-2000.
XX

```

PF 07-JUL-1997; 97US-00889108.
XX 08-MAR-1993; 93US-00056886.
PR 13-SEP-1993; 93US-00120601.
PR 13-SEP-1994; 94US-00305518.
XX
PA (INDV ) UNIV INDIANA.
XX
PI Yu L;
DR WPI; 2000-542550/49.
DR P-PSDB; AAB07868.
XX
PT Novel nucleic acids encoding mu opioid receptor for expressing large
PT quantities opioid receptors which are useful for screening and evaluating
PT subtype-selective drugs and as probes or primers.
XX
PS Example 9; Col 105-110; 86pp; English.
XX
CC The present sequence encodes a mu opioid receptor protein. The
CC specification also describes a transcription regulatory polypeptide and
CC an opioid receptor-like polypeptide. Human mu opioid receptor
CC polynucleotides are useful as a source of probes and primers, which may
CC be used as diagnostic tools to detect normal and abnormal DNA sequences
CC in DNA derived from patients cells. They are also used as a means for
CC detecting and isolating other members of the polypeptide family and
CC related polypeptides from a DNA library potentially containing such
CC sequences. The polynucleotide is used for preparing large quantities of
CC cDNA receptor which on expression in microorganism can be useful for
CC evaluating subtype-selective drugs
XX
SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 U; 0 Other;

```

Query Match 32.7%; Score 377.6; DB 3; Length 1567;
Best Local Similarity 63.9%; Pred. No. 1.4e-82;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

```

QY 153 GCGGCACTCTCCCGGCACTCCGGTATCATACAGCGGGTCTACTCCGTAGTGTGCT 212
DB 292 GCGCTTCTGCCCCCTTGACTCAAGTACCATGTGGGCTCTACTTGGCTGTGTGAT 351
QY 213 CGTGGGCTTGTGTGGCACTCGCTGTATGTTGTGTATCTCCGATACCAAGATGAA 272
DB 352 CGGGGGGCTCCTGGGGAACCTGCTGTATGTATGATCTCAGGCAACCAAGATGAA 411
QY 273 GACGCAACCAATTATATTTTAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
DB 412 GACAGCTAACCAATTATATTTTAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 471
QY 333 CATGCCCTTCAAGTACGGTCTACTGATGATATTCCTGGGCTTTGGGAGTGTGTG 392
DB 472 ACTGCCCTTCAAGGCAACAGACATCTACTGTGGCTTCTGGGCAATTTGGGAATGAC 531
QY 393 CAAGATAGTAAATTCATGATTACTACAAAGTTCACACAGATCTTCACCTTGACAT 452
DB 532 CAAGACTGTGATCTGATCTGATCTACACATGTTTACAGACCTTTACTCTGACCGC 591
QY 453 GATGACGCTGACCCGCTACATTCGCTGTGCAACCCCGTGAAGGCTTTGACCTCGCAC 512
DB 592 CATGAGCGTAGAACCGCTATGTGGCTATCTGCAACCTTACCGGCTTGATGATTTGAGAC 651
QY 513 ACCCTTGAAGGCAAAAGATCATATATCTGCAATCTGGCTGTGTGCTCATCTGTTGGCAT 572
DB 652 ATCCAGCAAGGCCAGGCTGTAAATGTGCAATATGGGCCCTTGAGCTTCAGTGGTGTGT 711
QY 573 CTCTGCAATAGTCTCTTGAGAGCAACCAAGTCAAGGGAAGCTGATGTGATTAAGAGTCTC 632
DB 712 TCCTGTGGCATCATAGGTTTCAGACACAACT-----GGAAGATGAAGATGAAGTGCCT 765
QY 633 CTTCGAGTTCCCAATGATGACTACTCTCTGTGGGACCTTTCAATGAAGATCTGGCTTT 692
DB 766 GGTGAGATCCCTGCCCCCTCAGAGACTATTGGGG---CCCTGATATCGCATCTGCATCTT 822

```



```

XX 11-DEC-2002 (first entry)
DT CDNA encoding human mu1 opioid receptor fragment.
XX
XX
XX
XX Human; mu1 opioid receptor; gene; ss; morphine; receptor;
XX intracellular calcium.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..945
XX FT /tag= a
XX FT /product= "Mu1 opioid receptor fragment"
XX FT /transl_except= (pos:885..887, aa:Leu)
XX
XX WO200268594-A2.
XX
XX 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005452.
XX
XX 22-FEB-2001; 2001US-0270479P.
XX PR
XX 05-DEC-2001; 2001US-0336677P.
XX PR
XX
XX (RESU-) RES FOUND SUNY.
XX
XX Cadet P, Stefano GB;
XX
XX WPI: 2002-706977/76.
XX DR
XX P-PSDB; ABG32258.
XX
XX New isolated nucleic acid molecule encoding a polypeptide having mu3
XX opiate receptor activity, useful as research tools for exploring the
XX interactions, molecular mechanisms and relationship of the mu3
XX opiate receptor.
XX
XX Claim 5; Page 32; 52pp; English.
XX
XX This invention relates to a novel nucleic acid molecule encoding a
XX polypeptide having mu3 opiate receptor activity. Mu opioid receptors
XX exhibit a high binding specificity for morphine. The invention also
XX comprises a method for identifying a mu3 opiate receptor agonist or
XX antagonist. The nucleic acids and polypeptides of the invention are
XX useful as research tools for exploring the interactions of morphine with
XX the mu3 opiate receptor, the molecular mechanisms by which morphine
XX induces intracellular calcium concentration changes and the relationship
XX of mu3 opiate receptors with other mu opioid receptors. They are also
XX useful for identifying a mu3 opiate receptor agonist or antagonist. The
XX present sequence represents a CDNA sequence encoding a fragment of the
XX human mu1 opioid receptor of the invention
XX
XX Sequence 945 BP; 250 A; 252 C; 171 G; 272 T; 0 U; 0 Other;
SQ
XX
XX Query Match 32.5%; Score 375.6; DB 6; Length 945;
XX Best Local Similarity 67.9%; Pred. No. 3.7e-82;
XX Matches 557; Conservative 0; Mismatches 254; Indels 9; Gaps 2;
XX
XX 268 ATGAAGACGACGAACCAACATTACATATTAACTGGCTTTGGCAGATCCTTAGTTACT 327
XX |||||
XX 1 ATGAAGACGACGACCAACATCTACATTTCACCTTGTCTGGCAGATGCTTAGGCACC 60
XX |||||
XX 328 ACAACCATCCCTTTAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTGGGGATGTC 387
XX |||||
XX 61 AGTACCCCTGCCCCCTTCAGAGTGTGAATTCCTAATGGAACATGGGCATTTGGAAACATC 120
XX |||||
XX 388 CTGTGCAAGATAGTATTTCCATTTGATTTCTACAACAGATTACCGCAGATCTTCACTTCG 447
XX |||||
XX 121 CTTTGCAAGATAGTATTTCTCATAGTACTATTAACATGTTTACCGCATATTCACCTTC 180
XX |||||
XX 448 ACCATGATGAGCGGTGACCGCTACATATGCGGTGTGACACCGCGTGAAGCTTTGAGCTTC 507
XX |||||
XX 181 TGCACATAGTGTGATGATGATACATTTGAGAGTGTGCACCGCTGTCAAGGCTTAAATTC 240
XX |||||

```

```

QY 508 CGCACACCTGTAAGGGCAAGATCATCAATATTCGATCGGCTGCTGTCATCTGTT 567
XX |||||
DB 241 GGTACTCCCGAAGATGCGAAGATTTATCAATGTCTGCACTGATCTCTTCCAGCCATT 300
XX |||||
QY 568 GGCATCTCTGCAATAGTCTCTTGAAGGCAACAAAGTCAGAGGAAGAGTGTATCTATTGAG 627
XX |||||
DB 301 GGTCTCTGTAATGTTCATGAGCTACCAACAAATACAGGCAA-----GGTTCATAGAT 354
XX |||||
QY 628 TGCTCTTGCAGTTCGCCAGATGATGACTACTCTGTGTGGGACCTTTCATGAAGATCTGC 687
XX |||||
DB 355 TGTACACATCAATTTCTC---TCAATCAACCTGTGTAAGGAAACCTGCTGAAGATCTGT 411
XX |||||
QY 688 GTCTTCATCTTTCGCTTGTGATCCCTGTCTCCATCATCATCGTCTGTACACCTGTATG 747
XX |||||
DB 412 GTTTTCATCTTCCCTTCAATATGCAATGCTCATCATTTACCGTGTGCTATGATGATG 471
XX |||||
QY 748 ATCTGCGTCTCAAGAGGCTCGGCTCTTTCTGGCTCCGAGAGAAAGATCGCAACTG 807
XX |||||
DB 472 ATCTGCGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAGAAAGAGAGCAATCTT 531
XX |||||
QY 808 CGTAGATCACCAAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 867
XX |||||
DB 532 CGAAGATCACCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
XX |||||
QY 868 ATTCAATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 927
XX |||||
DB 592 ATTCAATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651
XX |||||
QY 928 TCCAGCTATTTACTTGTGATGCTGCTTGAAGCTATACCAACAGTACCTGAATCCATTCTC 987
XX |||||
DB 652 GTTCTGTGCACTTGTGATGCTGCTTGAAGCTATACCAACAGTACCTGAATCCATTCTC 711
XX |||||
QY 988 TACGCTTTTCTGATGAAATCTTCAAGGCGTGTTCGGGACTTGTGCTTCCACTGAAG 1047
XX |||||
DB 712 TATGATTTCTGATGAAATCTTCAAGGCGTGTTCGGGACTTGTGCTTCCACTGAAG 771
XX |||||
QY 1048 ATGAGATGAGCGGCGAGAGCACTAGCAGAGTCCGAATA 1087
XX |||||
DB 772 TCCACATTTGAGCAACAAATCTCCATCGAATTCGTGAGA 811
XX |||||
RESULT 94
AAT90381
ID AAT90381 standard; cDNA; 1452 BP.
XX
XX AAT90381;
XX
XX 23-JAN-1998 (first entry)
XX
XX DE Rat methadone-specific opioid receptor MSOR cDNA.
XX
XX XX Methadone-specific opioid receptor; MSOR; rat; psychoactive drug; ss.
XX
XX OS Rattus sp.
XX
XX XX
XX FT Key Location/Qualifiers
XX FT CDS 182..1285
XX FT /tag= a
XX
XX PN US5658783-A.
XX
XX PD 19-AUG-1997.
XX
XX XX
XX PF 08-NOV-1993; 93US-00149093.
XX
XX XX
XX PR 08-NOV-1993; 93US-00149093.
XX
XX XX
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX XX
XX PI Civeilli O, Grandy DK, Bunzow JR;
XX
XX DR WPI; 1997-424240/39.

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DR P-PSDB; AAM26582.

XX New isolated mammalian methadone-specific opioid receptor gene - used to
PT develop products for screening for compounds which can be used as
PT psychoactive drugs.

XX Claim 1; Col 17-20; 26pp; English.

XX This nucleotide sequence encodes a novel, claimed rat methadone-specific
CC opioid receptor (MSOR) (see AAM26582). It was isolated from a rat brain
CC library using degenerate primers (see AAT90382-83) based on the putative
CC 3rd and 7th transmembrane regions of a mouse delta-opioid receptor. Also
CC claimed are: (1) a hybridisation probe; (2) a recombinant expression
CC construct that is capable of expressing the MSOR in eukaryotic or
CC prokaryotic cell transformants; and (3) a transformed cell culture that
CC expresses the MSOR. The probes can be used to determine the pattern,
CC amount and extent of expression of the MSOR gene in various tissues of
CC mammals, including humans, as well as in the detection and diagnosis of
CC genetic disease, or the detection of novel related receptor genes

XX Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 GCGGCACTCTCCCGCCATCCCGGTCAATCAGCGGGGTCTACTCCGTAGTTCGT 212
DB 301 CCCCTTCCGCCCCCTTGAGACTCAAGGTCAACATCGGGGCTCATCTTGCTGTGCAT 360
QY 213 CGTGGGCTTGTTGGGCACTCGGTGTCATGTTGATCATCCGATACACAAGATGAA 272
DB 361 CCGGGGGCTCTGGGGAACCTGCTCAATGATGATCTCAGACACCCAGATGAA 420
QY 273 GACAGCAACCAATTATGATATTAACCTGCTTGGAGATGCTTATGATTAACAAC 332
DB 421 GACAGCTACCAATTATGATATTAATCTGGACATGGCGATACCTGTCTGTAC 480
QY 333 CATGCCCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392
DB 481 ACTGCCCTTTCAGAGGACAGACATCTACTGCGCTTCTGCGCATTTGGGAAAGCACTTCG 540
QY 393 CAAGATGATATTTCCATGATGATTAACAACATGTTACACAGATCTTACCTGACAT 452
DB 541 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 453 GATGAGCGTGAACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 512
DB 601 CATGAGCGTGAACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 513 ACCCTTGAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 572
DB 661 ATCCAGCAAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 573 CTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
DB 721 TCTCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
QY 633 CTTCGAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
DB 775 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 693 CATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
DB 832 CTTTTCCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891
QY 753 GGTTCAGAGAGTCCGCTCTCTCTGCTCCGAGGAAAGATGCAACTGTGATG 812
DB 892 AGGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
QY 813 GATCAGCAGAGTGTCTGT 872
DB 952 TATCAGTCACTGT 1011

QY 873 CATATTCATCTGTGAGAGGCTGTGGGAGACATCCACAGACAGTCTCTCCAG 932
DB 1012 GGTGTTGTTCTGTGTTCAAGAGCTGGGTCTTACGACAGGTATGAGACTGTGACAT 1071
QY 933 CTATTACTTCTGCATCGCTTGAAGCTATACCAAGATGACCTGAATCCATTTCTTACGC 992
DB 1072 CCGGCTTCTGCACAGCGCTGGGTATGTCAAGTGTCTCAATCCATTTCTTATGC 1131
QY 993 CTTTCTGATGAAACTTCAACCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGAG 1052
DB 1132 TTTCTGTGATGAACTTCAACCGGTGTTTGAAGTCTGCTGCTTCAATCCCTGCA 1191
QY 1053 GATGAGGCGGACAGACATGACAGAGTCCGAATACGTTCAAGATCCCTG 1102
DB 1192 CCGGAGATGACAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1241

RESULT 95

AAT89585
ID AAT89585 standard; cDNA; 1452 BP.

XX AAT89585;

XX 12-JAN-1998 (first entry)

DE Rat orphanin FQ receptor cDNA clone LC132.

XX Orphanin FQ receptor; binding; locomotor disease; diagnosis; treatment;

KW opioid inhibitor; opiate induced hypothermia; drug design;

KW morphine induced analgesia; methadone specific opioid receptor; ss.

XX Rattus sp.

XX Location/Qualifiers

FT 5'UTR 1..181

FT CDS 182..1285

FT 3'UTR 1286..1452

FT /*tag= c

PN MO9707212-A1.

PD 27-FEB-1997.

PF 12-AUG-1996; 96WO-US013305.

PR 11-AUG-1995; 95US-00514451.

PR 03-NOV-1995; 95US-00553058.

XX (UYOR-) UNIV OREGON HEALTH SCI.

PI Griesel JE, Mogil JS, Grandy DK, Bunzow JR, Civelli O;

PI Reinscheid RK, Nothacker H, Monnema FJ;

DR WPI; 1997-165296/15.

DR P-PSDB; AAM25217.

PS Mammalian orphanin FQ receptor inhibitor - used in the diagnosis and

PS treatment of locomotor disease.

XX Claim 5; Page 42-43; 68pp; English.

XX AAT89585 is rat orphanin FQ (OFQ) receptor cDNA clone LC132. Highly

XX specific peptides that bind the OFQ receptor were identified as OFQ

XX receptor inhibitors. The peptides can be used to antagonise a

XX physiological effect of an opiate in an animal. The peptides antagonise

XX opiate induced hypothermia and morphine induced analgesia in animals.

XX They may also be used in the diagnosis and treatment of locomotor

XX disease. The peptides may also be used in the design of a methadone

XX specific opioid receptor (MSOR), in drug design and for the isolation of

XX endogenous receptors for anti-opioid agonists and antagonists found in

CC plasma, serum, lymph, cerebrospinal fluid etc
XX Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGCACTCTCCCGGCATCCCGTCACTACACGGGGGTCTACCTCGTAGTGTCT 212
DB 301 CGCCTTCCGCCCCCTTGAAGTCAAGGTCACATCGGGGCTCATCTTGGCTGTGCAT 360
QY 213 CGTGGGCTTGTGGCACTCGCTGTGTCATGTTCCGATCCGATACACAAGATGAA 272
DB 361 CGGGGGGCTTCCGGGAATGCGCTGTGATGTATGTCAATCCAGACCCAAAGTGA 420
QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTTAGTTACTACAAC 332
DB 421 GACAGCTACCAATTATTAATTTAACTGGCACTGGCTGATACCTGTCTGTGTAAC 480
QY 333 CATGCCCTTTCAGAGTACGCTACTGTATGTAATTCCTGGCCTTTGGGGATGTCTGT 392
DB 481 ACTGCCCTTCCAGGGGACAGACATCTACTGGGCTTGGCCATTTGGGAAAGCACTTG 540
QY 393 CAAGAATGATTTTCATTTATTTACTACAACATGTTACACAGCATCTTACCTGACCAT 452
DB 541 CAAGACTGTCAATTTGATGATGATCACTACAACATGTTTACACAGCATTTTACTGTACCC 600
QY 453 GATGACGCTGACCCGCTACATTTCCGCTGTGCCACCCCGTAAAGCTTTGGACTTCCGAC 512
DB 601 CATGACGCTGACCCGCTATGTGGCTATCTGCCACCTATCCGCTTGAATGTTCCGAC 660
QY 513 ACCCTTGAAGGAAGATATCAATATCTGCATCTGGCTGTGTGATCTGTGGCAT 572
DB 661 ATCCAGCAAGCCCGCTTAAATGTGGCCATATGGCCCTTCAGCTGTGGTGT 720
QY 573 CTCTGCAATAGTCTTGTGAGGACCAAGTCAAGGGAAGACGTGATGATGAGTGTCT 632
DB 721 TCCTGTGTCATCATGCTGTGACGACAACT-----GGAAGATGAAGATGAGTGTCT 774
QY 633 CTTCGAGTTCCAGATGATGACTACTCTGTGTGGGACCTTTTCAATGAATGTGCGTCT 692
DB 775 GGTGAGATCCCTGCCCCCTCAGGACTAATGGGG---CCCTGATTCGCATCTGATCTT 831
QY 693 CATCTTGGCTTCGATATCCCTGTCTCTCATCATATCCGTCTCTCAACCTGATATCTCT 752
DB 832 CTTTTTTCCTTCAATCATCTGTGTGTATCATCTCTGTCTCAAGCTTATGATTCG 891
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGTGCTCCGAGAGAAAGATCGCAACCTGCTAG 812
DB 892 AGGACTGTGTGTGTCGCTGTCTCTTCAAGGCTCCGGGAGAAAGAACCTGCGGGG 951
QY 813 GATCACCAAGCTGTCTGT 872
DB 952 TATCACTGCACTGT 1011
QY 873 CATATTCATCCCTGT 932
DB 1012 GGT 1071
QY 933 CTATATCTTCTGATCGCTTGTAGGCTATATCAACAGTATGATATCCCATCTCTACGC 992
DB 1072 CCGTGGCTTCTGCAACGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1131
QY 993 CTTTCTTGTATGAAAATTGACGCGGTGTTTCGGGAATTCTGTCTTTTCACTGAAGATGAG 1052
DB 1132 TTTTCTGTATGAACTTCAAGGCTTGTGAAGATTTCTGTGTGTGTGTGTGTGTGTGTGT 1191
QY 1053 GATGAGCGGCGAGACACTAGACAGTCCGAATATACGTTACAGATCTCG 1102
DB 1192 CCGGAGATGACGGTTTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

RESULT 96
AAV56017
ID AAV56017 standard; cDNA; 1452 BP.

XX AC AAV56017;
XX AC AAV56017;
XX DT 08-DEC-1998 (first entry)

DE Rat methadone-specific opioid receptor (MSOR) protein encoding cDNA.
KW MSOR, methadone-specific opioid receptor; screening assay; inhibition;
KW psychotropic agent; therapeutic drug; ss.
OS Rattus sp.

PH Key Location/Qualifiers
FT 5'UTR 1..181
FT /tag= a
FT CDS 182..1285
FT /tag= b
FT /product= "Rat MSOR"
FT 3'UTR 1283..1452
FT /tag= c

XX US5821067-A.
XX PN 13-OCT-1998.

XX PF 15-AUG-1997; 97US-00911245.
XX PR 08-NOV-1993; 93US-00149093.

XX PA (OREG-) STATE OF OREGON.
XX PI Civeili O, Bunzow JR, Grandy DK;
XX DR WPI, 1998-567655/48.
XX DR P-PSDB; AAM80549.

PT Screening assays for opioid receptor ligands - using cells expressing
PT recombinant methadone-specific opioid receptor.

XX Example 1; Fig 1A-C; 26pp; English.

CC This cDNA encodes a rat methadone-specific opioid receptor (MSOR)
CC protein. A recombinant expression construct containing the MSOR encoding
CC nucleic acid can be used to transform a host cell for the recombinant
CC production of the protein. This can be used in the screening assays of
CC the invention for screening for a compound that binds to a mammalian
CC MSOR. The method is for quantitatively measuring inhibition of the
CC methadone-specific opioid receptor, which is useful for screening
CC psychotropic agents for use as therapeutic drugs which do not have
CC deleterious side effects

XX Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGCACTCTCCCGGCATCCCGTCACTACACGGGGGTCTACCTCGTAGTGTCT 212
DB 301 CGCCTTCCGCCCCCTTGAAGTCAAGGTCACATCGGGGCTCATCTTGGCTGTGCAT 360
QY 213 CGTGGGCTTGTGGCACTCGCTGTGTCATGTTCCGATCCGATACACAAGATGAA 272
DB 361 CGGGGGGCTTCCGGGAATGCGCTGTGATGTATGTCAATCCAGACCCAAAGATGA 420
QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTTAGTTACTACAAC 332
DB 421 GACAGCTACCAATTATTAATTTAACTGGCACTGGCTGATACCTGTCTGTGTAAC 480
QY 333 CATGCCCTTTCAGAGTACGCTACTGTATGTAATTCCTGGCCTTTGGGGATGTCTGTG 392

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Db      481 ACTGCCCTTCCAGGCGACAGACATCTACTGGGCTTCTGGCCATTGGGAAAGCACTCTG 540
Qy      393 CAAGATAGTAATTTTCATGATTACTACAAACATGTTCCACAGATCTTCACTTACCAAT 452
Db      541 CAAAGCTGTCATTTGATGACTACTACAAACATGTTTACCAAGACTTTTACTTGACCCG 600
Qy      453 GATGACCGTGACCGCGTACATTGCGGTGACCAACCGCGTGAAGGCTTTGAACTTCCGAC 512
Db      601 CATGACCGTAGACCGGTATGTGCTATCTGCCACCTTACCGCCCTTGATGTTGGAC 660
Qy      513 ACCCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGCTGCTCATCTGTTGGCAT 572
Db      661 ATCCAGCAAAAGCCAGCGTGTATATGTGGCATATGAGCCCTGCTTCAAGTGGTGTGT 720
Qy      573 CTCTGCATATGCTCTTGGAGGACCAAAATCAGGGAAGAGCTGATGTCAATGAGTCTC 632
Db      721 TCCTGTGGCATCATATGGGTTTCAAGCACAGT-----GGAAGATGAAGATCGAGTGCCT 774
Qy      633 CTTCAGATTCCAGATGATGACTACTCCTGTGGGAGCTCTTATGAAGATCTGGCTTT 692
Db      775 GGTGAGATCCCTGCCCCCTCAGACATATTGGG---CCCTGATTTGCCATCTGCATCTT 831
Qy      693 CATCTTTGCTTCTGTGATCCCTGTCTCTCATCATCATCTGTCTGACACCCCTGATGATCCT 752
Db      832 CTTTTTTTCTTCATCATCCCTGTGCTGATCATCTGTCTGCTACAGCTCATGATTTGG 891
Qy      753 GCGTCTCAAGAGCGTCCGCTCTTTCTGTGCTCCGAGAGAAAGATCGCAACCTGCTGAG 812
Db      892 AGGACTCTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 951
Qy      813 GATCACACAGATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      952 TATCACTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011
Qy      873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
Db      1012 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1071
Qy      933 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
Db      1072 CTTGCGCTTCTCACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1131
Qy      993 CTTTCTGTGTAATAATTGAAGCGGTGTTCGGGAGCTTCTGTCTTCACTGAAGATGAG 1052
Db      1132 TTTCTGTGATGAAGACTTCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1191
Qy      1053 GATGAGCGGACAGACTAGACAGATCCGAAATACAGTTCAAGATCTGTG 1102
Db      1192 CCGGAGATGACAGGTTTCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

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RESULT 97

AA291047
ID AA291047 standard; cDNA; 1452 BP.

XX AA291047;

XX 06-JUN-2000 (first entry)

XX Rat methadone-specific opioid receptor gene.

XX Mammalian; Norway rat; PCR primer; methadone-specific opioid receptor;
KM psychotropic drug; 88.

XX Rattus norvegicus.

XX Key Location/Qualifiers

XX FT CDS 182..1285

XX /tag= a /product= "methadone-specific opioid receptor"

XX US6028175-A.

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XX      22-FEB-2000.
PD      13-OCT-1998; 98US-00170331.
XX      08-NOV-1993; 93US-00149093.
PR      15-AUG-1997; 97US-00911245.
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX      Clive11 O, Bunzow JR, Grandy DK;
PI      MPI; 2000-194856/17.
XX      P-PSDB; AAY80493.
DR      New isolated mammalian opioid receptor protein used for the development
PT      of agents with pharmacological uses related to opioid receptors.
XX      Example 2; Fig 1; 26pp; English.
PS      This sequence represents the gene encoding a novel mammalian opioid
XX      receptor. The gene was isolated from Norway rat (Rattus norvegicus) by
CC      PCR with the primers AA291048-291049. The gene encodes a novel receptor
CC      which is designated the rat methadone-specific opioid receptor. The
CC      receptor protein can be used for the development of agents with
CC      pharmacological uses related to the receptors e.g. psychotropic drugs
XX      Sequence 1452 BP; 275 A; 415 C; 377 G; 385 T; 0 U; 0 Other;
SQ
Query Match      31.9%; Score 368; DB 3; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;
Qy      153 CCGGACATCTCCCGGCGCATCCGCTCATCATCACGGGCTTACTCCGTATGTTCCGT 212
Db      301 CCCTCTTCCCTGCGCCCTTGGACTCAGGTCAACATCGTGGGCTCATCTTGGCTGTGCAT 360
Qy      213 CGTGGGCTGTGGGGAATCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
Db      361 CGGGGGGCTCTGTGGGAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy      273 GACAGCAACCAATTTATATATTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
Db      421 GACAGTACCAATTTATATATTTATGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy      333 CATGCCCTTTCAGAGTACGTCTACTTGAATTCCTGCGCTTTTGGGAGTGTGCTGTG 392
Db      481 ACTGCCCTTCCAGGCGACAGACATCTACTGTGGGCTTCTGGCCATTGGGAAAGCACTCTG 540
Qy      393 CAAGATAGTAATTTTCATGATTACTACAAACATGTTCCACAGATCTTCACTTACCAAT 452
Db      541 CAAAGCTGTCATTTGATGACTACTACAAACATGTTTACCAAGACTTTTACTTGACCCG 600
Qy      453 GATGACCGTGACCGCGTACATTGCGGTGACCAACCGCGTGAAGGCTTTGAACTTCCGAC 512
Db      601 CATGACCGTAGACCGGTATGTGCTATCTGCCACCTTACCGCCCTTGATGTTGGAC 660
Qy      513 ACCCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGCTGCTCATCTGTTGGCAT 572
Db      661 ATCCAGCAAAAGCCAGCGTGTATATGTGGCATATGAGCCCTGCTTCAAGTGGTGTGT 720
Qy      573 CTCTGCATATGCTCTTGGAGGACCAAAATCAGGGAAGAGCTGATGTCAATGAGTCTC 632
Db      721 TCCTGTGGCATCATATGGGTTTCAAGCACAGT-----GGAAGATGAAGATCGAGTGCCT 774
Qy      633 CTTCAGATTCCAGATGATGACTACTCCTGTGGGAGCTCTTATGAAGATCTGGCTTT 692
Db      775 GGTGAGATCCCTGCCCCCTCAGACATATTGGG---CCCTGATTTGCCATCTGCATCTT 831
Qy      693 CATCTTTGCTTCTGTGATCCCTGTCTCTCATCATCATCTGTCTGACACCCCTGATGATCCT 752
Db      832 CTTTTTTTCTTCATCATCCCTGTGCTGATCATCTGTCTGCTACAGCTCATGATTTGG 891

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Db 1132 TTCTCTGATGAGACTTCAAGCCCTGCTTTAGAAAGTTCTCTGCTTATCCCTTGA 1191
 QY 1053 GATGAGCGGACAGACCTAGACAGAGTCCGAATACATTTCAGATCTCTG 1102
 Db 1192 CCGGAGATGACAGTTTCTGATCTGTGTGCGAGCATTTGCCAAGATGTTG 1241
 RESULT 100
 AA260659
 ID AA260659 strand: DNA; 1134 BP.
 XX
 AC AA260659;
 XX
 DT 16-MAY-2000 (first entry)
 DE DNA encoding a kappa3-related opioid receptor KOR-3D splice variant.
 XX
 KW Splice variant; kappa3 opioid receptor; muopioid receptor-1; KOR-3;
 KW morphine analgesia; opioid-mediated ingestive response; opioid;
 KW analgesic; gastrointestinal motility; respiration; immune system;
 KW endocrine system; autonomous nervous system; peristalsis regulator;
 KW body weight; neuroendocrine disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 16..1113
 FT /*tag= a
 FT /product= "KOR-3D splice variant"
 XX
 PN WO200004151-A2.
 XX
 PD 27-JAN-2000.
 XX
 PF 15-JUL-1999; 99WO-US015977.
 XX
 PR 16-JUL-1998; 98US-0093002P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Pasternak G, Pan Y;
 XX
 DR WPI; 2000-182421/16.
 DR P-PSDB; AAY68862.
 XX
 PT New splice variants of the kappa-opioid receptor, useful in screening for
 PT selective analgesics and for regulating morphine analgesia or body
 PT weight.
 XX
 PS Claim 34; Fig 15; 61pp; English.
 XX
 CC The present sequence encodes a splice variant of the human kappa3 opioid
 CC receptor (muopioid receptor-1, KOR-3). The splice present variant
 CC comprises exons 1a, 2 and 3. The specification describes four new exons
 CC of the KOR-3 gene, which combine to yield seven new KOR-3 splice variants
 CC of human, mouse and rat origin. These splice variants are potential
 CC targets for modulating morphine analgesia and opioid-mediated ingestive
 CC responses. The KOR-3 polypeptide are used to screen compounds for opioid
 CC activity. Such compounds are potential analgesics or more generally
 CC agents that affect gastrointestinal motility, respiration or the immune,
 CC endocrine or autonomous nervous systems, e.g., regulators of peristalsis.
 CC Antagonists, agonists and ligands of KOR-3, as well as DNA vectors
 CC expressing KOR-3-encoding nucleic acids, or sequences antisense to KOR-3
 CC nucleic acids, are used to regulate morphine analgesia and body weight.
 CC The level of KOR-3 or tissue distribution of KOR-3 can be measured to
 CC diagnose KOR-3 related pharmacological abnormalities or neuroendocrine
 CC disorders, particularly inherited disorders. Transgenic animals with
 CC extra copies of the KOR-3 gene, or with endogenous alleles deleted, are
 CC used to study loss or gain of function phenotypes
 CC
 CC Sequence 1134 BP; 177 A; 384 C; 319 G; 254 T; 0 U; 0 Other;

Query Match 31.9%; Score 367.8; DB 3; Length 1134;
 Best Local Similarity 62.1%; Pred. No. 3.3e-80;
 Matches 617; Conservative 0; Mismatches 367; Indels 9; Gaps 2;

QY 105 GCCGACAGCAACGCGACGCGGCTGGAGAGACCGGACGTGAGACCCGGGCATCTC 164
 Db 81 GTCCCTCTGAGCCCAACACAGTCTGCTCCCCCGCATCTGCTGCTCAATGCGACGCA 140
 QY 165 CCGGACCATCCCGGATCATCAAGGGGTCTACTCCGTAGTGTGCTGGGCTTGT 224
 Db 141 CGGCGCTTCTGCGCCCTCGGAGCTCAAGGTACATCTGGGGCTTACTCGGCGGTGTG 200
 QY 225 GGGCAACTCGGTGATGTTCTGTATCATCCGATACCAAGATGAAGACAGCACCA 284
 Db 201 TGTGAGAGGCTCTCGGGAACTGCTGTATGACACCAAAATGAAGACAGCACCA 260
 QY 285 CATTTACATATTAACTGTGGCTTTGGAGATGCTTTAATTACTACCAACATGACCTTCA 344
 Db 261 TATTTACATCTTTAACTGGCCCTGGCCGACATCTGTCTGTGACGCTGCTTCA 320
 QY 345 GAGTAGGTTACTGATGAATTCCTGGCTTTTGGAGATGCTGTGCAAGATAGTAAT 404
 Db 321 GGGCAGGACATCTCTGAGCTTCTGGACCTTTGGAAATGCGCTGTGCAAGACGTAT 380
 QY 405 TTCCATTGATTACTACCAATGTTCAACGACATCTTCACTTACCATGATGAGCTGCA 464
 Db 381 TGCCATTGACTACTACCAATGTTCAACGACATCTTCACTTACCATGATGAGCTGCA 440
 QY 465 CCGTACATTTGCGGTGGTCCACCCGTGAAGCTTTGACCTTCCGACACCCCTTGAAGG 524
 Db 441 TCGCTATGATGACATCTGACACCCCATCGTCCCTGACAGTCCGACGTCAGCAAAAGC 500
 QY 525 AAAGATCATATATCTGATCTGCTGCTGTGCTCATCTGTGTGACATCTGCAATAGT 584
 Db 501 CCAGGCTGTCAATGAGCCATCTGGGCCCTTGACCTCTGTGTGCGTGTCCGTTGCCAT 560
 QY 585 CCTTGAGGACACCAAGTCAAGGAAGACGTGATCTATTGAGTGTCTCTTGCATTTCCC 644
 Db 561 CATGGGCTGGCAGACAGTCAAGATGAAGAG-----ATCGAGTCTGTGTGAAGATCCC 614
 QY 645 AGATGATGACTACTCTGTGTGGACCTCTTCAATGAAGATCGGCTTCATCTTGGCTT 704
 Db 615 TACCCCTCAGGATTC--TGAGGCCCGGTGTGTGACATCTGCAATCTTCTCTCTT 671
 QY 705 CGTGAATCCCTGCTCATCATCATGCTGTGTATACCCCTGATGATCTGCTCAAGAG 764
 Db 672 CATGTCCTCCGCTGCTGATCTCTGTGTGACAGCTCATGATCCGCGGCTCGGTGG 731
 QY 765 CGTCCGGCTCTTTTGTGCTCCGAGAGAAAGATGCAACTGCTGATGATCAACGAT 824
 Db 732 AGTCGCGCTGCTCTCGGGCTCCGAGAGAAAGACCGGAACCTGCGCGCATCATCTCGGCT 791
 QY 825 GGTCTGT 884
 Db 792 GGT 851
 QY 885 GGTGAGGCTTGGGGAGCACTCCACAGCAACAGTGTCTCTCAAGTATTACTTCTG 944
 Db 852 GGGCCACAGGCTGTGGGTTCAACCGACAGCGAGACTGCGTGGCATCTCGGCTTCTG 911
 QY 945 CATGCGTTAGGCTATACCAAGATGCTGAATCCATTTCTTACAGCTTCTTGTGATGA 1004
 Db 912 CAGGCGCTTGGGCTACGTCAACAGCTGCTCAACCCATCTCTTACGCTTCTGTGATGA 971
 QY 1005 AAATCTCAAGCGGTGTTTCCGGAAGTCTGCTTTCATGAGATGAGATGAGAGCGGCA 1064
 Db 972 GAATCTCAAGCGCTGCTTCCGGAAGTCTGCTTGTGATGATGCTGCGCGGACGTGCA 1031
 QY 1065 GAGCACTAGCAGAGTCCGAATACAGTTGAGA 1097
 Db 1032 GGTGTGTACCGGTGCGGACAGATTGCCAAGGA 1064

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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1154	100.0	1154	12	US-09-904-584-1
2	1152.4	99.9	1154	12	US-09-904-584-2
3	1152.4	99.9	1154	12	US-09-904-584-3
4	1152.4	99.9	1154	12	US-09-904-584-4
5	1152.4	99.9	1154	12	US-09-904-584-5
6	1152.4	99.9	1154	12	US-09-904-584-6
7	1152.4	99.9	1154	12	US-09-904-584-7
8	1146	99.3	1182	15	US-10-225-567A-147
9	1146	99.3	1182	15	US-10-345-680-19
10	1146	99.3	1182	16	US-10-305-720-117
11	1143	99.3	1182	17	US-10-283-975A-80
12	1143	99.0	1143	15	US-10-318-661-1
13	1137.8	98.6	1284	15	US-10-318-661-3
14	1135	98.4	1143	15	US-10-345-680-21

15	1131.8	98.1	1143	11	US-09-826-509-542	Sequence 542, App
16	1001	86.7	1275	15	US-10-318-661-5	Sequence 5, Appli
17	996.2	86.3	1275	15	US-10-318-661-7	Sequence 7, Appli
18	981	85.0	1875	15	US-10-318-661-13	Sequence 13, Appli
19	965	83.6	1875	15	US-10-318-661-15	Sequence 15, Appli
20	910.8	78.9	1408	9	US-09-214-904-5	Sequence 5, Appli
21	879.4	76.2	1911	15	US-10-318-661-17	Sequence 17, Appli
22	470.6	40.8	585	13	US-10-027-632-188121	Sequence 188121,
23	470.6	40.8	585	13	US-10-027-632-188122	Sequence 188122,
24	470.6	40.8	585	16	US-10-027-632-188121	Sequence 188121,
25	470.6	40.8	585	16	US-10-027-632-188122	Sequence 188122,
26	446.4	38.7	1618	10	US-09-841-720-1	Sequence 1, Appli
27	446.4	38.7	1618	10	US-09-841-720-3	Sequence 3, Appli
28	436.2	37.8	1464	15	US-10-195-083-25	Sequence 25, Appli
29	436.2	37.8	1464	15	US-10-194-595-25	Sequence 25, Appli
30	434.8	37.7	1239	15	US-10-080-917-10	Sequence 10, Appli
31	434.8	37.7	1245	15	US-10-080-917-8	Sequence 8, Appli
32	434.8	37.7	1388	15	US-10-185-083-26	Sequence 26, Appli
33	434.8	37.7	1388	15	US-10-194-595-26	Sequence 26, Appli
34	434.8	37.7	1431	15	US-10-080-917-6	Sequence 6, Appli
35	434.8	37.7	2149	15	US-10-080-917-12	Sequence 12, Appli
36	434.8	37.7	2162	16	US-10-225-567A-185	Sequence 185, App
37	434.8	37.7	2162	16	US-10-305-720-1379	Sequence 1379, Ap
38	433.2	37.5	1176	10	US-09-935-061-11	Sequence 11, Appli
39	433.2	37.5	1176	17	US-10-692-071-11	Sequence 11, Appli
40	433.2	37.5	1473	15	US-10-080-917-13	Sequence 13, Appli
41	432.6	37.5	2951	15	US-10-185-083-21	Sequence 21, Appli
42	432.6	37.5	2951	15	US-10-194-595-21	Sequence 21, Appli
43	432.4	37.5	1332	15	US-10-185-083-22	Sequence 22, Appli
44	432.4	37.5	1332	15	US-10-194-595-22	Sequence 22, Appli
45	432.4	37.5	1334	9	US-09-761-962-3	Sequence 3, Appli
46	432.4	37.5	1334	15	US-10-283-300-3	Sequence 3, Appli
47	432.4	37.5	1365	9	US-09-761-962-11	Sequence 11, Appli
48	432.4	37.5	1365	15	US-10-283-300-11	Sequence 11, Appli
49	432.4	37.5	1373	15	US-10-185-083-51	Sequence 51, Appli
50	432.4	37.5	1373	15	US-10-194-595-51	Sequence 51, Appli
51	432.4	37.5	1423	9	US-09-761-962-1	Sequence 1, Appli
52	432.4	37.5	1423	15	US-10-283-300-1	Sequence 1, Appli
53	432.4	37.5	1440	15	US-10-185-083-15	Sequence 15, Appli
54	432.4	37.5	1440	15	US-10-194-595-15	Sequence 15, Appli
55	432.4	37.5	1569	15	US-10-185-083-17	Sequence 17, Appli
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57	432.4	37.5	1610	9	US-09-761-962-16	Sequence 16, Appli
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65	432.4	37.5	2045	9	US-09-761-962-10	Sequence 10, Appli
66	432.4	37.5	2045	15	US-10-283-300-10	Sequence 10, Appli
67	432.4	37.5	2588	15	US-10-185-083-23	Sequence 23, Appli
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69	431.6	37.4	1203	11	US-09-826-509-546	Sequence 546, App
70	431.6	37.4	1203	11	US-09-826-509-544	Sequence 544, App
71	430.8	37.3	2229	9	US-09-214-904-1	Sequence 1, Appli
72	430.4	37.3	1149	9	US-09-993-844-10	Sequence 10, Appli
73	429.2	37.2	1542	15	US-10-283-300-4	Sequence 4, Appli
74	429.2	37.2	1542	15	US-10-823-114-15	Sequence 15, Appli
75	429.2	37.2	1981	15	US-10-290-748-15	Sequence 15, Appli
76	429.2	37.2	1829	9	US-09-823-114-7	Sequence 7, Appli
77	422.6	36.6	1829	15	US-10-290-748-7	Sequence 7, Appli
78	422.6	36.6	2218	9	US-09-214-904-3	Sequence 3, Appli
79	422.6	36.6	2219	15	US-10-112-599A-1	Sequence 1, Appli
80	422.6	36.6	2219	17	US-10-435-655-1	Sequence 1, Appli
81	422.6	36.6	1176	10	US-09-935-061-13	Sequence 13, Appli
82	415.6	36.0	1176	17	US-10-692-071-13	Sequence 13, Appli
83	415.6	36.0	1346	9	US-09-761-962-12	Sequence 12, Appli
84	411	35.6	1346	15	US-10-283-300-12	Sequence 12, Appli
85	411	35.6	1773	15	US-10-112-599A-3	Sequence 3, Appli
86	408.6	35.4	1773	15	US-10-225-567A-107	Sequence 107, App
87	408.6	35.4	1773	15		


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Db 421 AACATGTTACCCAGCATCTTCACTTGACCATGATGAGGTGACCGCTACATTTGCCGTG 480
Oy 481 TGGCAACCCCGTAGAGCTTTGGAGCTTCGCGACACCCCTTGAAAGCAAGATCATCATATTC 540
Db 481 TGGCAACCCCGTAGAGCTTTGGAGCTTCGCGACACCCCTTGAAAGCAAGATCATCATATTC 540
Oy 541 TGGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TGGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Oy 601 GTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Oy 661 TGGTGGAGCTCTTTCATGAAAGATGCGCTCTTTCATGCTTGGCTGCTGCTGCTGCTGCTGCT 720
Db 661 TGGTGGAGCTCTTTCATGAAAGATGCGCTCTTTCATGCTTGGCTGCTGCTGCTGCTGCTGCT 720
Oy 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Oy 781 GGGTCCGAGAGAAAGATGCAACCTGGGAGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 GGGTCCGAGAGAAAGATGCAACCTGGGAGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTG 840
Oy 841 GCACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Oy 901 AGCACTCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 AGCACTCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 ACCAAGCTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 ACCAAGCTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Oy 1021 TTCCGGGACTTCTGCTTTCACATGAAAGTGAAGAGCGGACAGACATGACAGATC 1080
Db 1021 TTCCGGGACTTCTGCTTTCACATGAAAGTGAAGAGCGGACAGACATGACAGATC 1080
Oy 1081 CGAAATTAAGTTGAGGATCTGCTTAAGGAGGAGCATGATGAGATGAATTAACCACTA 1140
Db 1081 CGAAATTAAGTTGAGGATCTGCTTAAGGAGGAGCATGATGAGATGAATTAACCACTA 1140
Oy 1141 TGAAGTGTGCTGA 1154
Db 1141 TGAAGTGTGCTGA 1154
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RESULT 3

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US-09-904-584-3
; Sequence 3, Application US/09904584
; Publication No. US2004009704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yulterov, Vadim
; APPLICANT: Laforge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285X
; CURRENT APPLICATION NUMBER: US/09/904,584
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
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ORGANISM: homo sapiens
US-09-904-584-3

Query Match 99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 ATGATCTCCCGATCCAGATTTTCCGGGGAGGCGCCCTTACTGCGCCCGAGGCGC 60
1 ATGATCTCCCGATCCAGATTTTCCGGGGAGGCGCCCTTACTGCGCCCGAGGCGC 60
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Db 61 TGGCTGCCCCCAACAGACAGCGCTGATTTCCGGGCTGAGGCGGAGCCGACAGACAGCGC 120
Oy 121 AGCGCGGCTGAGAGAGCGGAGCTGAGAGCGCGAGCATCTCCCGGCGATCCGATC 180
Db 121 AGCGCGGCTGAGAGAGCGGAGCTGAGAGCGCGAGCATCTCCCGGCGATCCGATC 180
Oy 181 ATCATCAAGGGGTCTACTCGGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 ATCATCAAGGGGTCTACTCGGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Oy 241 ATGTTGATGATCATCCGATACAAAGATGAAGACAGCAACCAATTACATTTTAAC 300
Db 241 ATGTTGATGATCATCCGATACAAAGATGAAGACAGCAACCAATTACATTTTAAC 300
Oy 301 CTGGCTTTGGAGAGTCTTTAGTTACTAACCAATGCTTTTACAGATGAGCTGCTACTTG 360
Db 301 CTGGCTTTGGAGAGTCTTTAGTTACTAACCAATGCTTTTACAGATGAGCTGCTACTTG 360
Oy 361 ATGAATTCCTGGGCTTTTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 ATGAATTCCTGGGCTTTTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Oy 421 AACATGTTACCAAGATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 421 AACATGTTACCAAGATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Oy 481 TGGCAACCCCGTAGAGCTTTGGAGCTTCGCGACACCCCTTGAAAGCAAGATCATCATATTC 540
Db 481 TGGCAACCCCGTAGAGCTTTGGAGCTTCGCGACACCCCTTGAAAGCAAGATCATCATATTC 540
Oy 541 TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Oy 601 GTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Oy 661 TGGTGGAGCTCTTTCATGAAAGATGCGCTCTTTCATGCTTGGCTGCTGCTGCTGCTGCTGCT 720
Db 661 TGGTGGAGCTCTTTCATGAAAGATGCGCTCTTTCATGCTTGGCTGCTGCTGCTGCTGCTGCT 720
Oy 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Oy 781 GGGTCCGAGAGAAAGATGCAACCTGGGAGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 GGGTCCGAGAGAAAGATGCAACCTGGGAGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTG 840
Oy 841 GCACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Oy 901 AGCACTCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 AGCACTCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 ACCAAGCTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
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Db      961  ACCAAGTAGAGCTGATGATCCATTTCTAGACCTTTCTTGTATGAAATACTTAAGCGGTGT 1020
Qy      1021  TTCGGGAGATTTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGACAGATC 1080
Db      1021  TTCGGGAGATTTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGACAGATC 1080
Qy      1081  CGAAATATACAGTTGAGGATCTGCTTACCTGAGGAGCATGATGGATGAATAAACAGTA 1140
Db      1081  CGAAATATACAGTTGAGGATCTGCTTACCTGAGGAGCATGATGGATGAATAAACAGTA 1140
Qy      1141  TGACTAGTGTGGA 1154
Db      1141  TGACTAGTGTGGA 1154

RESULT 4
US-09-904-584-4
; Sequence 4, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-4

Query Match      99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGGAATCTCCCGATCCAGATCTTCCGCGGAGAGCCGCGCTTAACCTGCGCCCGGAGCGGC 60
Db      1  ATGGAATCTCCCGATCCAGATCTTCCGCGGAGAGCCGCGCTTAACCTGCGCCCGGAGCGGC 60
Qy      61  TSCCTGCGCCCGCAAGAGAGCGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCCGAGCAAGAGCGC 120
Db      61  TSCCTGCGCCCGCAAGAGAGCGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCCGAGCAAGAGCGC 120
Qy      121  AGCGCGCGCTGGAGAGAGCGCGAGCTGAGAGCCCGCGGACATCTCCCGGCAATCCCGGATC 180
Db      121  AGCGCGCGCTGGAGAGAGCGCGAGCTGAGAGCCCGCGGACATCTCCCGGCAATCCCGGATC 180
Qy      181  ATCATCAAGCGCGCTCTACTCCGTAAGTTCCTGCTGCGGCTTGGTGGGCAACTCGCTGCTC 240
Db      181  ATCATCAAGCGCGCTCTACTCCGTAAGTTCCTGCTGCGGCTTGGTGGGCAACTCGCTGCTC 240
Qy      241  ATCATCAAGCGCGCTCTACTCCGTAAGTTCCTGCTGCGGCTTGGTGGGCAACTCGCTGCTC 240
Db      241  ATCATCAAGCGCGCTCTACTCCGTAAGTTCCTGCTGCGGCTTGGTGGGCAACTCGCTGCTC 240
Qy      301  CTGGCTTTGGAGATGCTTTAGTTACTACTAACACATGCGCTTTCAAGATAGGCTACTTGG 360
Db      301  CTGGCTTTGGAGATGCTTTAGTTACTACTAACACATGCGCTTTCAAGATAGGCTACTTGG 360
Qy      361  ATGAATCTCTGGCTTTTGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db      361  ATGAATCTCTGGCTTTTGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420
Qy      421  AACATGTTCAACAGCATCTTCACTTGAACCATGATGAGGTGAGACCGCTACATTTGCCGTG 480
Db      421  AACATGTTCAACAGCATCTTCACTTGAACCATGATGAGGTGAGACCGCTACATTTGCCGTG 480
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Db      421  AACATGTTCAACAGCATCTTCACTTGAACCATGATGAGGTGAGACCGCTACATTTGCCGTG 480
Qy      481  TGCACACCCCGTGAAGGCTTTGAGATTTCCGCAACCTTTGAAGCAAAATCATCAATATC 540
Db      481  TGCACACCCCGTGAAGGCTTTGAGATTTCCGCAACCTTTGAAGCAAAATCATCAATATC 540
Qy      541  TGCATCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db      541  TGCATCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy      601  GTGAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      601  GTGAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy      661  TGTGGGACCTTTTATGAAGATCTGCGCTTTCATCTTTCCTTGTGATTCCTGCTGCTC 720
Db      661  TGTGGGACCTTTTATGAAGATCTGCGCTTTCATCTTTCCTTGTGATTCCTGCTGCTC 720
Qy      721  ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      721  ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy      781  GGTCTCCGAGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 840
Db      781  GGTCTCCGAGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 840
Qy      841  GCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db      841  GCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy      901  AGCACTCCCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      901  AGCACTCCCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy      961  ACCAAGTAGAGCTGATGATCCATTTCTAGACCTTTCTTGTATGAAATACTTAAGCGGTGT 1020
Db      961  ACCAAGTAGAGCTGATGATCCATTTCTAGACCTTTCTTGTATGAAATACTTAAGCGGTGT 1020
Qy      1021  TTCGGGAGATTTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGACAGATC 1080
Db      1021  TTCGGGAGATTTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGACAGATC 1080
Qy      1081  CGAAATATACAGTTGAGGATCTGCTTACCTGAGGAGCATGATGGATGAATAAACAGTA 1140
Db      1081  CGAAATATACAGTTGAGGATCTGCTTACCTGAGGAGCATGATGGATGAATAAACAGTA 1140
Qy      1141  TGACTAGTGTGGA 1154
Db      1141  TGACTAGTGTGGA 1154

RESULT 5
US-09-904-584-5
; Sequence 5, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
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US-09-904-584-5

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Query Match      99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCCGGGCGCTTACCGCGGCCCGGAGCGGC 60
OY 61 TCCCTGCCCCCAACAGACGCGCTGGTTTCCCGGCTGGGCGGAGCCGACAGCAACGCGC 120
DB 61 TCCCTGCCCCCAACAGACGCGCTGGTTTCCCGGCTGGGCGGAGCCGACAGCAACGCGC 120
OY 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGGCACATCTCCCGGCGCATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGGCACATCTCCCGGCGCATCCCGGTC 180
OY 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 240
DB 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 240
OY 241 ATGTTGCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 300
DB 241 ATGTTGCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 300
OY 301 CTGGCTTTGGGAGATGCTTACTACTCAACCATGCCCTTCAAGATACGGTCTACTG 360
DB 301 CTGGCTTTGGGAGATGCTTACTACTCAACCATGCCCTTCAAGATACGGTCTACTG 360
OY 361 ATGAATTCCTGGACCTTTTGGGGATGTGCTGTCACAGATAGTAATTTCCATTTACTAC 420
DB 361 ATGAATTCCTGGACCTTTTGGGGATGTGCTGTCACAGATAGTAATTTCCATTTACTAC 420
OY 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGACCGCTACATTCGCGTG 480
DB 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGACCGCTACATTCGCGTG 480
OY 481 TGCCACCCCGGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCATCATATC 540
DB 481 TGCCACCCCGGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCATCATATC 540
OY 541 TGCATCTGGCTGCTGTCTGATCTGTGGCATCTCTGCAATAGTCTTTGAGAGCACCAA 600
DB 541 TGCATCTGGCTGCTGTCTGATCTGTGGCATCTCTGCAATAGTCTTTGAGAGCACCAA 600
OY 601 GTCAAGGAAAGAGTGAATGTCATTGAGTCTCTTGCAGTTCCCAAGATGATGACTACTCC 660
DB 601 GTCAAGGAAAGAGTGAATGTCATTGAGTCTCTTGCAGTTCCCAAGATGATGACTACTCC 660
OY 661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCACTTTGCTTGCTTGCTGTAATCCCTGTC 720
DB 661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCACTTTGCTTGCTTGCTGTAATCCCTGTC 720
OY 721 ATCATCATCTGTCTGTACACCCCTGATGATCTGCGTCTCAAGAGGCTCCGCTCTTCT 780
DB 721 ATCATCATCTGTCTGTACACCCCTGATGATCTGCGTCTCAAGAGGCTCCGCTCTTCT 780
OY 781 GGCCTCCCAAGAAAGATCGCAACTGGGTAGAGTACACAGATGCTCTGTGTGTGTG 840
DB 781 GGCCTCCCAAGAAAGATCGCAACTGGGTAGAGTACACAGATGCTCTGTGTGTGTG 840
OY 841 GCACTCTTCGTCTGTCTGAGTCTCCATTCATATTCATCTCTGTGTGTGTGTGTG 900
DB 841 GCACTCTTCGTCTGTCTGAGTCTCCATTCATATTCATCTCTGTGTGTGTGTGTG 900
OY 901 AGCACTTCCACAGACAGCTGCTCTCCAGCTATTACTCTGTCAGCTTCTAGGCTAT 960
DB 901 AGCACTTCCACAGACAGCTGCTCTCCAGCTATTACTCTGTCAGCTTCTAGGCTAT 960
OY 961 ACCAAGTACCTGATATCCCATTTCTTACGCTTTTCTTGAATGAATACTTCAAGCGGTG 1020
DB 961 ACCAAGTACCTGATATCCCATTTCTTACGCTTTTCTTGAATGAATACTTCAAGCGGTG 1020
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OY 1021 TTCCGGGACCTTCTGCTTTCACCTGAAGATGAGATGAGACGGGACAGACATTCAGCAGATC 1080
DB 1021 TTCCGGGACCTTCTGCTTTCACCTGAAGATGAGATGAGACGGGACAGACATTCAGCAGATC 1080
OY 1081 GGAATACAGTTTCAGAGATCTGCTTACCTGAGGAGACATCGATGGAGATGAATTAACAGATA 1140
DB 1081 GGAATACAGTTTCAGAGATCTGCTTACCTGAGGAGACATCGATGGAGATGAATTAACAGATA 1140
OY 1141 TGACTAGTCTGGGA 1154
DB 1141 TGACTAGTCTGGGA 1154

RESULT 6
US-09-904-584-6
; Sequence 6, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yufeyev, Vadim
; TITLE OF INVENTION: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods using Said Alleles, and
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-6

Query Match      99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCCGGGCGCTTACCGCGGCCCGGAGCGGC 60
DB 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCCGGGCGCTTACCGCGGCCCGGAGCGGC 60
OY 61 TCCCTGCCCCCAACAGACGCGCTGGTTTCCCGGCTGGGCGGAGCCGACAGCAACGCGC 120
DB 61 TCCCTGCCCCCAACAGACGCGCTGGTTTCCCGGCTGGGCGGAGCCGACAGCAACGCGC 120
OY 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGGCACATCTCCCGGCGCATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGGCACATCTCCCGGCGCATCCCGGTC 180
OY 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 240
DB 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 240
OY 241 ATGTTGCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 300
DB 241 ATGTTGCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 300
OY 301 CTGGCTTTGGGAGATGCTTACTACTCAACCATGCCCTTCAAGATACGGTCTACTG 360
DB 301 CTGGCTTTGGGAGATGCTTACTACTCAACCATGCCCTTCAAGATACGGTCTACTG 360
OY 361 ATGAATTCCTGGACCTTTTGGGGATGTGCTGTCACAGATAGTAATTTCCATTTACTAC 420
DB 361 ATGAATTCCTGGACCTTTTGGGGATGTGCTGTCACAGATAGTAATTTCCATTTACTAC 420
OY 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGACCGCTACATTCGCGTG 480
DB 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGACCGCTACATTCGCGTG 480
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Accession	Sequence	Position
QY	ITTCGGGAGCTTCTGCTTTTCCACTGAAGATGAGATGAGCGGACAGGACATGACGAGTTC	1080
Db	1021 TTCCGGGAGCTTCTGCTTTTCCACTGAAGATGAGAGTGGAGCGCGAGACACTGACGAGTTC	1080
QY	1081 CGAAATTAAGTTCCAGGATTCCTGCTTAACTGAGGAGCATTCGATGGGATGAATTAACCACTA	1140
Db	1081 CGAAATTAAGTTCCAGGATTCCTGCTTAACTGAGGAGCATTCGATGGGATGAATTAACCACTA	1140
QY	1141 TGACTAGTCGTGGA	1154
Db	1141 TGACTAGTCGTGGA	1154

RESULT 8

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: Sequence 147: Application US/10225567A
: Publication No. US20030113796A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenn C.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 147
: LENGTH: 1162
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-225-567A-147

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Query Match	99.3%	Score 1146;	DB 15;	Length 1182;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1149; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

OY	1	ATGACATCCCCGATCATANATCTTCCGGGGGAGACCGGGCCCTTACTGTGGCCCCGAGAGCC	60
Db	14	ATGAATATCCCGATTCAATCTTCCGGGGAGCCTGGCCCTTACTGTGGCCCCGAGAGCC	73
OY	61	TGCGTGCCCCCAACAGCAGCGCGCTGTGTTCCCGGCTGAGCGCCGACAGCAAGCGC	120
Db	74	TGCGTGCCCCCAACAGCAGCGCGCTGTGTTCCCGGCTGAGCGCCGACAGCAAGCGC	133
OY	121	AGCGCCGGCTTGGAGAGATGCGGAGCTGGAGCCCGGACATCTCCCGGGCATTCGGCTC	180
Db	134	AGCGCCGGCTTGGAGAGATGCGGAGCTGGAGCCCGGACATCTCCCGGGCATTCGGCTC	193
OY	181	ATCATCAAGCGGAGTCTACTCCGTAGTGTTCGTGCGGACTTGGTGGGCAATCGCTGATC	240
Db	194	ATCATCAAGCGGAGTCTACTCCGTAGTGTTCGTGCGGACTTGGTGGGCAATCGCTGATC	253
OY	241	ATGTTCGTATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTTTAAAC	300
Db	254	ATGTTCGTATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTTTAAAC	313
OY	301	CTGGCTTGGAGAGATGCTTTAGTTACTATCAACATAGCCCTTTCAGAGAGCGTCTACTGTG	360
Db	314	CTGGCTTGGAGAGATGCTTTAGTTACTATCAACATAGCCCTTTCAGAGAGCGTCTACTGTG	373
OY	361	ATGAATTCCTGGCCCTTTTGGGAGATGTGCTGTGCAAGATAGTAATTTCCATTGATTAATAC	420
Db	374	ATGAATTCCTGGCCCTTTTGGGAGATGTGCTGTGCAAGATAGTAATTTCCATTGATTAATAC	433
OY	421	AAAGATTTCAACAGATCTTCAACCTTGCACATATATAGAGCGCGGACCGGTATATGCCGTG	480
Db	434	AAAGATTTCAACAGATCTTCAACCTTGCACATATATAGAGCGCGGACCGGTATATGCCGTG	493
OY	481	TGCCACCCCGTGAAGGCTTTTGGACTTCCGCAACACCCCTTGAAGGCAAAATCATCATATATC	540

Db	494	TGCAACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGAGAAATCATCAATATTC	553
QY	541	TGCATCTGGCTGCTGCTGCTCATCTGTTGGACATCTCTGCATATAGTCTTTGGAGGACCAAA	600
Db	554	TGCATCTGGCTGCTGCTGCTCATCTGTTGGACATCTCTGCATATAGTCTTTGGAGGACCAAA	613
QY	601	GTCAGGGAGAACGTGCATGTCATTGAGTGCTCTCTTGCAGTTCCTCAAGATGATGACTATCC	660
Db	614	GTCAGGGAGAGACGTGCATGTCATTGAGTGCTCTCTTGCAGTTCCTCAAGATGATGACTATCC	673
QY	661	TGAGGGAGACCTTCATATGAAGAATCTGGGCTTCATCTTTGGCTTCGTGATCCCTGCTCTC	720
Db	674	TGAGGGAGACCTTCATATGAAGAATCTGGGCTTCATCTTTGGCTTCGTGATCCCTGCTCTC	733
QY	721	ATCATCATCGCTGCTGTACACCTGTATGATCTGTGGCTCAAGAGCGTCCGCTCTTCTCT	780
Db	734	ATCATCATCGCTGCTGTACACCTGTATGATCTGTGGCTCAAGAGCGTCCGCTCTTCTCT	793
QY	781	GAGCTCCGAGAGAAAGATCGCACCTGCTGATGATCACACAGACTGTGTCCTGTGTGTGTG	840
Db	794	GAGCTCCGAGAGAAAGATCGCACCTGCTGATGATCACACAGACTGTGTCCTGTGTGTGTG	853
QY	841	GCAGCTTCGCGTCTGTGTGAGACTCCCATTCACATATTCATCTGGTGAAGGCTCTGGGG	900
Db	854	GCGGTTTTGCGTGTGTGTGAGACTCCCATTCACATATTCATCTGGTGAAGGCTCTGGGG	913
QY	901	AGCACTTCCACACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGCTAT	960
Db	914	AGCACTTCCACACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGCTAT	973
QY	961	ACCAACAGTAGCCTGATCCCATTTCTTACGCGCTTTCTTATGAAAACTTCAAGCGGTGT	1020
Db	974	ACCAACAGTAGCCTGATCCCATTTCTTACGCGCTTTCTTATGAAAACTTCAAGCGGTGT	1033
QY	1021	TTCCGGGAGCTCTGTCTTCCACTGAAGATGAGATGAGACGGCAGAGCACTAGCAGAGTTC	1080
Db	1034	TTCCGGGAGCTCTGTCTTCCACTGAAGATGAGATGAGACGGCAGAGCACTAGCAGAGTTC	1093
QY	1081	CGAAATACAGTTACAGATCTCTGTTACTCTGAGGAGCATTCGATGGGATGAATTAACCACTA	1140
Db	1094	CGAAATACAGTTACAGATCTCTGTTACTCTGAGGAGCATTCGATGGGATGAATTAACCACTA	1153
QY	1141	TGACTAGTCTGTGA 1154	
Db	1154	TGACTAGTCTGTGA 1167	

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/ RESULT 9
/ US-10-345-680-19
/ Sequence 19, Application US/10345680
/ Publication No. US20030148394A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Silos-Santiago, Inmaculada
/ APPLICANT: Venkateswarlu, Karicheti
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
/ TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
/ TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES
/ FILE REFERENCE: MPI02-012PIKRM.OMNI
/ CURRENT APPLICATION NUMBER: US/10/345, 680
/ CURRENT FILING DATE: 2003-01-16
/ PRIOR APPLICATION NUMBER: US 60/349, 511
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/360, 500
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/365, 041
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/374, 063
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/403, 468
/ PRIOR FILING DATE: 2002-08-14
/

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PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1182
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (14)...(1156)
US-10-345-680-19

Query Match 99.3%; Score 1146; DB 15; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAACTCCCGATCCAGATCTTCGCGGGAGCGGAGCCCTTACCTGCGCCCGAGCGCC 60
DB 14 ATGAAATCCCGATTCAGATCTTCGCGGGAGCGCTGGCCCTTACCTGCGCCCGAGCGCC 73
QY 61 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGGCGAGCCCGACAGCAAGCGC 120
DB 74 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGGCGAGCCCGACAGCAAGCGC 133
QY 121 AGCGCGGCTCGAGAGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCAATCCCGGTC 180
DB 134 AGCGCGGCTCGAGAGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCAATCCCGGTC 193
QY 181 ATCATCAAGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGTGTGGGCAATCCGTGTC 240
DB 194 ATCATCAAGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGTGTGGGCAATCCGTGTC 253
QY 241 ATGTTCGATCATCCGATACCAAAAGATGAAGAGCAACCAATTTACATATTAAAC 300
DB 254 ATGTTCGATCATCCGATACCAAAAGATGAAGAGCAACCAATTTACATATTAAAC 313
QY 301 CTGGCTTGGAGAGTGTCTTGTACTCAACCAATGCGCTTTCAGATGCGGTCTACTTG 360
DB 314 CTGGCTTGGAGAGTGTCTTGTACTCAACCAATGCGGTCTTTCAGATGCGGTCTACTTG 373
QY 361 ATGAATTCCTGCGCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTAC 420
DB 374 ATGAATTCCTGCGCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTAC 433
QY 421 AACATGTTCAACAGCATTTCACTTGAACATGATGAGCGGTGAGCGGTACATTCGGTG 480
DB 434 AACATGTTCAACAGCATTTCACTTGAACATGATGAGCGGTGAGCGGTACATTCGGTG 493
QY 481 TGGCAACCCCGGAGAGCTTGGAGCTTCGCGACACCCCTTGAAGGCAAAATATCAATATC 540
DB 494 TGGCAACCCCGGAGAGCTTGGAGCTTCGCGACACCCCTTGAAGGCAAAATATCAATATC 553
QY 541 TGCATTCGCTGTCTGTCTGTCACTGTGGCATCTCTGCATATGCTCTTGGAGGCAACAA 600
DB 554 TGCATTCGCTGTCTGTCTGTCACTGTGGCATCTCTGCATATGCTCTTGGAGGCAACAA 613
QY 601 GTCAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 614 GTCAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
QY 661 TGGTGGGAGCTCTTCATGAAGATCGGCTTCACTTTCGCTTCGCTTCGCTTCGCTTCG 720
DB 674 TGGTGGGAGCTCTTCATGAAGATCGGCTTCACTTTCGCTTCGCTTCGCTTCGCTTCG 733
QY 721 ATCATCATCTGTCTGTCAACCCGTGATGATGATGATGATGATGATGATGATGATGATG 780

DB 734 ATCATCATCTGTCTGTCAACCCGTGATGATGATGATGATGATGATGATGATGATGATG 793
QY 761 GAGCTCCGAGAGAAAGATGCAACCTGGATGATGATGATGATGATGATGATGATGATGATG 840
DB 794 GAGCTCCGAGAGAAAGATGCAACCTGGATGATGATGATGATGATGATGATGATGATGATG 853
QY 841 GAGCTCTTCGCTGTCTGTCACTGTGGCATCTCTGCATATGCTCTTGGAGGCTTGAGG 900
DB 854 GAGCTCTTCGCTGTCTGTCACTGTGGCATCTCTGCATATGCTCTTGGAGGCTTGAGG 913
QY 901 AGCACTCCCAAGACAGAGCTGCTCTTCACAGCTATTAATCTTGCATGCGCTTAGGCTAT 960
DB 914 AGCACTCCCAAGACAGAGCTGCTCTTCACAGCTATTAATCTTGCATGCGCTTAGGCTAT 973
QY 961 ACCAAGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 974 ACCAAGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1033
QY 1021 TTCCGGGACTTCTGCTTTCACAGTGAAGATGAGATGAGCGGACAGCACTAGACAGATC 1080
DB 1034 TTCCGGGACTTCTGCTTTCACAGTGAAGATGAGATGAGCGGACAGCACTAGACAGATC 1093
QY 1081 CGAAATACAGTTCAAGATCTGCTTACCTGAGGACATGATGATGATGATGATGATGATG 1140
DB 1094 CGAAATACAGTTCAAGATCTGCTTACCTGAGGACATGATGATGATGATGATGATGATG 1153
QY 1141 TGACTAGTCGTGGA 1154
DB 1154 TGACTAGTCGTGGA 1167

RESULT 10
US-10-305-720-1417
; Sequence 1417, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1417
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 9532059
US-10-305-720-1417

Query Match 99.3%; Score 1146; DB 16; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAACTCCCGATCCAGATCTTCGCGGGAGCGGAGCCCTTACCTGCGCCCGAGCGCC 60
DB 14 ATGAAATCCCGATTCAGATCTTCGCGGGAGCGCTGGCCCTTACCTGCGCCCGAGCGCC 73
QY 61 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGGCGAGCCCGACAGCAAGCGC 120
DB 74 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGGCGAGCCCGACAGCAAGCGC 133
QY 121 AGCGCGGCTCGAGAGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCAATCCCGGTC 180
DB 134 AGCGCGGCTCGAGAGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCAATCCCGGTC 193
QY 181 ATCATCAAGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGTGTGGGCAATCCGTGTC 240
DB 194 ATCATCAAGGCGGTCTACTCCGTAGTGTTCGTGTGGCTTGTGTGGGCAATCCGTGTC 253

241 ATGTTGCTGATCCTCCATACAAAGATGAAGACGACCAACCACTTTACATATTAC 300
254 ATGTTGCTGATCCTCCATACAAAGATGAAGACGACCAACCACTTTACATATTAC 313
301 CTGGTTGGGAGATGCTTTAGTTACTACCAACCATGCCCTTTGAGATGAGTCTACTG 360
314 CTGGCTTTGGGAGATGCTTTAGTTACTACCAACCATGCCCTTTGAGATGAGTCTACTG 373
361 ATGAATTCCTGGCTTTGGGAGATGCTGTCGCAAGATAGTAATTTCCATGATTACTAC 420
374 ATGAATTCCTGGCTTTGGGAGATGCTGTCGCAAGATAGTAATTTCCATGATTACTAC 433
421 AACATGTTACACAGATCTTACCTTGACCAATGATGACCGTGACCCGTTACATGCCCTG 480
434 AACATGTTACACAGATCTTACCTTGACCAATGATGACCGTGACCCGTTACATGCCCTG 493
481 TGCCACCCCGTGAAGGCTTTGGAATCTTCGCAACACCTTGAAAGGCAAAAGATCAATATC 540
494 TGCCACCCCGTGAAGGCTTTGGAATCTTCGCAACACCTTGAAAGGCAAAAGATCAATATC 553
541 TGCAATCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTTGAGGACCAAA 600
554 TGCAATCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTTGAGGACCAAA 613
601 GTCAGGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
614 GTCAGGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
661 TGGTGGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTTGGATCGCTGCTGCTG 720
674 TGGTGGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTTGGATCGCTGCTGCTG 733
721 ATCATCATCTGCTGCTACACCTGATGATGATGATGATGATGATGATGATGATGATG 780
734 ATCATCATCTGCTGCTACACCTGATGATGATGATGATGATGATGATGATGATGATG 793
781 GGCCTCCGAGAGAAAGATCGCAACCTGCGTGAAGATCACAGACATGCTGCTGCTGCTG 840
794 GGCCTCCGAGAGAAAGATCGCAACCTGCGTGAAGATCACAGACATGCTGCTGCTGCTG 853
841 GCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
854 GCGGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
901 AGCACTCCCAAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
914 AGCACTCCCAAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
961 ACCAATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
974 ACCAATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1033
1021 TTCCGGGACCTCTGCTTCCACTGAAGATGAGATGAGCGGACAGCACTAGCAGATC 1080
1034 TTCCGGGACCTCTGCTTCCACTGAAGATGAGATGAGCGGACAGCACTAGCAGATC 1093
1081 CGAATATACAGTTCAGAGATCTGCTTACCTGAGGACATGATGGATGAATTAACAGTA 1140
1094 CGAATATACAGTTCAGAGATCTGCTTACCTGAGGACATGATGGATGAATTAACAGTA 1153
1141 TGACTAGTCTGGA 1154
1154 TGACTAGTCTGGA 1167

RESULT 11
US-10-283-975A-80
; Sequence 80, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia

FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283, 975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340, 938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338, 997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340, 081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341, 012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-80

Query Match 99.3%; Score 1146; DB 17; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ATGGAATCCCGATCCAGATCTTCCGCGGAGCGGACCTTACCTGCGCCCGAGCGCC 60
14 ATGGAATCCCGATCCAGATCTTCCGCGGAGCGGACCTTACCTGCGCCCGAGCGCC 73
61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGACCGACAGCAAGCGC 120
74 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGACCGACAGCAAGCGC 133
121 AGCGCGGCTGCGAGAGCGGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGG 180
134 AGCGCGGCTGCGAGAGCGGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGG 193
181 ATCATCAAGCGGCTCTACTCCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
194 ATCATCAAGCGGCTCTACTCCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
241 ATGTTGCTGATCCTCCATACAAAGATGAAGACGACCAACCACTTTACATATTAC 300
254 ATGTTGCTGATCCTCCATACAAAGATGAAGACGACCAACCACTTTACATATTAC 313
301 CTGGCTTTGGGAGATGCTTTAGTTACTACCAACCATGCCCTTTGAGATGAGTCTACTG 360
314 CTGGCTTTGGGAGATGCTTTAGTTACTACCAACCATGCCCTTTGAGATGAGTCTACTG 373
361 ATGAATTCCTGGCTTTGGGAGATGCTGTCGCAAGATAGTAATTTCCATGATTACTAC 420
374 ATGAATTCCTGGCTTTGGGAGATGCTGTCGCAAGATAGTAATTTCCATGATTACTAC 433
421 AACATGTTACACAGATCTTACCTTGACCAATGATGACCGTGACCCGTTACATGCCCTG 480
434 AACATGTTACACAGATCTTACCTTGACCAATGATGACCGTGACCCGTTACATGCCCTG 493
481 TGCCACCCCGTGAAGGCTTTGGAATCTTCGCAACACCTTGAAAGGCAAAAGATCAATATC 540
494 TGCCACCCCGTGAAGGCTTTGGAATCTTCGCAACACCTTGAAAGGCAAAAGATCAATATC 553
541 TGCAATCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTTGAGGACCAAA 600
554 TGCAATCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTTGAGGACCAAA 613
601 GTCAGGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
614 GTCAGGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
661 TGGTGGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTTGGATCGCTGCTGCTG 720
674 TGGTGGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTTGGATCGCTGCTGCTG 733
721 ATCATCATCTGCTGCTACACCTGATGATGATGATGATGATGATGATGATGATGATG 780

Db 734 ATCATCATGTCGTCTGACACCTGTATGATTCCTGCTCAAGAGCGCTCCCTTCT 793
 Qy 781 GGCCTCCGAGAGAAAGATCGCAACCTGGGTAGGATCACAGACTGGTCTGGTGGTG 840
 Db 794 GGCCTCCGAGAGAAAGATCGCAACCTGGGTAGGATCACAGACTGGTCTGGTGGTG 853
 Qy 841 GCAGCTTCGTGTCGTGTCGATCCCATTCATATTCATCTGGTGGAGCTTGAGG 900
 Db 854 GCGGTTTTGTCGTGTCGTGTCGATCCCATTCATATTCATCTGGTGGAGCTTGAGG 913
 Qy 901 AGCACTCCACAGACAGCTGCTCTCTCCAGCTATTAATTCTGATGCGCTTAGCTAT 960
 Db 914 AGCACTCCACAGACAGCTGCTCTCTCCAGCTATTAATTCTGATGCGCTTAGCTAT 973
 Qy 961 ACCAAGCTAGCTGAATCCCATTTCTACGCTTTCTTGATGAAGAACTTCAAGGGGTG 1020
 Db 974 ACCAAGCTAGCTGAATCCCATTTCTACGCTTTCTTGATGAAGAACTTCAAGGGGTG 1033
 Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGCGGACAGCACTAGCAGATC 1080
 Db 1034 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGCGGACAGCACTAGCAGATC 1093
 Qy 1081 CGAAATACAGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
 Db 1094 CGAAATACAGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1153
 Qy 1141 TGACTAGTCGTGA 1154
 Db 1154 TGACTAGTCGTGA 1167

RESULT 12

US-10-318-661-1
 ; Sequence 1, Application US/10318661
 ; Publication No. US20030167476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conklin, Bruce R.
 ; TITLE OF INVENTION: Selective Target Cell Activation By
 ; Expression of A G Protein-coupled Receptor Activated
 ; TITLE OF INVENTION: Superiorly By Synthetic Ligand
 ; FILE REFERENCE: UCAL-049CIP2
 ; CURRENT FILING DATE: US/10/318,661
 ; PRIOR APPLICATION NUMBER: US 09/341,446
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334
 ; PRIOR FILING DATE: 1997-03-25
 ; PRIOR APPLICATION NUMBER: US 08/622,348
 ; PRIOR FILING DATE: 1996-03-26
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-318-661-1

Query Match 99.0%; Score 1143; DB 15; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATCTCCGATTCATATCTTCCGCGGAGAGCGGCGCTTACTTGGCGCCCGAGCGCC 60
 Db 1 ATGACATCTCCGATTCATATCTTCCGCGGAGAGCGGCGCTTACTTGGCGCCCGAGCGCC 60
 Qy 61 TGCCGTGCGCCCGACAGAGCGGCGCTTCTCCGCGGCTGAGCGCGGCGGACGAGCAAGAGG 120
 Db 61 TGCCGTGCGCCCGACAGAGCGGCGCTTCTCCGCGGCTGAGCGCGGCGGACGAGCAAGAGG 120
 Qy 121 AGCGCGGCTCGAGAGCGGCGAGCTGAGCGCGGCGGACATCTTCCCGGCGCATCCCGGTC 180
 Db 121 AGCGCGGCTCGAGAGCGGCGAGCTGAGCGCGGCGGACATCTTCCCGGCGCATCCCGGTC 180

Qy 181 ATCATCAGGCGGCTCTACTCCGTAAGTGTGTCGTGAGGCTTGATGGGCAACTCGGTGTC 240
 Db 181 ATCATCAGGCGGCTCTACTCCGTAAGTGTGTCGTGAGGCTTGATGGGCAACTCGGTGTC 240
 Qy 241 ATGTCGTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTATATTAAAC 300
 Db 241 ATGTCGTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTATATTAAAC 300
 Qy 301 CTGGTTTGGAGAGATGCTTGTACTCAACCAATGCCCTTCAAGATAGGTCATCTTG 360
 Db 301 CTGGTTTGGAGAGATGCTTGTACTCAACCAATGCCCTTCAAGATAGGTCATCTTG 360
 Qy 361 ATGAATTCCTGAGCTTTTGGGAGATGTCGTGCAAGATAGTAATTTCCATTGATTAAC 420
 Db 361 ATGAATTCCTGAGCTTTTGGGAGATGTCGTGCAAGATAGTAATTTCCATTGATTAAC 420
 Qy 421 AACATGTCACAGATCTTCACTTGCATATGATGAGCGGTGACCGCTACATTCGCTG 480
 Db 421 AACATGTCACAGATCTTCACTTGCATATGATGAGCGGTGACCGCTACATTCGCTG 480
 Qy 481 TGCCACCCCGTGAAGGCTTTGGAATCTCCGACACCCCTTGAAGGCAAGATCATTAATC 540
 Db 481 TGCCACCCCGTGAAGGCTTTGGAATCTCCGACACCCCTTGAAGGCAAGATCATTAATC 540
 Qy 541 TGCAATCTGCTGCTGTCATCTGATGAGATCTCTGCAATAGTCTTGAGAGGACCAAA 600
 Db 541 TGCAATCTGCTGCTGTCATCTGATGAGATCTCTGCAATAGTCTTGAGAGGACCAAA 600
 Qy 601 GTCAAGGAGAGAGTCGATGATGATGAGTCTCTTGCAGTTCCAGATGATGACTACTCC 660
 Db 601 GTCAAGGAGAGAGTCGATGATGATGAGTCTCTTGCAGTTCCAGATGATGACTACTCC 660
 Qy 661 TGGTGGGACTCTCTTCAATGAATGCTGCTTCAATCTTGGCTTGTGATCCCTGCTC 720
 Db 661 TGGTGGGACTCTCTTCAATGAATGCTGCTTCAATCTTGGCTTGTGATCCCTGCTC 720
 Qy 721 ATCATCATGTCGTGTAACCCGTATGATTCCTGGGCTCAAGAGGCTCCGCTCTTCT 780
 Db 721 ATCATCATGTCGTGTAACCCGTATGATTCCTGGGCTCAAGAGGCTCCGCTCTTCT 780
 Qy 781 GGCCTCCGAGAGAAAGATCGCAACCTGGGTAGGATCAACAGACTGGTCTGGTGGTG 840
 Db 781 GGCCTCCGAGAGAAAGATCGCAACCTGGGTAGGATCAACAGACTGGTCTGGTGGTG 840
 Qy 841 GCAGCTTCGTGTCGTGTCGTAAGTCCCATTAATTCATCTGCTGAGGCTCTGAGG 900
 Db 841 GCAGCTTCGTGTCGTGTCGTAAGTCCCATTAATTCATCTGCTGAGGCTCTGAGG 900
 Qy 901 AGCACTCCACAGACAGCTGCTCTCCAGCTATTAATTCTGATGCGCTTAGGCTAT 960
 Db 901 AGCACTCCACAGACAGCTGCTCTCCAGCTATTAATTCTGATGCGCTTAGGCTAT 960
 Qy 961 ACCAAGCTAGCTGAATCCCATTTCTCAAGCTTTCTTGATGAAGAACTTCAAGCGGTG 1020
 Db 961 ACCAAGCTAGCTGAATCCCATTTCTCAAGCTTTCTTGATGAAGAACTTCAAGCGGTG 1020
 Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGCGGACAGCACTAGCAGATC 1080
 Db 1021 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGCGGACAGCACTAGCAGATC 1080
 Qy 1081 CGAAATACAGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
 Db 1081 CGAAATACAGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
 Qy 1141 TGA 1143
 Db 1141 TGA 1143

RESULT 13
 US-10-318-661-3
 ; Sequence 3, Application US/10318661
 ; Publication No. US20030167476A1

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? GENERAL INFORMATION:
? APPLICANT: Conklin, Bruce R.
? TITLE OF INVENTION: Selective Target Cell Activation By
? TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
? TITLE OF INVENTION: Superiotically By Synthetic Ligand
? FILE REFERENCE: UCAL-049CIP2
? CURRENT APPLICATION NUMBER: US/10/318,661
? PRIOR FILING DATE: 2003-05-05
? PRIOR APPLICATION NUMBER: US 09/341,446
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US97/05334
? PRIOR FILING DATE: 1997-03-25
? PRIOR APPLICATION NUMBER: US 08/622,348
? PRIOR FILING DATE: 1996-03-26
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 1284
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: modified KOR
? US-10-318-661-3

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Query Match	98.6%	Score 1137.8	DB 15	Length 1284
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1139	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

Qy	2	TGGA	CTCCCCCAATCCAGATCTTCCGGGGGAAACGGGGGCTCTACCTGGGCCCCGAGCGCT	61
Dp	113	TGCATCTCCCGATCCAGATCTTCCGGGGAAACGGGGGCTCTACCTGGGCCCCGAGCGCT	172	
Qy	62	GCTG	CCCCCAACAGCAGCGCGCTGGTTCCCGGTGGGCGGAGCCCGACAGCAACGGCA	121
Dp	173	GCTG	CCCCCAACAGCAGCGCGCTGGTTCCCGGTGGGCGGAGCCCGACAGCAACGGCA	232
Qy	122	GCGC	CGGCTTCGAGAGACGGCAGCTGGAACCCGGCCCAATCTCCCGGCCATCCCGGTCA	181
Dp	233	GCGC	CGGCTTCGAGAGACGGCAGCTGGAACCCGGCCCAATCTCCCGGCCATCCCGGTCA	292
Qy	182	TCAT	CAACGGGAGTCTACCTCCGTAAGTTCGTGCGGGCTTGGTGGGCAATCGCTGGTCA	241
Dp	293	TCAT	CAACGGGAGTCTACCTCCGTAAGTTCGTGCGGGCTTGGTGGGCAATCGCTGGTCA	352
Qy	242	TGTT	CGTGATCATCCGATACCAAAAGTAGAAGACACACCAATTTACATATTTAAC	301
Dp	353	TGTT	CGTGATCATCCGATACCAAAAGTAGAAGACACACCAATTTACATATTTAAC	412
Qy	302	TGGC	TTGGCAGATGGTTTAGTTAGTTACACACATGCCCTTACAGAGTACGGTCTTACA	361
Dp	413	TGGC	TTGGCAGATGGTTTAGTTAGTTACACACATGCCCTTACAGAGTACGGTCTTACA	472
Qy	362	TGAAT	TCTGGCCTTTTGGGGATGTGTCTGTGCAGAGTAGTAATTTCAATTGATTACTCA	421
Dp	473	TGAAT	TCTGGCCTTTTGGGGATGTGTCTGTGCAGAGTAGTAATTTCAATTGATTACTCA	532
Qy	422	ACAT	GTTCACACAGCATCTTCAACCTTGACCATATAGAGGTGACCGCTACATTCGCGT	481
Dp	533	ACAT	GTTCACACAGCATCTTCAACCTTGACCATATAGAGGTGACCGCTACATTCGCGT	592
Qy	482	GCCAC	CCCCGTGAAGGCTTTGACCTTCGACACCCCTTGAAGGCAAAAGTCAATCATCT	541
Dp	593	GCCAC	CCCCGTGAAGGCTTTGACCTTCGACACCCCTTGAAGGCAAAAGTCAATCATCT	652
Qy	542	GCAAT	CTGGCTGTGTGTCTCTGTGGCATCTCTGCATAATGTCCTTGAAGGCACAAAG	601
Dp	653	GCAAT	CTGGCTGTGTGTCTCTGTGGCATCTCTGCATAATGTCCTTGAAGGCACAAAG	712
Qy	602	TCAG	GGGAAGACGTCAATGTCATTGAGTGTCTCTGCAGTCCGACAGATATACATCTCT	661
Dp	713	TCAG	GGGAAGACGTCAATGTCATTGAGTGTCTCTGCAGTCCGACAGATATACATCTCT	772
Qy	662	GGTGG	AGCCTCTTCAAGAAATCTGCGTCTTCACTTTGCTTCGTATCCCTGTCTCA	721

Db	773	GGTGGACCTCTTCATGAAGATCGCGCTTTCATCTTTGCGTTGCGTATCCCTGCTCCA	832
Qy	722	TCATCATGCTGTGTACACCCGTATGATCCTGGGCTCAAGAGGCTCGGCTCTTCTG	781
Db	833	TCATCATGCTGTGTACACCCGTATGATCCTGCGCTTCMAAGCGCTCGGCTCTTCTG	892
Qy	782	GCTCCCGAGAAAGATCGCAACTGCGTAGATCAACGACTGCTGTGTTGTTGG	841
Db	893	GCTCCCGAGAAAGATCGCAACTGCGTAGATCAACGACTGCTGTGTTGTTGG	952
Qy	842	CAGCTTGCTGTGTGCTGAGCTCCCAATTCATATTTCATCTGTGAGGCTCTGGGA	901
Db	953	CAGCTTGCTGTGTGCTGAGCTCCCAATTCATATTTCATCTGTGAGGCTCTGGGA	1012
Qy	902	GCACCTCCACAGACAGCTGCTCTTCCAGCTATTACTCTGCATGCGCTTAGGCTATA	961
Db	1013	GCACCTCCACAGACAGCTGCTCTTCCAGCTATTACTCTGCATGCGCTTAGGCTATA	1072
Qy	962	CCACAGTAGCTGAATGCCATTCTCAACGCTTCTGTATGAGAACTTCAAGCGTGT	1021
Db	1073	CCACAGTAGCTGAATGCCATTCTCAACGCTTCTGTATGAGAACTTCAAGCGTGT	1132
Qy	1022	TCCGGAATCTTCTTTCATGAAGATGAGATGAGCGGCAAGCATTAAGCATGCC	1081
Db	1133	TCCGGAATCTTCTTTCATGAAGATGAGATGAGCGGCAAGCATTAAGCATGCC	1192
Qy	1082	GAAATTAAGTTCAAGATCTGCTTACCTGAAGGACATCGATGGAGTGAATAAACAGTAT	1141
Db	1193	GAAATTAAGTTCAAGATCTGCTTACCTGAAGGACATCGATGGAGTGAATAAACAGTAT	1253
Qy	1142	G 1142	
Db	1253	G 1253	

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RESULT 14
US-10-345-680-21
/ Sequence 21, Application US/10345680
/ Publication No. US20030148394A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Siles-Santiago, Immaculada
/ APPLICANT: Venkateswarlu, Karicheti
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
/ TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
/ TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES
/ FILE REFERENCE: MP102-012P1NM OMNI
/ CURRENT APPLICATION NUMBER: US/10/345, 680
/ CURRENT FILING DATE: 2003-01-16
/ PRIOR APPLICATION NUMBER: US 60/349, 511
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/360, 500
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/365, 041
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/374, 063
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/403, 468
/ PRIOR FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: US 60/414, 262
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: US 60/419, 986
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 60/423, 809
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: US 60/429, 797
/ PRIOR FILING DATE: 2002-11-26
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 1143

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; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1143)
 US-10-345-680-21

Query Match 98.4%; Score 1135; DB 15; Length 1143;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1138; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGGAATCCCGGATTCAGATCTTCCGCGGAGAGCCGCGCTTACCTGCGCCCCGAGCGC 60
DB 1 ATGGAATCCCGGATTCAGATCTTCCGCGGAGAGCCGCGCTTACCTGCGCCCCGAGCGC 60
QY 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCAAGCAAGC 120
DB 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCAAGCAAGC 120
QY 121 AGCGCGGCTGGAGAGAGCGCGAGCTGAGAGCCGCGCAATCTCCCGGCAATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGAGCGCGAGCTGAGAGCCGCGCAATCTCCCGGCAATCCCGGTC 180
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTGTCTGCTGCGCTTGGGCAACTCGCTGGTC 240
DB 181 ATCATCAGGCGGCTTACTCCGTAAGTGTCTGCTGCGCTTGGGCAACTCGCTGGTC 240
QY 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTATTTAAC 300
DB 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTATTTAAC 300
QY 301 CTGGCTTTGGAGATGCTTTAGTTACTACACCATGCGCTTCAAGATACGCTTACTTG 360
DB 301 CTGGCTTTGGAGATGCTTTAGTTACTACACCATGCGCTTCAAGATACGCTTACTTG 360
QY 361 ATGAATTCCTGCGCTTTGGGGATGTGCTGTCAGATAGTATTTCCATTACTAC 420
DB 361 ATGAATTCCTGCGCTTTGGGGATGTGCTGTCAGATAGTATTTCCATTACTAC 420
QY 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGAACCGCTACATTCG 480
DB 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGAACCGCTACATTCG 480
QY 481 TGGCAACCCCGTGAAGGCTTTGGAATTCGCGCAACCTTGAAGGCAAAATCATCATC 540
DB 481 TGGCAACCCCGTGAAGGCTTTGGAATTCGCGCAACCTTGAAGGCAAAATCATCATC 540
QY 541 TGCATCTGGCTGCTGCTGATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAAA 600
DB 541 TGCATCTGGCTGCTGCTGATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAAA 600
QY 601 GTCAAGGAAGAGCTGATGATGATGAGTCTCTTGAAGTCCAGATGATGATCTAC 660
DB 601 GTCAAGGAAGAGCTGATGATGATGAGTCTCTTGAAGTCCAGATGATGATCTAC 660
QY 661 TGGTGGAGACTTTCATGAAATCTGCGCTTTCATCTTTGCTTGTGATCCCTGCTC 720
DB 661 TGGTGGAGACTTTCATGAAATCTGCGCTTTCATCTTTGCTTGTGATCCCTGCTC 720
QY 721 ATCATCATGCTGCTGATACACCTGATGATCTGCTGCTCAAGAGGCGCGGCTCTTCT 780
DB 721 ATCATCATGCTGCTGATACACCTGATGATCTGCTGCTCAAGAGGCGCGGCTCTTCT 780
QY 781 GGCCTCCGAGAAAGATCGCAACCTGCGTAGAGATCAACAAGCTGCTGCTGCTG 840
DB 781 GGCCTCCGAGAAAGATCGCAACCTGCGTAGAGATCAACAAGCTGCTGCTGCTG 840
QY 841 GCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 GCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 AGCACTCCCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 AGCACTCCCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
  
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DB 901 AGCACTCCCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 ACCAACAATGAGCTTAAATCCCATTTCTTACAGCTTTCTTGAAGAAACTTCAAGCGGT 1020
DB 961 ACCAACAATGAGCTTAAATCCCATTTCTTACAGCTTTCTTGAAGAAACTTCAAGCGGT 1020
QY 1021 TTCGGGACTTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TTCGGGACTTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGAGATGATGAGTGAATTAACCACTA 1140
DB 1081 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGAGATGATGAGTGAATTAACCACTA 1140
QY 1141 TGA 1143
DB 1141 TGA 1143
  
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RESULT 15

US-09-826-509-542
 ; Sequence 542, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 542
 ; LENGTH: 1143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-826-509-542

Query Match 98.1%; Score 1131.8; DB 11; Length 1143;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 ATGGAATCCCGGATTCAGATCTTCCGCGGAGAGCCGCGCTTACCTGCGCCCCGAGCGC 60
DB 1 ATGGAATCCCGGATTCAGATCTTCCGCGGAGAGCCGCGCTTACCTGCGCCCCGAGCGC 60
QY 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCAAGCAAGC 120
DB 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGCTGGGCGGAGCCGAGCAAGCAAGC 120
QY 121 AGCGCGGCTGGAGAGAGCGCGAGCTGAGAGCCCGCGCAATCTCCCGGCAATCCGCTC 180
DB 121 AGCGCGGCTGGAGAGAGCGCGAGCTGAGAGCCCGCGCAATCTCCCGGCAATCCGCTC 180
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 ATCATCAGGCGGCTTACTCCGTAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTATTTAAC 300
DB 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTATTTAAC 300
QY 301 CTGGCTTTGGAGATGCTTTAGTTACTACACCATGCGCTTCAAGATACGCTTACTTG 360
DB 301 CTGGCTTTGGAGATGCTTTAGTTACTACACCATGCGCTTCAAGATACGCTTACTTG 360
QY 361 ATGAATTCCTGCGCTTTTGGGGATGTGCTGTCAGATAGTATTTCCATTACTAC 420
DB 361 ATGAATTCCTGCGCTTTTGGGGATGTGCTGTCAGATAGTATTTCCATTACTAC 420
  
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Db 361 ATGATTCCTGGCCCTTTGGGGATGCTGTGCAAGATGATTAATTTCATGATTACTAC 420
Qy 421 AACATGTTACACAGCATCTTCACTTGAACATGATGAGCGTGAGCCGCTACATGCGGTG 480
Db 421 AACATGTTACACAGCATCTTCACTTGAACATGATGAGCGTGAGCCGCTACATGCGGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTGGAATCTGCGACACCCCTTGAAGGCAAAATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGGAATCTGCGACACCCCTTGAAGGCAAAATCATCAATATC 540
Qy 541 TGCATCTGGCTGTGCTGTCACTGTGTGGCATCTCTGCAATAGTCTTGAAGGCAACCAA 600
Db 541 TGCATCTGGCTGTGCTGTCACTGTGTGGCATCTCTGCAATAGTCTTGAAGGCAACCAA 600
Qy 601 GTCAGGGAAGACGTGATGTCAATGAGTCTCTTGCACTTCCAGATGATGACTACTCC 660
Db 601 GTCAGGGAAGACGTGATGTCAATGAGTCTCTTGCACTTCCAGATGATGACTACTCC 660
Qy 661 TGGTGGGACCTCTTCATGAAGATCGGCTTTCATCTTGGCTTGATGCTGCTGCTC 720
Db 661 TGGTGGGACCTCTTCATGAAGATCGGCTTTCATCTTGGCTTGATGCTGCTGCTC 720
Qy 721 ATCATCATCTGTCTGTCAACCTGTATGATCCTGTGCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATCATCTGTCTGTCAACCTGTATGATCCTGTGCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GCGTCCGAGAGAAAGATCGCACTGCGTGAAGATCACCAGATCTGCTGCTGCTGCTG 840
Db 781 GCGTCCGAGAGAAAGATCGCACTGCGTGAAGATCACCAGATCTGCTGCTGCTGCTG 840
Qy 841 GCAGTCTGTGTGTGTGTGTGAGCTCCATTCATCATTCATCTGCTGCTGCTGCTGCTG 900
Db 841 GCAGTCTGTGTGTGTGTGTGAGCTCCATTCATCATTCATCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCACTCTCCACAGACAGCTGTCTCTCACTATTAATCTGTGATGCTTGAAGCTAT 960
Db 901 AGCACTCTCCACAGACAGCTGTCTCTCACTATTAATCTGTGATGCTTGAAGCTAT 960
Qy 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1021 TTCGGGACCTCTGTCTTCACTGAAGATGAGATGAGCGGACAGACTAGAGAGATC 1080
Db 1021 TTCGGGACCTCTGTCTTCACTGAAGATGAGATGAGCGGACAGACTAGAGAGATC 1080
Qy 1081 CGAAATACAGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGATGATGATGATGAT 1140
Db 1081 CGAAATACAGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGATGATGATGATGAT 1140
Qy 1141 TGA 1143
Db 1141 TGA 1143

RESULT 16
US-10-318-661-5

; Sequence 5, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: USAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348

; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASL OR1
US-10-318-661-5

Query Match 86.7%; Score 1001; DB 15; Length 1275;
Best Local Similarity 93.1%; Pred. No. 1.2e-279;
Matches 1062; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

Qy 2 TGAATCCCGCATTCAGATCTTCCGCGGGAGCCGGCCCTTACTGCGGCCCGGAGCGCT 61
Db 113 TCGACTCCCGCATTCAGATCTTCCGCGGGAGCCGGCCCTTACTGCGGCCCGGAGCGCT 172
Qy 62 GCGTCCCGCCCAAGAGAGCGCTGTTCCTCCGCGTGGAGCCGAGCCGAGCAAGAGCA 121
Db 173 GCGTCCCGCCCAAGAGAGCGCTGTTCCTCCGCGTGGAGCCGAGCCGAGCAAGAGCA 232
Qy 122 GCGCGGCTGGAGAGCGCGAGCTGAGCCCGGCAATCTCCGCGCATCCGCTGCA 181
Db 233 GCGCGGCTGGAGAGCGCGAGCTGAGCCCGGCAATCTCCGCGCATCCGCTGCA 292
Qy 182 TCATCAAGGCGGTATCTCCGTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
Db 293 TCATCAAGGCGGTATCTCCGTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
Qy 242 TGTTCGTATCATCCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 301
Db 353 TGTTCGTATCATCCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 412
Qy 302 TGGCTTTGGAGATGCTTATGATTCATCAACCATGCTTTCAGAGTACGCTTACTTGA 361
Db 413 TGGCTTTGGAGATGCTTATGATTCATCAACCATGCTTTCAGAGTACGCTTACTTGA 472
Qy 362 TGAATTCCTGCTTGTGGGATGCTGTGCAAGATGATGATGATGATGATGATGATGAT 421
Db 473 TGAATTCCTGCTTGTGGGATGCTGTGCAAGATGATGATGATGATGATGATGATGAT 532
Qy 422 ACATGTTACACAGATCTTCACTTGAACATGATGAGCGGCTACATGCTGCTGCT 481
Db 533 ACATGTTACACAGATCTTCACTTGAACATGATGAGCGGCTACATGCTGCTGCTGCT 592
Qy 482 GCCACCCCGTGAAGCTTTGACTTCCGACACCCCTTGAAGGCAAAATCATCAATATCT 541
Db 593 GCCACCCCGTGAAGCTTTGACTTCCGACACCCCTTGAAGGCAAAATCATCAATATCT 652
Qy 542 GCATCTGCTGCTGTGCTCATCTGTGCAATCTGTGCAATCTGTGCAATCTGTGCAATCT 601
Db 653 GCATCTGCTGCTGTGCTCATCTGTGCAATCTGTGCAATCTGTGCAATCTGTGCAATCT 712
Qy 602 TCAGGAAGAGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
Db 713 CCGGAGATGAGAGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
Qy 662 GGTGGACCTCTTCATGAAGATCTGCTTTCATCTTGTGCTTGTGATCTGCTGCTCA 721
Db 764 ACTGGACACTGTACCAAGATCTGCTTTCATCTTGTGCTTGTGATCTGCTGCTCA 823
Qy 722 TCATCATCTGTGCTTACACCTGTATATCTGCTGCTTCAAGAGGCTGCTGCTTCTG 781
Db 824 TCATCATCTGTGCTTACACCTGTATATCTGCTGCTTCAAGAGGCTGCTGCTTCTGCT 883
Qy 782 GCTCCGAGAGAAAGATCGCAACTGCTGATGATGATGATGATGATGATGATGATGATGAT 841
Db 884 GCTCCGAGAGAAAGATCGCAACTGCTGATGATGATGATGATGATGATGATGATGATGAT 943
Qy 842 CAGTCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901

Db	944	CAGTCTTGTCGTCTGCTGAGACTCCCATTCACATTTATCTCTGATGAGGCTCTGGGGA	1003
Qy	902	GCACCTCCCAAGCAGCAGACTGCTCTCTCCAGCTATTACTTTCGATCGCTTTAAGGCTATA	961
Db	1004	GCACCTCCCAAGCAGCAGACTGCTCTCTCCAGCTATTACTTTCGATCGCTTTAAGGCTATA	1063
Qy	962	CCAACAGTAGGCTGATCCCATTTCTCTACGCGCTTCTTGATGAAACTTCAAGGCGTAT	1021
Db	1064	CCAACAGTAGGCTGATCCCATTTCTCTACGCGCTTCTTGATGAAACTTCAAGGCGTAT	1123
Qy	1022	TCCGGGACTTCTGCTTTCCACTGAAAGATGAGATGAGCGGCAAGCATCTAGCAGATCC	1081
Db	1124	TCCGGGACTTCTGCTTTCCACTGAAAGATGAGATGAGCGGCAAGCATCTAGCAGATCC	1183
Qy	1082	GAAATACAGTTCAGGATCCTGCTTACCTGAGGAGCATGATGGATGTAATAACACATAT	1141
Db	1184	GAAATACAGTTCAGGATCCTGCTTACCTGAGGAGCATGATGGATGTAATAACACATAT	1243
Qy	1142	G	1142
Db	1244	G	1244

RESULT 17
US-10-318

; Sequence 7, Application US/10318661
; Publication No. US20030167476A1

; GENERAL INFORMATION:

APPLICANT: Conklin, Bruce R.

TITLE OF INVENTION: Selective Target Cell Activation By

TITLE OF INVENTION: Superiorly By Synthetic Ligand

FILE REFERENCE: UCAL-049CIP2

CURRENT APPLICATION NUMBER: US/10/318,661

; CURRENT FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: US 09/341,446

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1997-03-25

PRIOR APPLICATION NUMBER: US 08/622,348

PRIOR FILING DATE: 1996-03-26

NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7
TTCCTT 1077TYPE: DNA
LENGTH: 1275

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: RASSL OR2

US-10-318-661-7

Query Match	86.3%;	Score 996.2;	DB 15;	Length 1275;
Best Local Similarity	92.8%;	Pred. No. 2.9e-278;		
Matches 1059;	Conservative 0;	Mismatches 73;	Indels 9;	Gaps 1;

Oy	2	TGGATCTCCCGCATCCAGATCTTCCGCGGGGGAGCCGGGCGCTAACCTCGCGCCCCCGAGCGGCT	61
Db	113	TGACATCCCCCGATCCAGATCTTCCGCGGGGAGCCGGGCGCTTAACCTCGCGCCCCGAGCGGCT	172
Oy	62	GCTTGCCTCCCGCAACGACGCGCTTGTTCCCGAGCTGGGCGGAGCCGACAGCAACGGCA	121
Db	173	GCTTGCCTCCCGCAACGACGCGCTTGTTCCCGAGCTGGGCGGAGCCGACAGCAACGGCA	232
Oy	122	GCGCGGGCTCGAGAGACGGACGAGCTGGAGCCCGGCACATCTCCCGGCGCATCCCGGTCGA	181
Db	233	GCGCGGGCTCGAGAGACGGACGAGCTGGAGCCCGGCACATCTCTCCCGGCGCATCCCGGTCGA	292
Oy	182	TCATACGGCGGATCTAATCTCCGTAAGTGTTCGTGCGGCTTGATGGGCAATCGCTGTCGA	241
Db	293	TCATACGGCGGATCTAATCTCCGTAAGTGTTCGTGCGGCTTGATGGGCAATCGCTGTCGA	352
Oy	242	TGTTTGTATCATCCGATACCAAGATGAGAGACGCAACCAACTTTACATATTAAAC	301

Db	355	TGTTGCGATATATCCGATACCAAGATGAAAGACAGCAACCAACTTATATTAAACC	412
Qy	302	TGGCTTTGGCAGATGCTTTAGTTACTATCAACCAATGCCCTTTCAGAGTACGGTCTACTTGA	361
Db	413	TGGCTTTGGCAGATGCTTTAGTTACTATCAACCAATGCCCTTTCAGAGTACGGTCTACTTGA	472
Qy	362	TGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATATGTAATTTCCATTGATTACTACA	421
Db	473	TGAATTCCTGGCCTTTTGGAGATTTCTGTGCAAGATATGTAATTTCCATTGATTACTACA	532
Qy	422	ACATGTTCAACGAGATCTTCACTTGCACATGATGAGGGCGAGACCGCTACATTTGGCGTGT	481
Db	533	ACATGTTTACAGCATATTCACCTTTGACCAATGATGAGTGTGACCGCTTACATTTGCCGTGT	592
Qy	482	GCCACCCCGTGAAGGCTTTGGACTTTCCGACACACCTTGAAGCAAAAGATCATCAATATCT	541
Db	593	GCCACCCCTGTGAAGCTTTGGATTTCCGAAACACCTTGAAGCAAAAGATCATCAATATCT	652
Qy	542	GCATCTGGCTCTGTCTGTATCTGTGGCATCTCTGCATATGTCTTTGGAGGACCAAG	601
Db	653	GCATTTGGCTCTGTGGCATCATCTGTGTATATCAGGCATATGTCTTTGGGAGTACCAC	712
Qy	602	TCAGGSAAGAGTGGATGTCAATTAAGTGTCTTGCAGTTCGCAATGATGATCACTACTCT	661
Db	713	CCCGGATGAGAGCAGTGGTATGACAGCGCTCAAGTTCGCCAGCC-----CAGTGT	763
Qy	662	GATGGGACCTTTCATGTAAGATCTGCGCTTCATCTTTGCTCTGTGATTCCTGTCTCA	721
Db	764	ACTGGGACACTGTATCCAAAGATCTGCGCTTCATCTTTGCTGTGATTCCTGTCTCA	823
Qy	722	TCATCATCTGTCTGCTACACCTGTATGATCTGTGCTCTCAGAGCGTCCGCTCCTTTCTG	781
Db	824	TCATCATCTGTCTGCTACACCTGTATGATCTGTGCTCTCAGAGCGTCCGCTCCTTTCTG	883
Qy	782	GCTCCCGAGAAAGATGCGAACCTGGGTAGAGTACACGAGCTGGTCTCGTGGGTG	841
Db	884	GCTCCCGAGAAAGATGCGAACCTGGGTAGAGTACACGAGCTGGTCTCGTGGGTG	943
Qy	842	CAGTCTTGTGTGTGTGCTGAGCTCCCATTCATATTCATCTGTGTGAGGCTCTGGGGA	901
Db	944	CAGTCTTGTGTGTGTGCTGAGCTCCCATTCATATTCATCTGTGTGAGGCTCTGGGGA	1003
Qy	902	GCACTCTCCACAGACACAGCTGCTCTCTCCAGCTATTACTTTGCACTGCGCTTAAAGCTATA	961
Db	1004	GCACTCTCCACAGACACAGCTGCTCTCTCCAGCTATTACTTTGCACTGCGCTTAAAGCTATA	1063
Qy	962	CCAACAGTAGCCTGAATCCCATTTCTTAAGGCTTTTGAAGAAACCTTCAAGCGGTGT	1021
Db	1064	CCAACAGTAGCCTGAATCCCATTTCTTAAGGCTTTTGAAGAAACCTTCAAGCGGTGT	1123
Qy	1022	TCGCGGACCTTGTGCTTTTCACTGAAGATGAGATGAGCGGACAGACACTAGACAGATCC	1081
Db	1124	TCGCGGACCTTGTGCTTTTCACTGAAGATGAGATGAGCGGACAGACACTAGACAGATCC	1183
Qy	1082	GAAATACAGTTCAAGATCTGTCTTACCTGAGGGAACATGATGGATGTAATAAACAGTAT	1141
Db	1184	GAAATACAGTTCAAGATCTGTCTTACCTGAGGGAACATGATGGATGTAATAAACAGTAT	1243
Qy	1142	G 1142	
Db	1244	G 1244	

RESULT 18

US-10-318-661-13

Sequence 13, Application US/10318661

GENERAL INFORMATION:

APPLICANT: Conklin,

; TITLE OF INVENTION: Selective Target Cell Activation By

TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated

10 TITLE OF INVENTION: Superiorly By Synthetic Ligand

FILE REFERENCE: UCAL-049C1P2

```

; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ro3 (Rig)
US-10-318-661-13
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Query Match      85.0%; Score 981; DB 15; Length 1875;
Best Local Similarity 92.6%; Pred. No. 9e-274;
Matches 1045; Conservative 0; Mismatches 75; Indels 9; Gaps 1;
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QY 15 CCAAGATCTTCCGCGGAGAGCCGCGCTTAACTGCGCCCGGAGCGCTGCTGCCCCCAA 74
DB 756 CGAGCTGTACCGCGGGAGCCGGGCTTAACCTGCGCCCGAGCGCTGCTGCCCCCAA 815
QY 75 CAGCAGCGCCCTGCTTCCCGGCTGGGCGGCGGAGCGGAGCGGAGCGGCGGCTCGGA 134
DB 816 CAGCAGCGCCCTGCTTCCCGGCTGGGCGGAGCGGCGGAGCGGAGCGGCGGCTCGGA 875
QY 135 GAGCAGCGAGCTGAGCGCCGCGCACATCTCCCGGCGCATCCCGGCTCATCTACGCGCGT 194
DB 876 GAGCAGCGAGCTGAGCGCCGCGCACATCTCCCGGCGCATCCCGGCTCATCTACGCGCGT 935
QY 195 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTGCGTGTGATGTTCTGATCAT 254
DB 936 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTGCGTGTGATGTTCTGATCAT 995
QY 255 CCGATACCAAGATGAGAGAGCAACCAATTATTAACCTGCGCTTGGGCGA 314
DB 996 CCGATACCAAGATGAGAGAGCAACCAATTATTAACCTGCGCTTGGGCGA 1055
QY 315 TGCCTTAGTACTACCAACCATGCGCTTTCAGAGTACGCTTCACTTATGAAATTCCTGGCC 374
DB 1056 TGCCTTAGTACTACCAACCATGCGCTTTCAGAGTACGCTTCACTTATGAAATTCCTGGCC 1115
QY 375 TTTTGGGAGTGTCTGTGCAAGATGATATTTCAATGTTATCTAACAATGTTCAACAG 434
DB 1116 TTTTGGAGATGTTCTGTGCAAGATGTTCAATGTTCAATGTTCAACAATGTTTACAG 1175
QY 435 CATCTTCACTTGAACATGATGAGGAGGAGCGGCTAACATGCGGAGTGCACCCGGTAA 494
DB 1176 CATCTTCACTTGAACATGATGAGGAGGAGCGGCTAACATGCGGAGTGCACCCGGTAA 1235
QY 495 GGCCTTTGAGCTTCCGACACCCCTTGAAGGCAAGATCATCATATCTGATCTGCTGCT 554
DB 1236 AGCTTTGAGATTTCCGAACACCTTTGAAGGCAAGATCATCATATCTGATCTGCTGCT 1295
QY 555 GTGCTGATCTGTGGCACTCTGCAATATGCTCTTGAAGGCAACAAAGTCAAGGAAGAGCT 614
DB 1296 GGCATCATCTGTTGGTATATCAGCATAGTCTTGGGAGTGAACCAACCCCGGAGTGAAGC 1355
QY 615 CGATGTCATATGAGTCTCTTGCAGTTCCTCAATATGATGATGATGATGATGATGATGAT 674
DB 1356 AGTGTATGACAGCTTCAGTTCCTCAATATGATGATGATGATGATGATGATGATGATGAT 1406
QY 675 CATGAGATCTGCGCTTTCATCTTTCCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 734
DB 1407 GACCAAGATCTGCGCTTTCATCTTTCCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1466
QY 735 CTACACCTGATGATCTGCGCTTCAAGAGCTCGGCGCTCTTTCGCTGCTCGGAGAA 794
DB 1467 CTACACCTGATGATCTGCGCTTCAAGAGCTCGGCGCTCTTTCGCTGCTCGGAGAA 1526
```

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QY 795 AGATCGCAACTGCGTAGATGATCACCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 854
DB 1527 AGATCGCAACTGCGTAGATGATCACCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1586
QY 855 CTGCTGAGCTCCCAATTCATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
DB 1587 CTGCTGAGCTCCCAATTCATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1646
QY 915 CACAGCTCTCTCCAGCTATTTCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
DB 1647 CACAGCTCTCTCCAGCTATTTCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1706
QY 975 GAATCCCATCTCTACGCTTCTTGTGATGAAACCTTCAAGCGGTGTTTCCGGGACTTCTG 1034
DB 1707 GAATCCCATCTCTACGCTTCTTGTGATGAAACCTTCAAGCGGTGTTTCCGGGACTTCTG 1766
QY 1035 CTTTCCACTGAAAGATGAGATGAGCGGAGAGCACTAGCAGAGTCCGAATTAACATTCA 1094
DB 1767 CTTTCCACTGAAAGATGAGATGAGCGGAGAGCACTAGCAGAGTCCGAATTAACATTCA 1826
QY 1095 GGATCTCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGATATGA 1143
DB 1827 GGATCTCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGATATGA 1875
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RESULT 19

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US-10-318-661-15
; Sequence 15, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Konklin, Bruce R.
; TITLE OF INVENTION: Selection Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ro3A (Rig A)
US-10-318-661-15
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Query Match      83.6%; Score 965; DB 15; Length 1875;
Best Local Similarity 91.7%; Pred. No. 4e-269;
Matches 1035; Conservative 0; Mismatches 85; Indels 9; Gaps 1;
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QY 15 CCAAGATCTTCCGCGGAGAGCCGCGCTTAACTGCGCCCGGAGCGCTGCTGCCCCCAA 74
DB 756 CGAGCTGTACCGCGGGAGCCGGGCTTAACTGCGCCCGAGCGCTGCTGCCCCCAA 815
QY 75 CAGCAGCGCCCTGCTTCCCGGCTGGGCGGAGCGGAGCGGAGCGGCGGCTCGGA 134
DB 816 CAGCAGCGCCCTGCTTCCCGGCTGGGCGGAGCGGAGCGGAGCGGCGGCTCGGA 875
QY 135 GAGCAGCGAGCTGAGCGCCGCGCACATCTCCCGGCGCATCCCGGCTCATCTACGCGCGT 194
DB 876 GAGCAGCGAGCTGAGCGCCGCGCACATCTCCCGGCGCATCCCGGCTCATCTACGCGCGT 935
QY 195 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTGCTGATGTTCTGATCAT 254
DB 936 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTGCTGATGTTCTGATCAT 995
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255 CCGATACCAAGATGAGAGACAGCAACCAATTTACATATTTAACTGGCTTTGGACGA 314
CGATACCAAGATGAGAGACAGCAACCAATTTACATATTTAACTGGCTTTGGACGA 1055
315 TGCCTTAGTACTACCAACCATGCGCTTTCAGAGTACGGTCTACTGTAAGTAATTCCTGGCC 374
TGCCTTAGTACTACCAACCATGCGCTTTCAGAGTACGGTCTACTGTAAGTAATTCCTGGCC 1115
375 TTTTGGGATGTCGTGTGCAAGATGTAATTTCCATTGTTACTACACATGTTCCACG 434
TTTGGAGATGTCGTGTGCAAGATGTAATTTCCATTGTTACTACACATGTTCCACG 1175
435 CATCTTCACTTGAACATGATGAGGTGAGCCGCAACATTTGCCGTGTGCAACCGGTGA 494
CATATTTCACTTGAACATGATGAGGTGAGCCGCAACATTTGCCGTGTGCAACCGGTGA 1235
495 GGCCTTTGACCTTCCGACACCCCTTGAAGCAAGATCATCATATCTGCATCTGCTGCT 554
AGCTTTGGATTTCCGAAACCTTTGAAGCAAGATCATCATATCTGCATTTGGCTACT 1295
555 GTGCTCATCTGTGGCATCTCTGCAATAGTCTTTGAGGACCAAAAGTCAGGAAAGCT 614
GGCATCATCTGTGGATATACGAGTAGTCTTGGGGTGAACCAACCCGGAGTGAAC 1355
615 CGATGCAATGAGTGTCTCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 674
AGTGTATGACACCTTCACCTTCCCAAGCTT-----CAGCTGTATGAGCACTGT 1406
675 CATGAAGATCTGCTCTTCTCATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 734
GACCAAGATCTGCTCTTCTCATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1466
735 CTACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
CTACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1526
795 AGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 854
AGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1586
855 CTGCTGATCTCCCATTTACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 914
CTGCTGATCTCCCATTTACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1646
915 CACAGCTGCTCTCTCAAGTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 974
CACAGCTGCTCTCTCAAGTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1706
975 GAATCCCATTTCTCAAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1034
GAATCCCATTTCTCAAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1766
1035 CTCTTCCATGAGATGAGATGAGACCGGACAGACTAGCAGAGTCCGAATATACCTTCA 1094
CTTTCATCTGAGATGAGATGAGACCGGACAGACTAGCAGAGTCCGAATATGCTTCTCA 1826
1095 GGATCTCTGCTTACCTGAGGACATGATGGATGATGATGATGATGATGATGATGATGAT 1143
GGATCTCTGCTTACCTGAGGACATGATGGATGATGATGATGATGATGATGATGATGATGAT 1875

RESULT 20
US-09-214-904-5
Sequence 5, Application US/09214904
Patent No. US20010047519A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
TITLE OF INVENTION: OF OPATE RECEPTORS IS MODIFIED
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/214,904
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR97/01282
FILING DATE:
APPLICATION NUMBER: FR 96.08810
FILING DATE: 15-JUL-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1323
US-09-214-904-5
Query Match 78.9%; Score 910.8; DB 9; Length 1408;
Best Local Similarity 86.8%; Pred. No. 1.9e-253;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
1 ATGACCTCCCGATCCAAATCTTCCGCGGAGCCGGGCTTACTGCGCCCGAGCGCC 60
184 ATGAGATCCCATTCAGATCTTCCGAGAGATCCAGGCCCTTACTGCTCTCCAGTGT 243
61 TGCCTGCCCCCAAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
244 TGCCTTCTCCCAAGAGAGCTTGTGTTCCCACTGAGGAGATCCGACGTAATGAGC 303
121 AGCGCGGCTGAGAGAGCGAGCTGAGAGCGCGGACATCTCCCGGACATCCCGGTC 180
304 AGTGGGCTCAGAGATCAGAGAGTGAAGTCCGGGACATCTCCCGGACATCCCGTGT 363
181 ATCATCAGCGGCTTACTCGGTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
364 ATCATCAGCGGCTTACTCGGTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
241 ATGTCGATCATCCGATACCAAGATGAAAGAGAGCAACCAATTTACTATTTAAC 300
424 ATGTTGATCATCCGATACCAAGATGAAAGAGAGCAACCAATTTACTATTTAAC 483
301 CTGCTTTGGAGATGCTTTAGTACTCAACCATGCTCTTTCAGAGTACGCTTACTTGG 360
484 CTGCTTTGGAGATGCTTTAGTACTCAACCATGCTCTTTCAGAGTACGCTTACTTGG 543
361 ATGAATCTCGGCTTTTGGGAGTGTCTGCAAGATGATGATGATGATGATGATGATGATG 420
544 ATGAATCTCGGCTTTTGGGAGTGTCTGCAAGATGATGATGATGATGATGATGATGATG 603
421 AACATGTTACAGAGATCTTACCTTGAACATGATGATGATGATGATGATGATGATGATG 480
604 AACATGTTACAGAGATCTTACCTTGAACATGATGATGATGATGATGATGATGATGATG 663
481 TGCACCCCGTGAAGGCTTTTGGACTTCCGACACCTTGAAGGCAAAATCATCATATTC 540
664 TGCACCCCGTGAAGGCTTTTGGACTTCCGACACCTTGAAGGCAAAATCATCATATTC 723
541 TGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
724 TGCATTTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
601 GTGCGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
784 GTGCGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843
661 TGTGGGACCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720


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/ Sequence 188121, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO: 188121
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188121
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Query Match      40.8%; Score 470.6; DB 13; Length 585;
Best Local Similarity 99.8%; Pred. No. 6.9e-126;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 684 CTGCGCTTTCAATCTTTCCTTCTGATATCCCTCTCCATCATCATGCTGTACACCT 743
DB 585 CTGCGCTTTCAATCTTTCCTTCTGATATCCCTCTCCATCATCATGCTGTACACCT 526

QY 744 GATGATCTGCGCTTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 803
DB 525 GATGATCTGCGCTTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 466

QY 804 CTGCGTGAAGATCAACAGACTGCTCTGATGATGAGTCTTCTGCTGTGAC 863
DB 465 CTGCGTGAAGATCAACAGACTGCTCTGATGATGAGTCTTCTGCTGTGAC 406

QY 864 TCCCATTCACATATTCAATCTGATGAGGCTCTGGGAGACCTCCACAGACAGCTGC 923
DB 405 TCCCATTCACATATTCAATCTGATGAGGCTCTGGGAGACCTCCACAGACAGCTGC 346

QY 924 TCTCTCAGCTATTACTTCTGATGAGCTTGAAGCTTAAACAGTACAGTACCTGAT 983
DB 345 TCTCTCAGCTATTACTTCTGATGAGCTTGAAGCTTAAACAGTACAGTACCTGAT 286

QY 984 TCTCTACGCTTTCTTGAATGAAAACCTTCAAGGGGTCTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGAATGAAAACCTTCAAGGGGTCTTCCGGGACTTCTGCTTCCACT 226

QY 1044 GAAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCCGAATATACAGTTCAAGATCTGC 1103
DB 225 GAAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCCGAATATACAGTTCAAGATCTGC 166

QY 1104 TTACCTGAGGACATCGATGGATGAAATTAACAGTATGACTAGTCTGGA 1154
DB 165 TTACCTGAGGACATCGATGGATGAAATTAACAGTATGACTAGTCTGGA 115
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RESULT 23
US-10-027-632-188121/c
/ Sequence 188122, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO: 188122
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188122
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Query Match      40.8%; Score 470.6; DB 13; Length 585;
Best Local Similarity 99.8%; Pred. No. 6.9e-126;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 684 CTGCGCTTTCAATCTTTCCTTCTGATATCCCTCTCCATCATCATGCTGTACACCT 743
DB 585 CTGCGCTTTCAATCTTTCCTTCTGATATCCCTCTCCATCATCATGCTGTACACCT 526

QY 744 GATGATCTGCGCTTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 803
DB 525 GATGATCTGCGCTTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 466

QY 804 CTGCGTGAAGATCAACAGACTGCTCTGATGATGAGTCTTCTGCTGTGAC 863
DB 465 CTGCGTGAAGATCAACAGACTGCTCTGATGATGAGTCTTCTGCTGTGAC 406

QY 864 TCCCATTCACATATTCAATCTGATGAGGCTCTGGGAGACCTCCACAGACAGCTGC 923
DB 405 TCCCATTCACATATTCAATCTGATGAGGCTCTGGGAGACCTCCACAGACAGCTGC 346

QY 924 TCTCTCAGCTATTACTTCTGATGAGCTTGAAGCTTAAACAGTACAGTACCTGAT 983
DB 345 TCTCTCAGCTATTACTTCTGATGAGCTTGAAGCTTAAACAGTACAGTACCTGAT 286

QY 984 TCTCTACGCTTTCTTGAATGAAAACCTTCAAGGGGTCTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGAATGAAAACCTTCAAGGGGTCTTCCGGGACTTCTGCTTCCACT 226

QY 1044 GAAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCCGAATATACAGTTCAAGATCTGC 1103
DB 225 GAAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCCGAATATACAGTTCAAGATCTGC 166

QY 1104 TTACCTGAGGACATCGATGGATGAAATTAACAGTATGACTAGTCTGGA 1154
DB 165 TTACCTGAGGACATCGATGGATGAAATTAACAGTATGACTAGTCTGGA 115
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RESULT 24
US-10-027-632-188121/c
/ Sequence 188121, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
```



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/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/841,720
/ FILING DATE: 24-Apr-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/120,601
/ FILING DATE: 13-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: INDA:002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1618 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 214..1407
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-841-720-1
Query Match      38.7%; Score 446.4; DB 10; Length 1618;
Best Local Similarity 66.9%; Pred. No. 1.2e-118;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
QY 110 ACAGCAGCGGCGGCGGCTGCGAGAGAGCGGCGAGCTGGAGCCCGGCAATCTCCCGG 169
DB 350 ACCGACCGGCGGCTTGCGGAGAGAGAGCGGCTTGCGGCGGCGGCGGCGGCGGCGG 409
QY 170 CCATCCCGGCTCATCATCAGCGGCGGCTTACTCCGTAAGTTCGTCGTGGCGTTGGTGGCA 229
DB 410 TCACAGCATTAACATCATGAGCGGCGGCTTACTATGATGATGATGATGATGATGATGATG 469
QY 230 ACTCGGTGTCATGTTCTGTCATCATCCATACAAAGATGAAGACAGACCAACATTT 289
DB 470 ACTTCCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
QY 290 ACATATTTAAGCTGCTTTGGAGAGATGCTTTAGTACTACAAACATGCGCTTTGAGAGTA 349
DB 530 ACATTTTCAACTCTCTCTGCGAGAGCGCTTAGCAGCAGTACACGCTGCGCTTTGAGAGTG 589
QY 350 CGGTCTACTGATGATTCCTGCGCTTTTGGGAGATGCTGTCGAAGATAGTAATTTCA 409
DB 590 TCAACTTACTGATGAGAGATGAGCGCTTCTCGAAGATGATGATGATGATGATGATGATGATG 649
QY 410 TTGATTTACTACAAATGTTTACACAGCATCTTACCTTGACATGATGAGCGTGAACGCT 469
DB 650 TAGATTACTACAAATGTTTACACAGCATCTTACCTTGACATGATGAGCGTGAACGCT 709
QY 470 ACATGCGGTGTCGAGCGGCGGAGAGGCTTTGAGATCTTCCGACACACCTTTGAGAGTA 529
DB 710 ACATGCGGTGTCGAGCGGCGGAGAGGCTTTGAGATCTTCCGACACACCTTTGAGAGTA 589
QY 530 TCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
DB 770 TCGTCAAGGTGTCGAGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 829
QY 590 GAGGACCAAAAGTCAAGGAGAGAGCGTGAATGATGATGATGATGATGATGATGATGATGATG 649
DB 830 CAACCAAAATTAAGGAGGCGGCGGCTC-----CATAGATTGACACCTCTCAGCTTCTCCACC 883

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QY 650 ATGACTACTCTGATGAGACCTTTCAATGAGATGCGGTCTTCACTTTGCTTGTGA 709
DB 884 CAACCTGCTACTGAGAGAGAGCTGCTC---AAATCTGCTGCTTTATCTTCTGCTTCAATCA 940
QY 710 TCCCTGCTCTCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
DB 941 TCCCATCTCTCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
QY 770 GCGCTCTTTGCGGCTCCGAGAGAGAGATGCGCAACCTGCTGATGATGATGATGATGATGATG 829
DB 1001 GCATCTTATCGGCGCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1060
QY 830 TGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 889
DB 1061 TGGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120
QY 890 AGGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 949
DB 1121 AAGCGCTGATCAGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1180
QY 950 CCTTAGGCTTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009
DB 1181 CTTGGGCTTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1240
QY 1010 TCAAGCGGTGTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1069
DB 1241 TCAAGCGGTGTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1300
QY 1070 CTAGCAGAGTCCGAATTAAGTTCAGATCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1358

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RESULT 27
US-09-841-720-3
/ Sequence 3, Application US/09841720
/ Publication No. US20030068672A1
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Lei
/ TITLE OF INVENTION: MU OPTOID RECEPTORS: COMPOSITIONS AND METHODS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: P.O. Box 4433
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/841,720
/ FILING DATE: 24-Apr-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/120,601
/ FILING DATE: 13-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: INDA:002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1618 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single

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TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1232
SEQUENCE DESCRIPTION: SBO ID NO: 3
US-09-841-720-3

Query Match 38.7%; Score 446.4; DB 10; Length 1618;
Best Local Similarity 66.9%; Pred. No. 1.2e-118;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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110 ACAGCAACGCGACGCGGCTGCGAGAGACGCGAGCTGAGCCCGGACATCTCCCGG 169
350 ACGGACCGCGGCTTGCGGGGAAACGACAGCTTGCCCTAGACCGGACCTTCCATG 409
170 CCATCCCGGTCATCATCAGCGGCTTACTCCGTAGTGTTCGTGCGCTTGAGGCA 229
410 TCACAGCCATACCATCATGCGCTTACTCTATCGTGTGTAGTGGGCTTCCGGA 469
230 ACTCGGTGTCATGTTCCGTGATCCGATACAAAGTGAAGACAGCAACCAATT 289
470 ACTCCGTGTCATGATGTGATGTGAATACACAAATGAAGCTGCCACCAATCT 529
290 ACATATTTACCTGCTTGCGAGATGCTTAGTTACTACACCAATGCCCTTGAAGTA 349
530 ACATTTTCACTTGTCTGCGAGAGCGCTTAGCGACAGTACACTGCCCTTTCAGATG 589
350 CGGTCTACTTGATGAATTCCTGGCTTTGGGAGATGCTGTGCAAGATGATTTCCA 409
590 TCACATCTACTGATGGAACATGCGCTTGGAAACATCTCTGCAAGATGCTGATCTCA 649
410 TTGATTACTACAAACATGTTACACAGATCTTACCTGACCATGATGAGCGTGACGCT 469
650 TAGATTACTACAAACATGTTACACAGATATTCACCTCTGCAACATGAGCGTGACGCT 709
470 ACATTCGCGTGTGCGACCGCGTGAAGGCTTGAAGCTTGCACACCTTGAAGGAAAG 529
710 ACATTGCTGTGCGACCGCAAGTCAAAAGCCCTGATTCGATACCCCGGAAATGCAAAA 769
530 TCATCAATATCTGCAATCTGCGTGTGTGTCATCTGTTGGCAATCTCTGCAATAGTCTTG 589
770 TCGTAAAGTCTGCAACCTGATCTCTCTTCTGCAATGCTGTGCTTAATGTTTCATG 829
590 GAGGACCAAAAGTCAAGGGAAGACGTCATGATGAGTGCCTTGAAGTCCCAAGT 649
830 CAACCAAAATATACAGGAGGAGGCTC-----CATGATTTGACCTCTCAAGTCTTCCAAC 883
650 ATGACTACTCTGATGAGGACCTCTTCAAGATCTGCGTCTTCAATCTTGTGCTGTA 709
884 CAACCTGATCTGGAAGAACTGCTC---AAATCTGTGTCTTAACTTCTGCTTTCATCA 940
710 TCCGTGTCTCATCATCTGCTGTCTACCTGATGATCTGCGTCTCAAGAGCTGC 769
941 TCCCATCTCTATCATCTGCTGTGTACGCGCTGATGATCTTACGATCAAGAGCTGTC 1000
770 GGCCTCTTTCGCGCTCCGAGAGAAAGATCGCACTGAGATGATCAACGAGCTGCGC 829
1001 GCATCTTATCGGCTTCAAAAGAAAGACAGAAATCTGCGAGATCAACCGGATGCTGC 1060
830 TGTGTGTGTGAGCTGCTGTGTCTGTCTGAGCTCCCATTCACATATTCCTGATG 889
1061 TGTGTGTGTGAGCTGCTGTGTATGCTGTGTGAGTCCCATCAATCTGATGATCA 1120
890 AGGCTCTGGGAGACCTTCCACAGCAAGCTGCTCTTCCAGCTATTAATCTTGATG 949
1121 AAGGCTGTATCAAGATTCAGAAACCAATTCAGACCGTTCCTGGGACATTCGCAATG 1180
950 CCTTAGGCTATACCAAGATGAGCTGAATCCATCTCTAGCGCTTGTGATGAAACT 1009
1181 CTTTGGGTTACAGCAAGCTGCTGATTCAGATTCATGCTTCTTGAAGTGAAGT 1240
1010 TCAAGCGTGTCTTCCGAGCTTCTGCTTTCATGAGATGAGATGAGGCGGAGCA 1069
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DB 1241 TCAGCGATGCTTACAGAGATTTCTGATCCCACTGCTCCAGCATGCAAGCAAACT 1300
QY 1070 CTAGCAGATCCGAAATACAGTTCCAGATCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTGACAACTAGGGAACATCCCTCC 1338
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RESULT 28

US-10-185-083-25
; Sequence 25, Application US/10185083
; Publication No. US2003050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Paternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 83002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-185-083-25

Query Match 37.8%; Score 436.2; DB 15; Length 1464;
Best Local Similarity 64.7%; Pred. No. 1e-115;
Matches 683; Conservative 0; Mismatches 363; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGACCGGACAGCAACGCGCGGCTCGAAGACGCGCACTGAGC 151
DB 174 CCGACCATGGGATCCGAACCGCACGACCTGGGCGGAGAGACGCTGACCTCCGA 233
QY 152 CCGGCAATCTCCCGGCAATCCCGGTCATCATCAAGGGGCTACTCCGTAGTGTG 211
DB 234 CCGGCAATCTCCCATATATACCGGCATCAAGATCAAGATGAGGCTTACTCATGCTGCG 293
QY 212 TCGGAGGCTTGATGAGCAATCGCTGCTCATGTTCTGATCATCCGATACAAAGATGA 271
DB 294 TGTGTGGGCTCTTGGAAATCTCTGATCATGATGTGATGTGATGATGATGATGATG 353
QY 272 AGACAGCAACCAATTTAATATTAACTGCTTTGGCAAGTCTTATGTTAATA 331
DB 354 AGACTGCACCAACATCATATTTCACCTGCTGCGAGATGCTTAGCCACAGTA 413
QY 332 CCATGCGCTTTCAGATGAGTCTACTGTGATGATTCCTGAGCTTTTGGGATGTGCT 391
DB 414 CCGGCGCTTTCAGATGAGTCTACTGTGATGATTCCTGAGCTTTTGGGATGTGCT 473
QY 392 GCAAGATGATTAATTTCAATGATTTACTACAAATGTTCAACAGATCTTACCTGACCA 451
DB 474 GCAAGATGATGATCTCATATGATTTATCATATAATGTTCAACAGATTTACCTCTGCA 533
QY 512 TGAATGAGTGAACCGCTTACATGCTGCTGTGCAACCGCTGAAAGCTTTGAACTTCCGA 511
DB 534 CCAATGATGTTGATTCGATATCATGATGCTGCAACCGCTTCAAGGCTTATGATTCGTA 593
QY 512 CACCTTGAAGGCAAGATATCATATATCTGATCTGAGCTGCTGTGATCTGTTGGCA 571
DB 594 CTCCCGCAATATGCAAAATATATATATATATATATATATATATATATATATATAT 653
QY 572 TCTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAAAGAGTGTGATGATGAGTCT 631
DB 654 TTCTCTGATATGTTTCAATGCTACAAACAAATACAGGCA-----GTTTCAATGATGTA 707
QY 632 CTTTGAAGTCCAGATGATGATCTCTCTGTTGGGACCTTTCAATGAGATCTGCGTCT 691
DB 708 CACTTAATCTCTC---TCATCAACCTGTGATGAGGAAACCTGTAAGATCTGTGTTT 764
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; PRIOR FILLING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/336,677
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-080-917-10

```

Query Match	37.7%;	Score 434.8;	DB 15;	Length 1239;
Best Local Similarity	66.3%;	Pred. No. 2.5e-115;		
Matches 660;	Conservative 0;	Mismatches 327;	Indels 9;	Gaps 2

OY		92	CCGGCTGGGCGCAGACCCGCACAGCAAGGACGCCCGCTTCGGAGACGCGACCTGGAGC	151
Dd		119	CCGACCATTGCGCGGTCCGGAACCGCACCGACTCTGGGCGGAGAGAAGCTGTGCCCTCCGA	178
OY		152	CCGCGCAGCATCTCCCCGGGCGCATCCGGGTATCATACAAGGCGGTCTACCTCGTATGTTTG	211
Dd		179	CCGGCAGTCCCTTCATGATACACGGCCATCCAGATCAATGGCCCTCTACTCATGTGTGGCG	238
OY		212	TGCTGGGCTTGGTGGGCACTCGCTGGTCATGTTCTGTGATCATCCCATACACAAAGATGA	271
Dd		239	TGCTGGGCTCTTCGGAACTTCCTGTGATGATGATGATGATGATGATGATGATGATGATGATG	298
OY		272	AACACAGCAACCAACATTTACATTTTAACCTGGCTTTGGCAGATGCTTTAATTACTAAC	331
Dd		299	AACATGCCAACCAACATCTACATTTTCAACCTTGCTCTGGGAGATGCTTAGCCACCAAGTA	358
OY		332	CCATGCCCCTTACAGAGTACGAGTCTACTGTATGAATTCCTGGCCCTTTGGGGAGATGTCGT	391
Dd		359	CCCTGCCCCCTCAGAGTGTGAATTTACTTAATGGAAACATGGCCATTGGAAACCATCTTT	418
OY		392	GCAAGATAGTAATTTTCATTTGATTTACTACAAACATGTTCAACAGACATTTTCACTTGACA	451
Dd		419	GCAAGATAGTATCTTCATAGATTACTATAACATGTTCAACAGCATATTCAACCTCTGCA	478
OY		452	TGATAGCGTGGACCGCTACATTCGCGTGTGCCACCCCGTGAAGGCTTTGACTTCGCA	511
Dd		479	CCATAGGTGTATGATACATTCATTTGACGTGGCCACCTGTCAAAGGCTTAGATTTCCGTA	538
OY		512	CACCCCTGAAGGCAAAAGATCATCAATATCTGCATCTGGCGCTGTGCTATCTGTTGGCA	571
Dd		539	CTCCCCGAATATCCAAAATTATCAATGTCTGCACCTGGATCTCTCTTTCAGCCATTGGTC	598
OY		572	TCTCTGCAATAGTCTCTTGGAGGCAACCAAGTCAGGGAAGCGTCGATGTCAATTGACTGTCT	631
Dd		599	TTCCTGTATGTTCATGCTTACAAACAAATATACGGCAAG-----TTCATATGATTTGA	652
OY		632	CCTTGCAGTGCCCAATGATGACTACTCCTGTGTGGACCTCTTTCAATGAAGATCTGTGCT	691
Dd		653	CACTAACATCTCTCATCCCAACCTGGTACTGGAAAACTGCG--TGAAGATCTGTGTTT	709
OY		692	TCATCTTGGCTTCGTGATACCTCTGTCTCATCATCATCTCTGTCTACACCTCGATATGCC	751
Dd		710	TCATCTTGGCTTCAATTATGCCAGTGTCAATTAACCTGTGTCTATGSACTGTATGATCT	769
OY		752	TGCGTCTCAAGAGCGTCCGGCTCTTTTCTGCTCCCGAGAGAAAGATGSCAACTTGCGTA	811
Dd		770	TGCGCTCAAGAGTGTCCGATGCTCTCTGCTCCAAAAGAAAGACAGAGATCTTCGAN	829
OY		812	GGATACACAGACTGGTCTCGTGTGTGTGTGTGTGGGACGTCTTGTGTGTGTGTGTGTGTGT	871
Dd		830	GGATACACAGAGT	889
OY		872	ACATATTCATCTGTGTGAGGCTCTGGGGAGACCTCCACAGCAACAGTGTCTCTCTCCA	931
Dd		890	ACATTTAGTATCATTTAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	949
OY		932	GCTATTACTTGTGATGCGCTTAGGCTATACCAACAGTAGCCTGAATCCCATTTCTTAG	991

Db 950 CTGGCACTTCGATTCCTCTAGATTACACAAACAGCTGCCTCAACCGACTCTTTATG 1009

Qy 992 CCTTCTTGATGAATACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGA 1051

Db 1010 CATTCTCGAAGAAACCTCAACGAAGCTTCAAGAGTTCTGTATCCCACTTTCCA 1069

Qy 1052 GGATGAGCGGCAGAGCACTAGCAGAGTCCGAAATA 1087

Db 1070 ACATTGAGCAACAAACTCCACTCGAATTTGCTCGA 1105

RESULT 31
US-10-080-917-8

Query Match	37.7%	Score 434.8;	DB 15;	Length 1245;
Best Local Similarity	66.3%;	Pred. No. 2.5e-115;		
Matches 660;	Conservative 0;	Mismatches 327;	Indels 9;	Gaps 2;

Qy	92	CCGGCTGGGGCCGAGCCCGACACGACCGGACGCGCGAGTCGGAGAGACGCGAGCTGGAGC	151
Db	125	CCGACCCCATGCGGATCCGAAACCGCACCGACCTGGGCGGGAGAGACGAGCTGTGCCCTCCGA	184
Qy	152	CCGCGCACATCTCCCCGGCCATCCCGGATCATCAACGGCGATCTACTCGTAGTGTTCG	211
Db	185	CCGGCAGTCCCTCCATGATCAACGGCATTACGATCAAGGCCCTTACTCCATGATGTGGC	244
Qy	212	TGCTGGGCTTGGTGGGCAACTGCGCTGTCATGTTCTGTATCATCCGATACCAAAAGTGA	271
Db	245	TGGTGGGGCTCTTCGAAAATTCCCGGACGATGATGGAATGTGCAGATACCAAGATGA	304
Qy	272	AGACAGCAACCAACATTTACATATTTAACTCGGCTTTGGGAGATGCTTATGTTACTACAA	331
Db	305	AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGCGAGATGCTTGGCCACACAGTA	364
Qy	332	CCATGCCCTTTGAGATACGGCTCTACTGATGAATCTCTGGCCTTTTGGGGAATGTGCTGT	391
Db	365	CCCTGCCCTTCAGAGTGTGAATTACCTAAAGGGAGATGGCCATTTGGAAACATCTT	424
Qy	392	GCAAGATAGTATTTCCATGATTAATCTACAAACATGTTCAACAGATCTTACCTTGACCA	451
Db	425	GCAAGTATGATCTCCATATGATTAATCTATACATGTTCAACAGATTAATCACTCTCGCA	484
Qy	452	TGATAGAGGTGACCGCTACATTTGCCGTGGCCACCCCGTGAAGGCTTTGAACTTCGCA	511
Db	485	CCATGAGTGTGATGATGATACATTCGACGTGCCACCTGTCAAGGCTTATGATTTCCGTA	544
Qy	512	CACCCTTGAAGGAAAGATCATCAATATCTGCACTGTGGCTGTGTGTATCATGTTGGCA	571
Db	545	CTTCCCCGAATGCCAAATATATCAATGTCTGGCACTGGATCTCTCTTTCAGCCATTGGTTC	604
Qy	572	TCTCTGCAATAGTCTTGGAGGCAACAAATCAGAGGAAGACGTGATGTCATTAGAGTCT	631
	605	TTCTCGTATGTTATGTGCTACCAACAAATACAGGCAAG-----TTCCATGATTTGA	658

Qy	632	CCCTGGACGTTCCCAAGATGATGACTACTCCTGGTGGAGCCTCTTTCATGAAGATCTGGCTCT	691
Db	659	CAGTAACATTTCTCATCCAACCTGGTAAGTGGGAAAACTGTC--TGAAGATCTGTGTTT	715
Qy	692	TCATCTTGGCCTTCGTGATCCCTGTCTCATCATCATCGTCTGTCAACCCGTGATGATCC	751
Db	716	TCATCTTGGCCTTCATTTATGCAAGTGTCTCATTTAACGTGTGGCTATGAGACGTGATGTCT	775
Qy	752	TGCGTCTCAAGAGCGTCCGGCTTCCTTTCTGGCTCCCGAGAGAAAGATGCGAACCTGGCTTA	811
Db	776	TGCGGCTCAAGAGGTGTCCGCATGCTCTCTGGGCTCCAAAAGGACAGGAATCTTCGAA	835
Qy	812	GGATCACCAGAGATGGGCTCGTGGTGGTGGTGGACAGTCTTGGTGGTGGTGGATCCCATTC	871
Db	836	GGATACACAGAGATGGTGTGCTGGTGGTGGTGGTGTGTGTTCATCGTCTGTGAGATCTCCCATTC	895
Qy	872	ACATATTCATCTGTGGTGGAGGCTCTGGGGAGACCTCCACAGACACAGTGTCTCTTCCA	931
Db	896	ACATTTAGGTGATCATTTAAAGCCTTGGTTACATCCACAAACTAGTTCCAGACTGTTT	955
Qy	932	GCTATTACTTCTGCGATCGCGCTTAGGCTATACCAACAGTAGCCGTGAATCCCATTTCTCTAG	991
Db	956	CTTGGACCTCTGCGATGTGCTTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG	1011
Qy	992	CCCTTCTTGATGAAAACTTCAGAACGCGATGTTTTCCGGGACTTCTGCTTTCACATGAAAGATGA	1051
Db	1016	CATTTCTGGATGAAAACTTCAGAACGATGTTCTAGAGAGTTCGTATCCCAACTCTTCCA	1071
Qy	1052	GGATGGAGCGCGACAGCACTAGACAGTCCGAAATA	1087
Db	1076	ACATTGAGCAACAAAACTCCATCGAAATTCGCAG	1111

```

RESULT 32
US-10-185-083-26
? Sequence 26, Application US/10185083
? Publication No. US20030050467A1
? GENERAL INFORMATION:
? APPLICANT: Memorial Sloan Kettering Cancer Center
? APPLICANT: Pasternak, Gavril
? APPLICANT: Pan, Yang-Xian
? TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
? FILE REFERENCE: 830002-2007.1
? CURRENT APPLICATION NUMBER: US/10/185,083
? CURRENT FILING DATE: 2002-06-28
? PRIOR APPLICATION NUMBER: 60/302,072
? PRIOR FILING DATE: 2001-06-29
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 26
? LENGTH: 1388
? TYPE: DNA
? ORGANISM: Homo Sapiens
US-10-185-083-26

```

Query Match	37.7%	Score 434.8;	DB 15;	Length 1388;
Best Local Similarity	66.3%	Pred. No. 2.6e-115;		
Matches 660; Conservative	0;	Mismatches 327;	Indels 9;	Gaps 2

QY	92	CCGCGTGGGCGAGGCCGACAGCAACAGGAGCGCGCTCCGAGGACCGGACGCTGGAGC	151
Db	174	CCGACCCCATGCGCGTCCGAACCGGACCGACCTGGGCGGAGACAGCGCTGTGCCCTCCGA	233
QY	152	CCGCGCACATCTCCCGGCGCATCCCGGTCATCTACAGGCGGTCATCTCGTATGTTTCG	211
Db	234	CCGGCAGTCCCTTCATGATCAGGCGCCATACGATCATGGGCCCTCTACCTCCATGTGTGCG	293
QY	212	TGCTGGGCTTGGTGGCACTCGCTGGTCATGTTCTGTATCATCCGATACACAAAGATGA	271
Db	234	TGGTGGGGCTCTTCGGAACCTTCGTGTATGTATGTGATTGTCAGATACCAAGATGA	353
QY	272	AGACAGCAACAACATTTTACATATTTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAA	331

Db	354	AGATGCGACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTACCCACAGTA	413
QY	332	CCATGACCCTTTCAGAGTACGGTCTACTGTGATGAATTCCTGGCCCTTTGGGAGTGTCTGT	391
Db	414	CCCTGCCCCCTTCAGACGTGTGAATTACCTAATGGGAACTGGCCATTGGAAACATCTCTTT	473
QY	392	GCAAGATATGTAATTTCCATTGATTACTTACACAAAGATTTCACCAAGACTTTCACCTTGAACA	451
Db	474	GCAAGATATGATCTCCATATGATTACTATATACATGTTTCACCGAGATATTTCCCTTCGCA	533
QY	452	TGATGAGGGTGAACCGGTACATTGCGGTGCGCAACCCCGTGAAGGCTTTGGACTTCCGCA	511
Db	534	CCATGAGGTGTGATCGATPACTTCGACGTGCGCACCCCTGTCAAGCCCTTGAATTTCCGTA	593
QY	512	CACCCCTTGAAGGCAAAAGTATCATTAATTCGATCTGGCTGCTGCTCATCTGTGTGACA	571
Db	594	CTCCCCGAAAGCCAAATTTATCAATGTCTGSCAACTGGATCTCTTTCAAGCCATTGGTC	653
QY	572	TCTGTGCAATAGTCTTTGGAGGCAACCAAGTCAGGGGAAGAGTCGATGTCAATTGAGTCT	631
Db	654	TTCCGTATATGTTTCATGGCTACAAACAAATTCAGGGCAAG-----TTCCATATGATTGTA	707
QY	632	CCTTGCACTTCCCAAGATGATGACTACATCTCGGTGGGACCTCTTATGAAGATCTGGCTCT	691
Db	708	CACITAACTTCTTCATCTCAACCTGGATCTGGGAAACCTGCG-----TGAAGATCTGTGTTT	764
QY	692	TCATCTTTGACCTTGGTGTATCCCTGCTCATCATCTGTCGTGTGATACACCCTGATGTCC	751
Db	765	TCATCTTTCGCTTCAATTATGCGAGTGCATCATCTTACCGTGTGCTATATGAGCTATGATCT	824
QY	752	TGCGTCTCAAGAGCGTCCGGCTCTCTTTCTGGCTCCGAGAAAGATCGCAACTGCGTA	811
Db	825	TGCGCTCAAGAGTGTCCGATGTCTCTGTGCTCTCAAAAGAAAGACAGGAATCTTGAA	884
QY	812	GGATTCACCAAGCTGGTCTGTGGTGTGGGAGATCTTGTGTGCTGTGCACTCCCATTC	871
Db	885	GGATTCACCGAGATGT	944
QY	872	ACATATTCATCTGTGTGAGGCTGTGGGGAGCACTCCACAGACAGCTGTCTTCGA	931
Db	945	ACATTTTAGTATATATTAAGCCTTGTGTATCAATCCAGAAACTAGCTTCCAGACTGTTT	1004
QY	932	GCTATTACTTGTGCATGCGCTTGTAGGCTATACCAACAGTAGCTGAATCCATTCTACAG	991
Db	1005	CTTGGCACTTGTGATGTCTGTAGGTTTACCAAAACAGCTGCTCAACCCAGTCTTTATG	1064
QY	992	CCTTTCTGTAGTAAACCTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGAAGATGA	1051
Db	1065	CATTTCTGATGAAGAACTTCAAGAGATGCTTCAAGAGGTTCTGTATCCAACTCTTCCA	1124
QY	1052	GGATGAGCGGCAAGACATAGCAGAGTCCGAATA	1087
Db	1125	ACATTTGAGCAACAAACTCCACTCGAATTCGTCTGA	1160

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RESULT 33
US-10-194-595-26
; Sequence 26, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561,523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53

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Qy	692	TCATCTTTGGCTTGGTATATCCCTGTCTCATATATATGTCTGTACACCTGATGATTC	751
Db	902	TCATCTTCGCTTCAATTAATGCAAGTCTATCATTAACCGTGTGATAGATGAATCT	961
Qy	752	TGCGCTCAAGAGCGTCCGGCTCTTTCTGGCTCCGAGAGAGAAATGCAACCTGGCTA	811
Db	962	TGCGCTCAAGAGTCTCCGCAATGCTCTCTGTGCTCCAAAAGAAAGACAGAAATCTTCCAA	1022
Qy	812	GGATCACCAAGCTGGTCTCGTGTGTGTGGCAGTCTTGTGCTGTGCTGACCTCCCAATTC	871
Db	1022	GGATCACCAAGATGGTGTGGGTGGTGGTGTGTATCGTGTGTGTGACTCCCAATTC	1082
Qy	872	ACATATTATCTCTGTGAGAGGCTCTGGGAGACCTCCACAGCACACTGCTCTCTCCA	931
Db	1082	ACATTTAGTATCATTTAAAGCTTTGGTTACATCCAGAACTAAGTTCACAGCTGTTT	1142
Qy	932	GCTATTACTTCTGCATCGCTTACGGCTTAACCAACAGTAGCGCTGAATCCACTTCTACAG	991
Db	1142	CTTGGCACTTCTGCACTTGTCTTAGTTACAAACAGCTGCTCAACCAAGTCTTTATG	1202
Qy	992	CCTTTCTTGATGAAAACTTCAAGCGGTATTTCCGGAACTTCTGTCTTCCACTGAAGATGA	1051
Db	1202	CATTTCTGATGAAAACTTCAAAAGATGCTTACAGAGGTCTGTATCCCAACTCTTCCA	1262
Qy	1052	GGATGAGAGCGGCAGAGCACTAGACAGATGCCAAATA	1087
Db	1262	ACATTTAGCAACAAACCTCACTCGAAATTTGTCACA	1297

RESULT 35

```

US-10-080-917-12
? Sequence 12, Application US/10080917
? Publication No. US20030054451A1
? GENERAL INFORMATION:
? APPLICANT: Cadet, Patrick
? APPLICANT: Stefano, George B.
? TITLE OF INVENTION: Opiate Receptors
? FILE REFERENCE: 09598-006001
? CURRENT APPLICATION NUMBER: US/10/080,917
? CURRENT FILING DATE: 2002-02-22
? PRIOR APPLICATION NUMBER: US 60/270,479
? PRIOR FILING DATE: 2001-02-22
? PRIOR APPLICATION NUMBER: US 60/336,677
? PRIOR FILING DATE: 2001-12-05
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 12
? LENGTH: 2149
? TYPE: DNA
? ORGANISM: Homo Sapiens
? US-10-080-917-12

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Query Match	37.7%;	Score 434.8;	DB 15;	Length 2149;
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Best Local Similarity 66.3%; Pred. No. 3.2e-115;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2.

Qy	92	CCGGCTGGGCGCAGGCCGACAGCAACGGCAGGCGCGGCTCGGAGGAGCGCGAGCTGGAGC	151
Db	334	CCGACCCATGCGGGTTCGAAACCGACCGACCTTGGCGGAGAGACAGCCTGTGGCCCTCCGA	3939
Qy	152	CCGCGACATCTTCCCGGCGCATCCGGTCATCATCAGCGCGGATCTACCTCGTAGTGTTCG	2111
Db	394	CCGGCAGTCCCTTCATGATTCAGGCGCATACATATGAGCCCTCTACCTCAATCGTGTGGC	453
Qy	212	TCGTGGGCTTGTGGGCAACTGCGTGTCATGTCGTATCATCCGATACCAAAAGTGA	2711
Db	454	TGGTGGGGCTCTTCGAAACTTCCTGTGTCATGTATGTGTCAGATACCAAGATGA	5133
Qy	272	AGACAGCAACCAATTATATTTAACTCTGGCTTTGGCAGATGCTTTAGTTACTTCAA	3311
Db	514	AGACTGCAACCAACTTATATTTTCAACTTGTCTCTGGCAGATGCTTTAGCCCAACAGTA	5733

OY	332	CCATGCCCCCTTCAGAGTAAGGCTCTACCTTGATGGAATATTCGGGCTTTGGGGATGTCCTG	391
Db	574	CCCTGCCCCCTTCAGAGTGAATTAACCTPAATGGGAACATGGCCATTGGAAACCATCTT	633
OY	392	GCAAGATATGTAAATTTCCATTGATTAATCTACCAACATGTTCAACAGACTCTTCACCTTGACCA	451
Db	634	GCAAGATATGTATCTCCATAGATTATCTATACATGTTTCCACAGCATATTCACCTCTGCA	693
OY	452	TGATGAGCGTGGACCGCTACATTGGCCGTGTGTCACCCCGTGAAGGCTTTGACCTTCCGA	511
Db	694	CCATGAGTGTGATGATACATATTGACGCTGCGCACCCCTGTCAAGGGCTTAGATTTCCGTA	753
OY	512	CACCTTTGAAGGCAAAAGATTCATCAATATCTGATATTGGTGTGTGCTCATCTGTTGGCA	571
Db	754	CTCCCCGAAATGCGAAAATTAATCAATGTCCTGCACTGGAATCCTCTCTTAGCCATTGGTC	813
OY	572	TCTGTCATATATGCTCTTGGAGGCAACAAAGTCAGGGAAGACGTCGATGTCAATTAAGTGTCT	631
Db	814	TTCTGTATATGTATGTATGCTGTACACAAAATTAACGGCAGG-----TTCCATATGATTGTA	867
OY	632	CTTGGAGTTCCCAAGATGATGACTACTCTGTGTGGACCTCTTCATGAAGATCTGCGTCT	691
Db	868	CACPAACATCTCTCATCCAACTGTAAGTGGTACTGGGAAACCTGC---TGAAGATCTGTGTT	924
OY	692	TCATCTTTGGCTTGTGTGATCCCTGTCTCTCATATCATGTGTCTGCTACACCTGATGATCC	751
Db	925	TCATCTTGTGCTTCAATTATGCCAGTGCATCATTAACCGTGTGCTATGAGCATGATGATCT	984
OY	752	TGCGCTCAAGAGCGATCCGGGCTCCTTCTTGCGCTCCGAGAGAAAGATGCGCAACCTGCGTA	811
Db	985	TGCGCTCAAGAGTGTCCGCATGCTCTGTGCTCCAAAGAAAGACAGAAATCTTCCGA	104
OY	812	GAATTCACCAACTGTGCTCTGTGTGTGTGTGACGCTTGTGCTGTGCTGAGCTCCCATTC	871
Db	1045	GGATCACCAAGATGGTGTGGTGGTGTGTGTGTGCTGTTCATCGTGTGCTGAGCTCCCATTC	110
OY	872	ACATATTATCTGTGTGAGGCTCTGGGGAAGCACTCCACAGCAGACTGCTCTCCCA	931
Db	1105	ACATTTAAGTATCATTAAGCCCTTGGTTACATATCCAGAAACTACGTTCAGACTGTT	116
OY	932	GCTATTACTTCTGCATCGCTTAAAGGCTATTAACCAACAGTAGCTGATATCCATTCTCTACG	991
Db	1165	CTTGGCACTTCTGCTATGCTCTAGTTTACAAACAGCTGCTTCAACCAAGTCTTTATG	122
OY	992	CCTTTCTTGATGAATACTTCAAGCGGTGTTTCCGGAATTCTTGCTTTCATGAAAGATGA	105
Db	1225	CATTCTGTGATGAATACTTCAAGCGATGCTTCAAGAGTGTGTATCCCAACTCTTCCA	128
OY	1052	GGATGAGAGCGGCAAGCACTGACAGAGTCCGAATA	1087
Db	1285	ACATTGAGCAACAAATCCCACTCGAAATTGTCAGA	1320

RESULT 36

US-10-225-567A-185
; Sequence 185, Application US/10225567A

```

: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenna C.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 185
:
: LENGTH: 2162
: TYPE: DNA

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2063)..(2063)
OTHER INFORMATION: unknown nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (2091)..(2091)
OTHER INFORMATION: unknown nucleotide
US-10-225-567A-185

Query Match 37.7%; Score 434.8; DB 15; Length 2162;
Best Local Similarity 66.3%; Pred. No. 3.2e-115;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACGACGACGACGAGCGCGGCTCGGAGGACCGCGAGCTGGAGC 151
DB 337 CCGAGCCGATCGGCTCGGAACTCGACCACTCGGCGGAGAGACAGCCCTGTCCTCCGA 396
QY 152 CCGGCGACATCTCCCGGCGATCCGCGATCATGACGCGCGGCTCACTCCGAGTTCG 211
DB 397 CCGGCGATCTCCATGATCAGCGCATGAGCCCTCACTCCATCGTGTGCG 456
QY 212 TCGTGGGCTTGGGCACTCGCTGTCATGTCGATCATCCGATACAAAGATGA 271
DB 457 TGTGGGGCTTTCGAAACTTCGTGTCATGTATGTGTGATGATGACAAAGATGA 516
QY 272 AGACGACACCAACATTTACATTTAACTTGGCTTGGCAGATCTTATTTACTCAA 331
DB 517 AGACGACCAACCAATTTACATTTAACTTGGCTTGGCAGATCTTATTTACTCAA 576
QY 332 CCATGCGCTTTCAGATGAGTCTACTTGTATGATTAATTCGCGCTTGGGAGTGTGCT 391
DB 577 CCGTCCCTTCAGAGTGTGATTAACCTTAATGGAAACATGGCATTTGGAACATCTTT 636
QY 392 GCAAGATAGTATTTCCATTTGATTAACCAATGTTCAACGATCTTTCACCTTGAACA 451
DB 637 GCAAGATAGTATTTCCATTTGATTAACCAATGTTCAACGATCTTTCACCTTGAACA 696
QY 452 TGAATAGGTGAGCCGCTACATGTCGCTGTGCGACCCGCTGAAAGCTTGGACTTCGCA 511
DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTGCTGATCTGTGTGCA 571
DB 757 CTCGCCGAATGCCAAATTTATCATGTCTGCACTGATCTCTCTTCAAGCCATTGCTC 816
QY 572 TCTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGAGTGTGATGATGATGATGATGAT 631
DB 817 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
QY 632 CTTGCAATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 871 CACTAACATTTCTCATCAACCTGTGTACTGGGAAACCTCG--TGAAGATCTGTGTT 927
QY 692 TCACTTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 928 TCACTTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
QY 752 TGGCTTCAAGAGCGTCCGCTCTTTTGTGCTCCGAGAGAAAGATGCAACTGTGCTA 811
DB 988 TGGCTTCAAGAGCGTCCGCTCTTTTGTGCTCCGAGAGAAAGATGCAACTGTGCTA 1047
QY 812 GGAATCAACAGCTGCTGT 871
DB 1048 GGAATCAACAGCTGCTGT 1107
QY 872 ACATATTCATCTGTGAGGCTCTGGGAGAGACCTCCACAGGACAGCTGCTCTTCCA 931
DB 1108 ACATATTCATCTGTGAGGCTCTGGGAGAGACCTCCACAGGACAGCTGCTCTTCCA 991
QY 932 GCTATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991

DB 1168 CTTGGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
QY 992 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
DB 1228 CATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287
QY 1052 GGAATGAGCGGAGAGGACCTTACGAGATGATGATGATGATGATGATGATGATGAT 1087
DB 1288 ACATTTGAGCAACAAATCTCCATCGAATTCGTGCA 1323

RESULT 37
US-10-305-720-1379

; Sequence 1379, Application US/10305720
; Publication No. US2004010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1379
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank ID No. US2004010136A1 9452072
; LOCATION: (1) ... (2162)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-1379

Query Match 37.7%; Score 434.8; DB 16; Length 2162;
Best Local Similarity 66.3%; Pred. No. 3.2e-115;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACGACGACGAGCGCGGCTCGGAGGACCGCGAGCTGGAGC 151
DB 337 CCGAGCCGATCGGCTCGGAACTCGACCACTCGGCGGAGAGACAGCCCTGTCCTCCGA 396
QY 152 CCGGCGACATCTCCCGGCGATCCGCGATCATGACGCGGCTCACTCCGAGTTCG 211
DB 397 CCGGCGATCTCCATGATCAGCGCATGAGCCCTCACTCCATCGTGTGCG 456
QY 212 TCGTGGGCTTGGGCACTCGCTGTCATGTCGATCATCCGATACAAAGATGA 271
DB 457 TGTGGGGCTTTCGAAACTTCGTGTCATGTATGTGTGATGATGATGATGATGATGATGAT 516
QY 272 AGACGACACCAACATTTACATTTAACTTGGCTTGGCAGATCTTATTTACTCAA 331
DB 517 AGACGACCAACCAATTTACATTTAACTTGGCTTGGCAGATCTTATTTACTCAA 576
QY 332 CCATGCGCTTTCAGATGAGTCTACTTGTATGATTAATTCGCGCTTGGGAGTGTGCT 391
DB 577 CCGTCCCTTCAGAGTGTGATTAACCTTAATGGAAACATGGCATTTGGAACATCTTT 636
QY 392 GCAAGATAGTATTTCCATTTGATTAACCAATGTTCAACGATCTTTCACCTTGAACA 451
DB 637 GCAAGATAGTATTTCCATTTGATTAACCAATGTTCAACGATCTTTCACCTTGAACA 696
QY 452 TGAATAGGTGAGCCGCTACATGTCGCTGTGCGACCCGCTGAAAGCTTGGACTTCGCA 511
DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTGCTGATCTGTGTGCA 571
DB 757 CTCGCCGAATGCCAAATTTATCATGTCTGCACTGATCTCTCTTCAAGCCATTGCTC 816

Qy	572	TCCTGCAATAGTCTCTTGGAGGCAACCAAGTACGGGAAAGCTGCATGTCATTGAGTGTCT	631
Db	817	TTCCGTATATGTTCAATAGGCTACAAACAAAATACAGGCAAG-----TTCCATGATGTGA	870
Qy	632	CCTTGACAGTTCACAGATGATGACTACTCGTGGGGGACCTCTTCATGAAGATCTGGCTCT	691
Db	871	CACTAACATTCTCTCATCCCACTGGTACTGGGAAAACTCG--TGAAAGATCTGTGTTT	927
Qy	692	TCATCTTTGCGCTTCGATATCCCTGTGCTCATCATCATCGTCTGCTACACCTGATGATCC	751
Db	928	TCATCTTGCCCTTCATATATGCCAGTCTCATATACCTGTGTCTATGACATGATGATCT	987
Qy	752	TGCGTCTCAAGAGCGCTCCGACTCTTTCTGCTCTCCGAGAGAAAGATTCGCAACTGCGTA	811
Db	988	TGCGCCTCAAGAGTGTCCGCAATGCTCTGCGCTCCAAAGAAAGACAGAAATCTTCGAA	104
Qy	812	GGATCAACCAAGCTGGTCTCTGTGTGTGTGTGGCAGTCTTCGTCTGCTGATCCCATTC	871
Db	1048	GGATCAACCGAGATGGTGTGTGTGTGTGTGGCTGTGTTCATCTGCTGCTGACCTCCATTC	110
Qy	872	ACATATTCATCTCGTGGAGGCTCTGGGGAGACCTCCACAGACAGCTGCTCTCTCCA	931
Db	1108	ACATTAGCTCATCATTTAAAGCCTGTGTTACATCCAGAAACTAGCTTCAGACTGTTT	116
Qy	932	GCTATTAATCTTCGATATCGCCTTAGGCTATACCAACAGTATGACCTGAATCCCATTTCTAG	991
Db	1168	CTTGGCATTCTTGCAATGTCTCTAGAGTTACACAAACAGCTGCTCAACCAAGTCTTTANG	122
Qy	992	CTTTTCTTGATGAAAACTTCAAGCGGTGTTTCGGGACTTCTGCTTTCCATGAAGATGA	105
Db	1228	CATTTCTGATGATAAACTTCAAAACGATGCTTCAGAGAAGTTGTGATCCACCTCTTCCA	128
Qy	1052	GGATGAGCGGCAAGACACTAGACAGTCCGAATA	1087
Db	1288	ACATTGAGCAACAAAATCTCCACTCGAATTCGTGAGA	1323
RESULT 38			
US-09-935-061-11			
; Sequence 11, Application US/09935061			
; Publication No. US20030129649A1			
; GENERAL INFORMATION:			
; APPLICANT: Kobilka, Brian M.			
; APPLICANT: Chanouni, Peiman			
; APPLICANT: Lee, Tae Weon			
; TITLE OF INVENTION: Conformational assays to detect binding			
; TITLE OF INVENTION: co G protein-coupled receptors			
; FILE REFERENCE: STAN213			
; CURRENT APPLICATION NUMBER: US/09/935,061			
; CURRENT FILING DATE: 2001-08-21			
; PRIOR APPLICATION NUMBER: 60/286,250			
; PRIORITY FILING DATE: 2001-04-24			
; NUMBER OF SEQ ID NOS: 16			
; SOFTWARE: PaeSeq for Windows Version 4.0			
; SEQ ID NO 11			
; LENGTH: 1176			
; TYPE: DNA			
; ORGANISM: homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1) ... (1176)			
; US-09-935-061-11			

Query Match	37.5%	Score 433.2;	DB 10;	Length 1176;
Best Local Similarity	66.2%;	Pred. No. 7e-115;		
Matches 659; Conservative	0;	Mismatches 328;	Indels 9;	Gaps 2

[illegible]

Db	185	CGGCGATGCCCTCCATGATACAGGCGCATACGATATAGGCCCTTACTTCATCGTGTGG	244
Qy	212	TCTGGGGCTTGGTGGGCAACTCGGTGTCATGTTCTGTATCATCCGATACCAAAAGATGA	271
Db	245	TGTTGGGGCTCTTGGGAAACTTCCTGGTCAATGTATGATTGTGAGATACACAAAGATGA	304
Qy	272	AGACAGCAACCAACATTATTAACATATTTAAACCTGGCTTTGGCAGANTGCTTTACTACAA	331
Db	305	AGACTGCCACCAACATCTACATTTTTCACCTTGGCTCTGGCAGANTGCCCTTAAGCACAAATGA	364
Qy	332	CCATGCCCTTTCAGAGTACGGGTCTACTGATGAATTCCTGGCCCTTTTGGGGATGTGCTGT	391
Db	365	CCCTGCCCTTTCAGAGTGTGAATTTACCTAAATGGGAACATGGCCATTTTGGAAACATCTTT	424
Qy	392	GCAAGATGATATTTTCCATTGATTACTACCAACATGTTTACACGACATCTTACCTTGACCA	451
Db	425	GCAAGATGATGATCTCCATAGATTATCTAAACATGTTTACACGACATATTTACCCCTGTCCA	484
Qy	452	TGATAGAGGTGGACCGGCTCAATTGGCCGTGTGCCACCCCGTGAAAGGCTTTGGACTTCGGCA	511
Db	485	CCATGAGTGTGATCGATACATATGCAAGTCTGCCACCCGTGCAAGGCCCTTAAATTTCCGTGA	544
Qy	512	CACCCCTTAAAGGCAAAAGATTCATCAATATCTGCATCTGCTGTCGTCATCTGTGGACA	571
Db	545	CTCCCCGAAATGCCAAATTTTCAATGTCCTGCMACTGATCTCTCTTCAAGCATTTGGTTC	604
Qy	572	TCTCTGCAATAGTCTTTGGAGGCAACCAAGTCAAGGGAAGACGTGATGATCTTGAAGTCT	631
Db	605	TTCTGTAATGTGTCATAGCTACCAACAAATACAGGCAAG-----TTCCTAATGATTGTA	658
Qy	632	CCTTGCAATTCOCAGATGATGATCTACTCTGTGTGGACCTCTTCAATGAAAGATTCGGCTCT	691
Db	659	CACTAACATTCCTCATCCAACTCTGTAACTGGGAAACCTTC--TGAAGATCTGTGTTT	715
Qy	692	TCATCTTGTGCTGTGTGATTCCTGTCCATCATCATCATGCTGTGCTACACCCGTAGATCC	751
Db	716	TCATCTTGTGCTTCAATTATGCAAGTGCATCATTTACGTGTGTGATGGAATGATGATCT	775
Qy	752	TGCGTCTCAAGAGCGTCCGGCTCCTTTTGTGGCTCCCAAGAAAGATGCAACCTGGCTA	811
Db	776	TGCGGCTCAAGAGTGTCCGCAATGCTCTCTGTGCTCCMAAGAAAGACAGGAATCTTCSAA	835
Qy	812	GGATCACAGACTGGTCTCTGGAGTGGAGGAGCTTGTGTCGTCTGCTGACTCCCATTC	871
Db	836	GGATCACAGATGT	895
Qy	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACTTCCACAGACAAGACTGCTCTTCCCA	931
Db	896	ACATTTAGTCATCATTTAAAGCTTTGTTACAAATCCGAAACATACGTTCCAGACTGTTT	955
Qy	932	GCTATTAATTTCTGCATGCGCTTAAGCTATACCAACAGTAGCTGAATCCCATTTCTTACG	991
Db	956	CTTGGACATTTGCAATGCTCTAGGTATACAAACAAGCTGCTTCAACCCAGATCTTTTATG	1015
Qy	992	CTTTCTTGTAGAAAACCTTAAAGCGGTATTTCCGGGACTTCTGCTTTCACATGAAGATGA	1051
Db	1016	CATTTCTGTAGAAAACCTTAAAGCAATGCTTCAAGAGATTTCTGTATCCCAACCTCTTCCA	1075
Qy	1052	GGATGAGCGGCAAGCACTAGCAAGAGTCCGAAATA	1087
Db	1076	ACATTTAGCAACAAAACTCCACTCGAATTTCTTCCGA	1111

RESULT 39
US-10-692-071-11
; Sequence 11, Application US/10692071
; Publication No. US20040157268A1

```

; APPLICANT: Kobilka, Brian K.
; APPLICANT: Chanount, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding

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; TITLE OF INVENTION:    to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CJP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Fastseq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1176)
US-10-692-071-11

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Db      601  CCAATGAGTGTGATGATACATGACATGAGCTGCGACCCCTGTCAAAGGCTTAGAATTCCTGTA 740
Oy      512  CACCCTTGAAAGGCAAAAGATCATCAATATCTGCATCTGAGCTGTCGTATCTGTTGGCA 571
Db      741  CTCCCGGAAATGTCAAAATATTATCAATGCTGCGACCTGAGATTCCTCTTACGACATTGGTC 800
Oy      572  TCTCTGCATAATGACTCCTTGGAGGCAACCAAAAGTCAGGAGAGAGCTGCATGTCATTGAGTCT 631
Db      801  TTCCCTGTAATGTTCATAGCTACACAAATAATACAGCGCAAG3-----TTCCATAGATTGTA 854
Oy      632  CCTTGACAGTTCACAGATGATGACTACTCCTGGGAGGAGCCTTTCATAGAAAGATCTGGCTCT 691
Db      855  CACTAACATTTCTCTCATCCACCTGGTACTGGGAAAACCTGC--TGAAAGATCTGTTT 911
Oy      692  TCATCTTTGGCCTTGCATGATCCCTGTCCTCATCATCATCTGTCATCAACCTGATGATCC 751
Db      912  TCATCTTGCCCTTCAATTATGACAGAGCTCATATTACGTTGTCATAGACATGATGATCT 971
Oy      752  TGCCTCTCAAGAGCGTCCGCGCTCTTCTGCTGCTCCCGAGAGAAAGATCCCAACTGCGTA 811
Db      972  TGCGGCTCAAGAGGTGTCCGCAAGCTCTCTGCGCTCCAAAAGGACAGAGAAATCTTCGAA 1033
Oy      812  GGATCACCAGACATGGCCCTGGTGGTGGTGGAGGAGCTTGTGCTGCTGCTGAGACTGCCATTC 871
Db      1032  GGATACACAGAGATGGTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1099
Oy      872  ACATATTCATCTCTGTGTGAGAGGCTCTGGGGAGACACTCCACAGACAGAGCTGCTCTTCCA 931
Db      1092  ACATTTAGCTCATCATTAAGGCTTGTTAGCAATCCCAAGAACTACGTTCCAGAGCTGTT 1155
Oy      932  GCTATTACTTCTGTGCATCGCCTTAGGCTATACCAACAGTAGTGCTGAAATCCACTTCTTAGC 991
Db      1152  CTGGACACTTCTGCATGTGCTCTAGGTTACAAACACAGCTGCCTCAACCCAGTCCCTTATG 1211
Oy      992  CCTTCTCTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAAGATGA 1055
Db      1212  CATTTCTGATGAAAACTTCAAAACGATGCTTCAAGAGAGTTCTGTATCCAACTCTTCCA 1277
Oy      1052  GGATGAGCCGCGACAGACACTAGACAGAGTCCGAATA 1087
Db      1272  ACATTGACCAACAAAACCTCCACTCGAATTGTCAG 1307

RESULT 41
US-10-185-083-21
; Sequence 21, Application US/10185083
; Publication No. US20030050467A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan Kettering Cancer Center
APPLICANT: Paeternak, Gavril
APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185, 083
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/502, 072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2951
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-185-083-21

```

Query Match	37.5%	Score 432.6	DB 15	Length 2951
Similarity	64.4%	Pred. No. 1,66-114		
Beet local	683	Conservative	0	Mismatches 9
Matches	683	Indels	9	Gaps 2
92	CCGCGTGGAGCCGAGCCGACGCAACGCGAGCGCCCGGCTCGGAGGAGACGCGGACCTTGAGAC	151		
185	CCGAGCCATGCGCGCTCTTAACCGCAACGGGGCTTGGGGGGAGCCACAGCCCTGTGCTCCCTCACA	244		

QY	152	CCGGGCAATCTCCCGGGCCATCCGGGCAATCAAGGGGGTCTACTCGTAGTTCG	211
Db	245	CCGGGAGCCCTTCCATGGTCAAGCAATCAATCAATGCCCCCTCTATTCTATCGGTGTC	304
QY	212	TCTGTGGCTTGGTGGGCACTCGGTGTGCATGTTTCGTGATCATCCGATACCAAAAGATGA	271
Db	305	TAGTGGGCTCTTTGGAAACTTCCGTGCATGTATGTATGTATGAAGATATACAAAATGA	364
QY	272	AGACAGCAACCAACATTATTCATATTTAACTGTGGCTTTTGGAGATGCTTTAAGTACTACA	331
Db	365	AGACTGCACCAACATCTACATTTTCAACCTGTGCTGGGAGATGCCCTTACCCACTACGA	424
QY	332	CCATGCCCCCTTCAGAGTACGGGTCTACTGTATGAATATCCGTGGCCTTTGGGGATGCGCT	391
Db	425	CGCTGCCCTTTCAGAGTGTATTACTAACCTGATGGAGACGTGGCCCTTTGGAAACATCTCT	484
QY	392	GCAAGATAGTAAATTTCCATTGATTACTACAACATGTTCCACGACGATCTTCACTTGACCA	451
Db	485	GCAAGATGTGATCTCAATAGACTACTACACATGTTCCACGATATCTTCAACCCGTCTGCA	544
QY	452	TGATGAGGTGTGACCCGCTACATTTGGCGGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGA	511
Db	545	CCATGAGGTGTGACCGCTACATTTGGCGGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGA	604
QY	512	CACCCCTTGAAGGCAAAAGATTCATCAATATCTGATCTGGCTCTGTGCTCATCTGTGGCA	571
Db	605	CCCCCCGAAATGCCAAATTTGTCAATGTCTGTGCAACTGATCTCTCTTCTGTGCATTTGGTC	664
QY	572	TCTGTCAATAGTCTTGTGAGGCAACAAAGTCAGGGAGAAGCTGTGATCTAATGAGTCT	631
Db	665	TGCCCGTAAATGTTATGGCAACCAAAATTCAGGCA-----GGGGTCCATTAATTTGCA	718
QY	632	CCTTGGCAATCCCAAGATATATGACTATCTCTGTGGGACCTTCTGATGAAGATCTGGCGCT	691
Db	719	CCCTCAGCTTCTCATCTCCACATGTGTATGTGGAGAACTGTCTC--AAATCTGTGTCT	775
QY	692	TCATCTTTTGCCTTGTGTGATCCCTGTCTCCATCATCATCATCTGTGCTACACCTGTAGATCC	751
Db	776	TCATCTTGCCTTATCATGTCCGGTCTCTCATCATCATCATGTGTGTATGTGCTGTGACCCCCATCC	835
QY	752	TGCGCTTCAGAGCGTCCGGCTCTCTTTCTGTGGCTCCGAGAGAAAGATTCGACCTGTGGTA	811
Db	836	TACGACTCAGAAAGTGTCCGCATGTCTGTCTGGGCTCAAAAGAAAGACAGAACTGTGGCA	895
QY	812	GGATCACACAGCTGTCTGTGTGTGTGGTGTGGAGTCTTGTCTGTCTGTGCACTGCCATTC	871
Db	896	GGATCACACCGGATGT	955
QY	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACTCCACAGACAGAGCTCTCTCTCA	931
Db	956	ACATCTATGTATCATCAAGCACTGTATCAACGATTCAGAAACACACTTTCAGACTGTTT	1015
QY	932	GCTATATCTTGTGATGCGCTTATAGGCTATACCAACAGTACGCTGAATCCATTCTACG	991
Db	1016	CTGTGCACTTCTGTGATTTGCTTGTGGTTTACACAAACAGCTGTCTAAACCCAGTCTTTATG	1079
QY	992	CCTTTCTTGAAGAAACTTCAAGGGGTGTTTCGGGCACTTGTGTTTCACTGAAGATGA	1051
Db	1076	CGTTCCTTGAAGAAACTTCAAGAGTGTTTTGAAGAGTTTGTGATCCCACTTCTCTCA	1135
QY	1052	GGATGAGCGGACAGACACTAGCAGAGTCCGAAATACAGTTCAAGATCTGTCTTACCTGA	1111
Db	1136	CAATCGAAGCAAACTCTGTGATTCGTTCAAAACACTAGAGGAAACACCCCTCACGG	1195
QY	1112	GGGACATTCGATGGGATGAATTAACCAAGTATGACTATGTCTGTG	1152
Db	1196	CTAATATACGTGATCGAACTTAACCAACAGTGTGTATGATG	1236

RESULT 42
US-10-194-595-21
; Sequence 21, Application US/10194595

```

; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561,523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2951
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-194-595-21

```

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Query Match      37.5%; Score 432.6; DB 15; Length 2951;
Best Local Similarity 64.4%; Pred. No. 1.6e-114;
Matches 683; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAAGCGAGCGCGCTCGGAGAGCGCGAGCTGGAGC 151
DB 185 CCGAGCCAGTCCGGTCTTAACCGGAGGGGCTGGCGGAGCCACAGCCCTGCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCTATCATCAAGCGGCTTACTCTCGAGTTCG 211
DB 245 CCGGAGCGCTTCCATGTCACAGGCAATCATCATGCGCTTATCTATCTCGTGTG 304
QY 212 TCGTGGGCTGGTGGAACCTGCTGTCATGTTGTATCATCGATACAAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAACCTTCTGTCATGTATGTATGAATACCAAAATGA 364
QY 272 AGACAGCAACCAATTTAATATTTAACTGCTTTGGCAGATCTTGAATTAAGTA 331
DB 365 AGACTGCCACCAACATCAATTTTCAACCTTGTCTGGCAGATGCTTGAACATTA 424
QY 332 CCATGCGCTTTGAGAGTACGCTCTGTTGATGTAATCTCGGCTTTGGGAGTGTCT 391
DB 425 CGCTGCGCTTTCAGAGTGTATTAATCTGATGGAACGCGCTTTGGAAACATCTCT 484
QY 392 GCAAGATGTAATTTCCATGATTAATTAACAATGTTCAACGATCTTTCACCTTGA 451
DB 485 GCAAGATGTAATTTCAATTAATTAAGCTTAACATGTTCAACGATCTTTCACCTTGA 544
QY 452 TGATGAGGTGAGACCGCTAATTTGCGATGTCACCCGCTGAAGCTTTGACTTCCGA 511
DB 545 CCATGAGTGTAGACCGCTAATTTGCGATGTCACCCGCTGAAGCTTTGACTTCCGA 604
QY 512 CACCTTGAAGCAAGATCAATATCTGATCTGCTGTCTGTCATCTGTGGCA 571
DB 605 CCCCCGAAATGCAAAATGTCATGTCGAACTGATCTTCTTCTTCCATTTGGTTC 664
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGAGTCAATGATAGTCT 631
DB 665 TGCCGTAAATGTTATGCAACCAAAATACAGCA-----GGGATCCATAGTTGCA 718
QY 632 CTTTGCAGTTCCCAAGATGATCACTCTCGTGGAGACCTTTCATGAAGATCTGCGCT 691
DB 719 CCGTCAAGTCTCTCATCCCAATGATGTAAGGAACTGCTC---AAAATCTGTGCT 775
QY 692 TCAATCTTGGCTGTGATCCCTGCTCATCATCATGTCTGCTCAACCTGATGATCC 751
DB 776 TCAATCTTGGCTGTGATCCCTGCTCATCATCATGTGTTATGATGATGATCT 835
QY 752 TGCGCTCAAGAGGCTCCGGCTCTTCTGAGCTCCGAGAGAAAGATGCAACCGGCTA 811
DB 836 TAGACATCAAGAGTCCGCAATGCTGTGGGCTCCAAAGAAAGACAGGAACCTTGCGCA 895

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QY 812 GGATCAGCAGACTGGTCTCGGAGTGGAGGAGTCTTGCTGCTGAGCTCCCATTC 871
DB 896 GGATCAGCAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 955
QY 872 ACATATTCATCTGTTGAGAGGCTCTGGGAGACACTCCCAAGACAGCACTGCTCTTCCA 931
DB 966 ACATCTATGATCATCAAAACACTGATCAGATTCAGAAACACTTTCAGAGCTGTTT 1015
QY 932 GCTATTTATTTGATGAGCTCTTGAAGCTATACCAACAGTATGATCTGATCTTCTAG 991
DB 1016 CCGGCACTTTCGATGAGTGGCTTGGGTTACAAACAGCTGCTGAACCCAGTCTTTATG 1075
QY 992 CTTTCTTGAATAAATCTTCAAGGAGTGTTCGAGGACTTGTCTTCTTCACTGAAGATGA 1051
DB 1076 CGTTCCTGATGAAACCTTCAAGAGTGTTCGAGGACTTGTCTTCTTCACTGAAGATGA 1111
QY 1052 GGATGAGCGGCGAGACCTAGCAGAGTCCGAAATPACAGTTCAAGATCTGCTTACCTGA 1111
DB 1136 CAATCGAAACAGCAAACTCTGCTCGAATCCGTCAAACACTAGGGAACACCCCTCCAGG 1195
QY 1112 GGAACATGATGGATGATAATAACAGATACATGATCTGCTG 1152
DB 1196 CTAATCAAGTATGATGAACTAACCACAGTGTATGATGATG 1236

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RESULT 43
US-10-185-083-22
; Sequence 22, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-22

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Query Match      37.5%; Score 432.4; DB 15; Length 1332;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAAGCGAGCGCGCTCGGAGAGCGCGAGCTGGAGC 151
DB 185 CCGAGCCAGTCCGGTCTTAACCGGAGGGGCTGGCGGAGCCACAGCCCTGCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCTATCATCAAGCGGCTTACTCTCGAGTTCG 211
DB 245 CCGGAGCGCTTCCATGTCACAGGCAATCATCATGCGCTTATCTATCTCGTGTG 304
QY 212 TCGTGGGCTGGTGGAACCTGCTGTCATGTTGTATGATGATCAACAAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAACCTTCTGTCATGTTATGATGTAAGATACCAAAATGA 364
QY 272 AGACAGCAACCAATTTAATATTTAACTGCTTTGGCAGATCTTGAATTAAGTA 331
DB 365 AGACTGCCACCAACATCAATTTTCAACCTTGTCTGAGAGATGCTTGAACATTA 424
QY 332 CCATGCGCTTTGAGAGTACGCTCTGATGTAATCTGCTGTCTTGGGAGTGTCTGT 391
DB 425 CGCTGCGCTTTCAGAGTGTAACTAATCTGATGGAAGTGGCCCTTTGAAACATCTCT 484
QY 392 GCAAGATGTAATTTCCATGATTAATTAACAATGTTCAACGATCTTTCACCTTGA 451

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485 GCAGATGCTGATCTCAATAGACTACTCAACATGTTCCAGATCTTCAACCTCTGCA 544
QY 452 TGATGAGGTGGACCGCTAATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTCCGA 511
Db 545 CCATGAGTGTAGACCGCTAATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTCCGA 604
QY 512 CACCTTTAAGGCAAGATCATCAATATCTGATCTGGCTGTGCTGCTATGTTGGCA 571
Db 605 CCCCCGAAATGCAAAATTTGCTCATGTCTGCACTGATCTCTCTTCTGCAATTTGGC 664
QY 572 TCTGTCAATAGTCTTGGAGGCGACCAAGTCCAGGAAAGCGTCGATGTCATTTAGTGT 631
Db 665 TGCCCGTATGTTCAATGCAACCAAAATATACAGGAGGGGTC-----CATAGATTGCA 718
QY 632 CTTTGACATTTCCCAATGATGATCTACTCTGCTGGGAACTCTTCAATGAAGATCTGCT 691
Db 719 CCTCAGCTTCTCTATCCCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775
QY 692 TCATCTTTGCTTCCGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
Db 776 TCATCTTTGCTTCCGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TGCGTCTCAAGACGCTCCGCTCTCTTCTGCTCCGAGAGAAAGATGCAACTGCGTA 811
Db 836 TACGACTCAAGAGTGTCCGCAATGCTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCAACAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 896 GGATCAACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 956 ACATATGATGCTATCATCAAGACATGATCAAGATTTCCAAACCACTTTCCAGACTGTT 1015
QY 932 GCTATTTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 1016 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
QY 992 CCTTTCTGATGAAATCTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGA 1051
Db 1076 GCTTCTGATGAAATCTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGA 1135
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGATCCGAAATATACAGTTCAAGATC 1099
Db 1136 CAATGAAACAGCAAACTCTGCTGCAATCCGTAACCACTAGGGAAC 1183

RESULT 44
US-10-194-595-22
; Sequence 22, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasteur, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OR INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10194.595
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561.523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent version 3.1
; SEQ ID NO 22
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-194-595-22

Query Match 37.5%; Score 432.4; DB 15; Length 1332;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;
QY 92 CCGGCTGGGCGGAGCGCGACAGCAAGCGCGCGCTCGGAGGAGACGGCGAGCTGGAGC 151
Db 185 CCGAGCCATGCGGCTTAACCGGACAGGAGGCTTTGGGAGGCGACAGGCTGTGCTCCAA 244
QY 152 CCGGACATCTCCCGGCGCATCCCGGCTATCATGACGGCGGTCTACTCCGATGTTGG 211
Db 245 CCGGAGCGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
QY 212 TCGTGGGCTGCTGGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
Db 305 TAGTGGGCTCTTTGGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
QY 272 AGACGCAACCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 331
Db 365 AGACGCAACCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
QY 332 CCATGCCCTTTCAGAGTACGGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 391
Db 425 CCGTCCCTTTCAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 484
QY 392 GCAGATGATATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 451
Db 485 GCAGATGATGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 544
QY 452 TGATGAGGTGGACCGCTAATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTCCGA 511
Db 545 CCATGAGTGTAGACCGCTAATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTCCGA 604
QY 512 CACCTTTAAGGCAAGATCATCAATATCTGATCTGGCTGTGCTGCTGCTGCTGCTGCTGCT 571
Db 605 CCCCCGAAATGCAAAATTTGCTCATGTCTGCACTGATCTCTCTTCTGCAATTTGGC 664
QY 572 TCTGTCAATAGTCTTGGAGGCGACCAAGTCCAGGAAAGCGTCGATGTCATTTAGTGT 631
Db 665 TGCCCGTATGTTCAATGCAACCAAAATATACAGGAGGGGTC-----CATAGATTGCA 718
QY 632 CTTTGACATTTCCCAATGATGATCTACTCTGCTGGGAACTCTTCAATGAAGATCTGCT 691
Db 719 CCTCAGCTTCTCTATCCCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775
QY 692 TCATCTTTGCTTCCGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
Db 776 TCATCTTTGCTTCCGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TGCGTCTCAAGACGCTCCGCTCTTCTGCTCCGAGAGAAAGATGCAACTGCGTA 811
Db 836 TACGACTCAAGAGTGTCCGCAATGCTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCAACAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 896 GGATCAACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 956 ACATATGATGCTATCATCAAGACATGATCAAGATTTCCAAACCACTTTCCAGACTGTT 1015
QY 932 GCTATTTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 1016 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
QY 992 CCTTTCTGATGAAATCTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGA 1051
Db 1076 GCTTCTGATGAAATCTTCAAGCGGTGTTTCCGGGACTTCTGCTTCCACTGAAGATGA 1135
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGATCCGAAATATACAGTTCAAGATC 1099
Db 1136 CAATGAAACAGCAAACTCTGCTGCAATCCGTAACCACTAGGGAAC 1183

RESULT 45
US-09-761-962-3

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; Sequence 3, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice
; TITLE OF INVENTION: Variants of Mu-
; TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
; FILE REFERENCE: 830002-2000.1
; CURRENT APPLICATION NUMBER: US/09/761,962
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-3

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```

Query Match      37.5%; Score 432.4; DB 9; Length 1334;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

```

QY 92 CCGGCTGGGCGGAGCCGACGACGAGCGCGGCTCGAGAGACGGGACGCTGGAGC 151
DB 105 CCGACCCATGGCGTCTTAACCGGAGCGGCTTGGGAGCCACGCTGCTCAGA 244
QY 152 CCGGACACATCTCCCGGCGCATCCGGTATCATGACGGCGGTCTACTCCGATGTTCC 211
DB 245 CCGGACGCGCTTCCATGGTACAGCCATCACCATATGCGCTTATCTATCGGTGG 304
QY 212 TCGTGGGCTTGGTGGGAACTCGCTGATCATTTGGTATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAACTCTCTGGTATGATATGATATGAATATCAAAATGA 364
QY 272 AGACGACACCAACATTTACATTTTAACTGGCTTGGAGATCTTATGTTACTACA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGGAGATCTTACGACTACGA 424
QY 332 CCATGCCCTTTGAGATGAGGTCTAATTGATGAATTTCTGCGCTTTGGGAGTGTCTGT 391
DB 425 CGCTGCCCTTTGAGATGAGGTCTAATTGATGAATTTCTGCGCTTTGGGAGTGTCTGT 484
QY 392 GCAAGATGATATTTCCATGATTTAATTACTAACAATGTTACACAGATCTTTCACCTTGAACA 451
DB 485 GCAAGATGATATTTCAATGATTTAATTACTAACAATGTTACACAGATCTTTCACCTTGAACA 544
QY 452 TGATGAGGTGAGACCGCTACATTTGCGTGGCAACCCGTAAGAGCTTGGACTTTCGCA 511
DB 545 CCATGATGATGAGACCGCTACATTTGCGTGGCAACCCGTAAGAGCTTTCGCA 604
QY 512 CACCTTTGAAGGCAAGATCATTAATATCTGATCTGCTGCTGCTGATCTGTGGCA 571
DB 605 CCCCCGAAAGGCCAAATGTCATATGTCGCAATGATCTCTCTTCTGCAATGGTC 664
QY 572 TCTCTGCAATGATCTCTTGGAGGACCAAAATGCAAGGGAAGAGTGTGATCTGATAGTCT 631
DB 665 TGCCCGTATATTTATGAGCAACCAAAATGCAAGGGAAGAGTGTGATCTGATAGTCT 718
QY 632 CTTTGACATTTCCAGATGATGATCTCTCTGATGGGACCTTCTCATGAAAGATCTGCGCT 691
DB 719 CCGTCAAGCTTCTCATCTCCACATGATGATCTGAGGAACCTGCTC---AAATCTGTGTCT 775
QY 692 TCACTTTTGGCTTGGTATCTCTGCTCTCATCATCTGCTGCTCAACCTGATATCC 751
DB 776 TCACTTTTGGCTTGGTATCTCTGCTCTCATCATCTGCTGCTCAACCTGATATCT 835
QY 752 TGCCTCTCAAGAGGCTCGGCTCTCTTCTGCTGCTCCGAGAGAAAGATGCAACCTGGGTA 811
DB 836 TAGACATCAAGAGTGTGCGGATGCTGTGGGCTCTCAAAAGAAAGAGAGAACTGGGCA 895
QY 812 GGATCACCAAGCTGTCTGTGGTGTGGGAGTCTTGTGTGTGTGTGATCTCCCATTC 871

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DB 896 GGATCACCCGAGATGTGTGGTGTGTGTGTGTGTATTTATTTGTCTGTGAGACCCCATCC 955
QY 872 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAACAGACAGCTCTCTCCA 931
DB 966 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAACAGACAGCTCTCTCCA 1015
QY 932 GCTATTTACTTGCATGCGCTTGAAGCTATACCAACAGTACGCTGAATCTCTTACG 991
DB 1016 CCGGACCTTCTGATGCTCTTGGGTTACCAAAACAGCTGCTGAACCCAGTCTTATG 1075
QY 992 CTTTCTTGATGAAACTCTCAAGCGGTCTTCCGGAATCTGCTTCCACTGAAGATGA 1051
DB 1076 GCTTCTGATGAAACTCTCAAGCGGTCTTCCGGAATCTGCTTCCACTGAAGATGA 1135
QY 1052 GGATGAGCGGACAGACATGACAGATCCGAATATGATTCAGATC 1099
DB 1136 CAATGCAACGACAAACTCTGCTGGAATCCGTCAAAACACTAGGAAAC 1183

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RESULT 46
US-10-283-300-3
; Sequence 3, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
; TITLE OF INVENTION: OF THE MU-OPIOID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-283-300-3

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Query Match      37.5%; Score 432.4; DB 15; Length 1334;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACGAGCGCGGCTCGAGAGACGGGACGCTGGAGC 151
DB 185 CCGACCCATGGCGTCTTAACCGGAGCGGCTTGGGAGCCACGCTGCTCAGA 244
QY 152 CCGGACACATCTCCCGGCGCATCCGGTATCATGACGGCGGTCTACTCCGATGTTCC 211
DB 245 CCGGACGCGCTTCCATGGTACAGCCATCACCATATGCGCTTATCTATCGGTGG 304
QY 212 TCGTGGGCTTGGTGGGAACTCGCTGATCATTTGGTATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAACTCTCTGGTATGATATGATATGAATATCAAAATGA 364
QY 272 AGACGACACCAACATTTACATTTTAACTGGCTTGGAGATCTTATGTTACTACA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGGAGATGCTTACGCACTGCA 424
QY 332 CCAATGCCCTTTGAGATGAGGTCTAATTGATGAATTTCTGCGCTTTGGGAGTGTCTGT 391
DB 425 CGCTGCCCTTTGAGATGAGGTCTAATTGATGAATTTCTGCGCTTTGGGAGTGTCTGT 484
QY 392 GCAAGATGATATTTCCATGATTTAATTACTAACAATGTTACACAGATCTTTCACCTTGAACA 451
DB 485 GCAAGATGATATTTCAATGATTTAATTACTAACAATGTTACACAGATCTTTCACCTTGAACA 544

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Oy	452	IGATGAGGGGTGACCGCGTACATATGCGGTGTGACACCCGCTGAAAGGCTTTGACCTTCCGCA	511
Db	545	CCATGAGTGTGAAACCGCTACATTGGCGTCTGACACCCGCTCAAGGCGCTTGATTTTCCGTA	604
Oy	512	CACCCCTTAAAGCAAAAGATTCATCATATCTGGCATCTGGCTGTGCTGATCTGTGTGCA	571
Db	605	CCCCCGAAATATGCCAAATTTGTGCATGTCTGGAACTGGATCCTCTCTTCTGCGCAATTGGTC	664
Oy	572	TCTCTGCAATATGTCTTGGAGGACCAAAATGACGGAAAGAGCTGCATGTCAATTGATGTCT	631
Db	665	TGCCCGTATGTCTCATGGCAACCAAAAATATCAGGACAGGGGTCTC-----CATAGATTCA	718
Oy	632	CCTTGACATGCCCAAGATGATGACTACTCCTGGTGGGACCTCTCTTATGAAAGATCTGACGTCT	691
Db	719	CCCTCAGCTTCTCTCATCTCCACATGTGTACTGGAGAACTGTCTC---AAATCTGTGCT	775
Oy	692	TCATCTTTGCTTGTGTGATCCCTGTCTCATCATCATGTGTGTGCTACACCTGATGATCC	751
Db	776	TCATCTTGCCTTCATCATGCGCGGTCTCATCATCATGTGTGTATGATGATGATGATCT	835
Oy	752	TGCGTCTAAAGAGCGTCCGGGCTCTTCTGTGCGTCCCGAGAAAGATGGCAACCTGGCGTA	811
Db	836	TACGACTAAAGAGTGTCCGCAATGCTGTGGGCTCCAAAGAAAGAACAGAAACCTGGCGCA	895
Oy	812	GGATCACCAGACTGTGCTCCGTGTGTGTGTGTGACAGTCTTGTGCTGTGCTGACTCCCATTC	871
Db	896	GGATCACC CGGATGGTGTGCGTGTGTGTGTGTGTATTTATGTGTGTGTGTGTGTGTGTGTGT	955
Oy	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACTCCACAGACAGCTGTCTCTTCCA	931
Db	956	ACATCTATGTCATTCATCAAGACACTGATACACATTCACAGAAACCACTTCCAGACTGTCT	1015
Oy	932	GCTATTACTTCTGCATCCGCTTATGAGCTATTACCAACAGTAGAGCTGATCCCATCTCTACG	991
Db	1016	CCTGGCACTTCTGCATTTGCTGT	1075
Oy	992	CCTTCTGTGATGAATCTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCACTGAAAGATGA	1051
Db	1076	CGTTCCTGTGATGAATCTTCAAGCGGTGTTTGAAGAGTTCGTGCACTCCCACTTCTCCCA	1135
Oy	1052	GGATGGAGCGGACAGCACTGACAGTAGTCCGAAATATACAGTTCAAGATC	1099
Db	1136	CAATGAAACAGCAAACTCTGCTCGAATCCGTCAAAACATGAGGAAAC	1183

RESULT 47
 US-09-761-962-11
 : Sequence 11, Application US/09761962
 : Patent No. US20020077285A1
 : GENERAL INFORMATION:
 : APPLICANT: Memorial Sloan-Kettering Cancer Center
 : TITLE OF INVENTION: Identification and Characterization of Multiple Splice
 : TITLE OF INVENTION: Variants of Mu-
 : TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
 : FILE REFERENCE: 830002-2000.1
 : CURRENT APPLICATION NUMBER: US/09/761,962
 : CURRENT FILING DATE: 2001-01-17
 : PRIOR APPLICATION NUMBER: 09/743,872
 : PRIOR FILING DATE: 2001-03-13
 : NUMBER OF SEQ ID NOS: 46
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 11
 : LENGTH: 1365
 : TYPE: DNA
 : ORGANISM: Mus musculus
 : US-09-761-962-11

	Query Match	37.5%	Score 432.4	DB 9	Length 1365
	Best Local Similarity	65.8%	Pred. No. 1.3e-114		
	Matches 663	Conservative	0	Mismatches 336	Indels 9
					Gaps 2
QY	92	CCGGCTGGGCCGACGCCGACGCAACGGCAGCCGCTCGAGGAGACGGCGCAGCTTGAGC	151		

Db	185	CCGACCATTGGGGTCTTAACCGGACGGGGGCTTGGCGGGAGCCACAGAGCTGTGGCCTCAGA	244
OY	152	CCGGCGACATCTCCCGGCGCATCCCGGTCATCATCACGGGGGTCTACTCCGTAGTGTTCG	211
Db	245	CCGGCAGACCCCTTCATAGTCAAGCCACTATCCATCATGGCCCTCTATTCTTCTGTGTG	304
OY	212	TCGTGGGCTTGGTGGGAATCGGTGGTCATGTTCGTGATCATCCGATPACAAAGATGA	271
Db	305	TATGGGGCTCTTGGAACTTCTGTGCATGATGTGATTTGTAAGATATACAAAATGA	364
OY	272	AGACAGCAACCAATTTACTATTTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACA	331
Db	365	AGATGCGACCAACATCTACATTTTCAACCTGTGTCTGGCAGATGCTTACCACTAGCA	424
OY	332	CCATGCCCTTTCAGATGACGGTCTACTTGTATGAATTCCTGGCTTTTGGGGATGTCTGT	391
Db	425	CGTGCCTTTCAGAGTGTTAACCTGATCGGAAAGTGGAACGTGGCCCTTTGGAAACATCTCT	484
OY	392	GCAAGATATGTAATTTCCATTGATTAATCAACAATGTTCAACAGATCTTCACTTCAACA	451
Db	485	GCAAGATGTGATCTCAATAGACTACTACAAACATGTTCAACAGATCTTCAACCTCTGCA	544
OY	452	TGATGACGCTGGACCGGCTACATTTGCCGTGTGCCACCCCGTGAAAGCTTTGGACTTCCGA	511
Db	545	CCATGAGTGTAGACCGGTACATTTGCCGTCTGCCACCCGGTCAAGGCCCTGGATTTCCGTA	604
OY	512	CACCTTGAAGGCAAGATCATTAATCTGCATCTGGCTGTCTGTCATCTGTGGCA	571
Db	605	CCCCCCCAAAATGGCAAAATGTCAATGTCTGCAACTGGAATCTCTCTTCTGCCATTTGGTC	664
OY	572	TCCTGTGAATATGCTCTTGGAGGCAACAAAGTCAAGGAAAGCTGATGTCAATGAGTCT	631
Db	665	TGCCGTATGTATGACCAACCAAAATACAGGACAGGGGTC-----CATGAAATTGCA	718
OY	632	CTTTGACATTCACAGATGATGACTACTCTGTGGGAGCCTTTGATGAAGATCTGCCT	691
Db	719	CCCTCAGTGTCTCATCTCCACATGTAATCTGGAGAACCTGTCTC---AAATCTGTGTCT	775
OY	692	TCATCTTTGCTTGTGTATCCCTGTCTCTCATCATCATCTGTCTGCTAACCTGTATATCC	751
Db	776	TCATCTTCGCTTCATCATGTCCGGTCTCTCATCATCATCTGTGTGTTATGATGATGATCT	835
OY	752	TGGCTTCAAGAGGCTCCGGCTCTCTTGGCTCCGAGAGAAAGATCGCAACTGGGTA	811
Db	836	TACACCTCAAGAGTGTCCGATGCTGTGGGCTCAAAAGAAAGACAGAACTTGGCGCA	895
OY	812	GGATTCACAGACTGTCTGTGTGTGTGGTGGCAGTCTTCTGTCTGTGTGACTCCCATTC	871
Db	896	GGATCACCCGGATGT	955
OY	872	ACATATTCATCTGT	931
Db	956	ACATCTATGTCTATCATCAAGCACCTGTATCTAGTCTCAGTAAGAACCATTTCCAGCTGT	1015
OY	932	GCTATTAATCTTGATGCGCTTGTAGGATACCAACAGTAGCTGAATCCCATTTCTACAG	991
Db	1016	CTTGGCACTTGTGATTTGCTTGGGTTTACAAACAGCTGCTTAAACCACTTTTATG	1075
OY	992	CTTTCTTGTATGAATACTTCAAGGAGTGTTCGGGACCTTCTGCTTTCACTGAAGATGA	1051
Db	1076	CGTTCCTGATGAAACCTTCAAGATGTTTATGAGAGTCTGTGATCCCAACTCTCTCA	1135
OY	1052	GGATGAGACGGCAGACCTAGCAGAGTCCGAATACAGTTACAGATC	1099
Db	1136	CAATCGAACGCAAACTGTGCTGAATCGTCAAAACACTTAGGGAAC	1183

RESULT 48
US-10-283-300-11
; Sequence 11, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center

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; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-283-300-11

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Query Match      37.5%; Score 432.4; DB 15; Length 1365;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGAGCGCTTGGGGAGGACCAAGCCTGTGCCCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGTATATCAAGCGGCTCTTACTCCGTAGTGTTCG 211
DB 245 CCGGAGCGCTTCCATGCTGACAGGACATCACCATATGGCCCTCTATCTATCGTGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGCTGATCATGTTCGTATCAATCCGATACCAAAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCCCTGGTATATGTATGTATGAATATACCAAAATGA 364
QY 365 AGACGACCAACCAATTTAATATTAACTTGGCTTGGAGATCTTGAATTAACA 331
DB 365 AGACTGCCACCAATCTAATTTCAACTTGTCTGGCAGATCTTGAACCACTAGCA 424
QY 332 CCATGCGCTTTCAGAGTACGGCTCTAATTTCAATTAATTTCTGCGCTTTGGGATGTGCTGT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTAATCTGATGGAGCGGCTTGGAAACATCTCT 484
QY 392 GCAAGATGATATTTCAATTTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 451
DB 485 GCAAGATGATATTTCAATTTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 544
QY 452 TGATAGCGTGGACCGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
DB 545 CCATGAGTGTAGACCGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604
QY 512 CACCTTGAAGGCAAAAGATCAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 571
DB 605 CCCCCCAAAATGCAAAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTA 664
QY 572 TCTGTGAATAGTCTTGTGAAGGCAACCAAGTCAAGGGAAGAGTGTGATGATGATGATGATGATG 631
DB 665 TGCCGCTATATGTTATAGGCAACCAAAATTAAGGCAAGGGGTG-----CATTAATTTGCA 718
QY 632 CCTTGCAATTTCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 719 CCGTCAAGTGTCTCATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 692 TCATCTTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 776 TCATCTTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
QY 752 TGGCTTCAAGAGCGTCCGCTCTTCTTGTGCTCCGAGAGAAAGATGCAACCTGTGCTA 811
DB 836 TACAGCTCAAGAGTGTGCGATGTGCTGCGGCTCAAAAGAAAGAGACAGGAACTGTGGCA 895
QY 812 GGATCACCAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871

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DB 896 GGATCACCAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
QY 872 ACATATTCATCTGTGTGAGGCTCTTGGGAGACACTCCACAGACAGACTGCTCTTCA 931
DB 966 ACATCTATGATCATCAAAAGCACTGATCAAGATTCAGAAACCACTTCCAGACTGTTT 1015
QY 932 GCTATTTACTTGTGATGCTCTTGAAGCTTATACCAAGATGCTGATATCCATTTCTTACG 991
DB 1016 CCGGCACTTGTGATGCTCTTGTGCTTACCAAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 992 CTTTCTGATGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
DB 1076 CGTTCCTGATGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
QY 1052 GGATGAGCGGCAAGCACTAGCAAGATCCGAAATTAAGATTCAAGATC 1099
DB 1136 CAATCGAAGCAAGCAAACTGTGCTGAAATCCGTCAAAACACTAGGGAAC 1183

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RESULT 49
US-10-185-083.51
; Sequence 51, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Mus Sp.
; US-10-185-083-51

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Query Match      37.5%; Score 432.4; DB 15; Length 1373;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGAGCGCTTGGGGAGGACCAAGCCTGTGCCCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGTATATCAAGCGGCTCTTACTCCGTAGTGTTCG 211
DB 245 CCGGAGCGCTTCCATGCTGACAGGACATCACCATATGGCCCTCTATCTATCGTGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGCTGATCATGTTCGTGATCATCCGATACCAAAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCCCTGGTATATGTATGTATGAATATACCAAAATGA 364
QY 365 AGACGACCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
DB 425 CGCTGCCCTTTCAGAGTGTAACTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 484
QY 392 GCAAGATGATATTTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 451
DB 485 GCAAGATGATATTTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 544
QY 452 TGATAGCGTGGACCGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
DB 545 CCATGAGTGTAGACCGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604

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QY 512 CACCTTGAAGGCAAAAGATCATATATCTGCATCTGCTGCTGTCATCTGTTGGA 571
DB 605 CCCCCGAAATGCAAAATTTGTCATGTCTGCAACCTGATCCTCTTCTTGCCATTGGTC 664
QY 572 TCTGTCAATAGTCTCTTGGAGGCAACCAAGTCAGGAGACGTGATCATTTAGTGTCT 631
DB 665 TGCCGCTATATGTTACATGCAACCAAAATACAGGACGGGGTC-----CATAGATTGCA 718
QY 632 CCTTGACGTCTCCAGATGATGACTACTCTGTGTGGGACCTCTTCATGAAAGATCTGCTCT 691
DB 719 CCTCAGCTTCTCTCATCCACATGATGATCTAGGAGAACTGTCTC-----AAATCTGTCT 775
QY 692 TCATCTTTCCTCTGATCCCTGATCCCTGTCATCATCTGTCATCTGTCACCTGATGATCC 751
DB 776 TCATCTGCTCTTTCATCATGCGGCTCTCTATCATCTGTGTGTATGAGACTGATGATCT 835
QY 752 TCGCTCTCAAGACGCTCCGCTCTCTTCTGCTCCGAGAGAAAGATGCAACTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGCTATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCACCAAGACTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGATCACCGGATGT 955
QY 872 ACATATTATCTCTGT 931
DB 956 ACATATTATGTCTATCATCAAGACATGATCAAGATTCAGAAACCACTTTCCAGACTGTTT 1015
QY 932 GCTATTACTTCTGCATCGCTTATAGGCTATATCAACAGTAGCTGATCCATTTCTCTAG 991
DB 1016 CTTGCACTTCTGCATGTGCTTGGGTTACAAACAGCTGCTGAACCAAGTTCTTTTANG 1075
QY 992 CTTTCTTGATGAAAACCTTCAACGCGTGTTCCTGGGACTTCTGCTTTCACCTGAAGATGA 1051
DB 1076 CTTTCTTGATGAAAACCTTCAACGATGTTTATGAGAGTTCTGCACTCCCACTTCTCTCA 1135
QY 1052 GGATGAGGCGGACAGCACTAGACAGATCCGAAATTCAGTTCAAGATC 1099
DB 1136 CAATGAAACAGCAAACTTGTCTGATCCGTCATCAAAACACTAGGGAAC 1183

RESULT 50
US-10-194-595-51
; Sequence 51, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasteur, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561,523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-194-595-51

Query Match 37.5%; Score 432.4; DB 15; Length 1373;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGAGCGCGGCTCGAGAGACGCGCAGCTGAGAC 151
DB 185 CCGACCCATGCGGCTCTAACCGACGGGCTTGGGGGAGCCACAGCCTGTGCTCCAGA 244

QY 152 CCGGCAACATCTCCCGGCAATCCGCTCATCAACGAGGCTACTCCGATGTTGGA 211
DB 245 CCGGAGCCCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
QY 212 TGTGGGCTGTGTGGGCAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 271
DB 305 TAGTGGGCTCTTGTGAAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 364
QY 272 AGACAGCAACCAATTTACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
DB 365 AGACTGCCACCAACATTTACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 424
QY 332 CCATGCGCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
DB 425 CCGTCCCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 392 GCAAGATGATTTTTCATTTGATTTTACATTTGATTTTACATTTGATTTTACATTTGAT 451
DB 485 GCAAGATGATTTTTCATTTGATTTTACATTTGATTTTACATTTGATTTTACATTTGAT 544
QY 452 TGATGAGGTGAGACCGCTACATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 511
DB 545 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
QY 512 CACCTTGAAGGCAAAAGATCATATATCTGCATCTGCTGCTGTCATCTGTTGGA 571
DB 605 CCCCCGAAATGCAAAATTTGTCATGTCTGCAACCTGATCCTCTTCTTGCCATTGGTC 664
QY 572 TCTGTCAATAGTCTCTTGGAGGCAACCAAGTCAGGAGACGTGATCATTTAGTGTCT 631
DB 665 TGCCGCTATATGTTACATGCAACCAAAATACAGGACGGGGTC-----CATAGATTGCA 718
QY 632 CTTGCACTTCTGCATGTGCTTGGGTTACAAACAGCTGCTGAACCAAGTTCTTTTANG 691
DB 719 CCTCAGCTTCTCTCATCCACATGATGATCAAGATTCAGAAACCACTTTCCAGACTGTTT 775
QY 692 TCATCTTTCCTCTGATCCCTGATCCCTGTCATCATCTGTCATCTGTCACCTGATGATCC 751
DB 776 TCATCTGCTCTTTCATCATGCGGCTCTCTATCATCTGTGTGTATGAGACTGATGATCT 835
QY 752 TCGCTCTCAAGACGCTCCGCTCTCTTCTGCTCCGAGAGAAAGATGCAACTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGCTATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCACCAAGACTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGATCACCGGATGT 955
QY 872 ACATATTATCTCTGT 931
DB 956 ACATATTATGTCTATCATCAAGACATGATCAAGATTCAGAAACCACTTTCCAGACTGTTT 1015
QY 932 GCTATTACTTCTGCATCGCTTATAGGCTATATCAACAGTAGCTGATCCATTTCTCTAG 991
DB 1016 CTTGCACTTCTGCATGTGCTTGGGTTACAAACAGCTGCTGAACCAAGTTCTTTTANG 1075
QY 992 CTTTCTTGATGAAAACCTTCAACGCGTGTTCCTGGGACTTCTGCTTTCACCTGAAGATGA 1051
DB 1076 CTTTCTTGATGAAAACCTTCAACGATGTTTATGAGAGTTCTGCACTCCCACTTCTCTCA 1135
QY 1052 GGATGAGGCGGACAGCACTAGACAGATCCGAAATTCAGTTCAAGATC 1099
DB 1136 CAATGAAACAGCAAACTTGTCTGATCCGTCATCAAAACACTAGGGAAC 1183

RESULT 51
US-09-761-962-1
; Sequence 1, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice Variants of Mu-

```

; TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
; FILE REFERENCE: 830002-2000.1
; CURRENT APPLICATION NUMBER: US/09/761,962
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-761-962-1

Query Match      37.5%; Score 432.4; DB 9; Length 1423;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAACGGGCGGCGCTCGGAGGACGGGCGAGCTGGAGC 151
DB 185 CCGAGCCATGCGGTCTTAACCGGAGGGGCTTGGCGGAGCCAGCAGCTGCTCCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCATCAACGGCGGTCTTACTCCGTAAGTTGG 211
DB 245 CCGGCGAGCCCTTCCATGCTCAGGCAATCAACCATATGAGCCCTTATTCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCAACTCGCTGCTCATTTGCTATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCCGTCGTGATGATATGTATGAATATCCAAAGATGA 364
QY 272 AGACAGCAACCAACATTTTACATATTTAACTGGCTTTGGAGAGTCTTTAGTACTACA 331
DB 365 AGACTGCCACCAACATCAATTTTCAACCTTGTCTGGAGATGCTCTTACGACTACGA 424
QY 332 CCATGCCCTTTGAGATAGGTCTTACTGATGATTTCTGCTGCTTTGGGAGATGCTGT 391
DB 425 CGCTGCCCTTTGAGATGTTAATCTAGATGGAGACGTGGCCCTTTGGAAACATCTCT 484
QY 392 GCAAGATGATATTTCCATGATTTACTAACAATGTTACCAAGCATCTTTCACTTTGACA 451
DB 485 GCAAGATGATATTTCAATTAAGCTAATCAACATGTTTCAACGATATCTTCACTTTGCA 544
QY 452 TGATAGGCTGGACCGGTACATTTGCGTGGCAACCCCGTGAAGCTTTGGACTTCCGA 511
DB 545 CCATAGGTGAGACCGGTACATTTGCGTGGCAACCCCGTGAAGCTTTGCGTGA 604
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGCTGCTCATCTGTTGCA 571
DB 605 CCCCCGAAATGCCAAATGTTGCAATGTTGCAATCTGATCTCTCTTCCATTGGCT 664
QY 572 TCTCTGCAATAGTCTTGGAGGCAACAAAGTCAAGGAGAGATGTCATTTAGAGTCT 631
DB 665 TGCCGTATATGTTATGAGCAACACAAATATCAGGAGAGGCTC-----CATAGATTGCA 718
QY 632 CTTTGACGTTCCAGATGATGATCTCTGCTGGGACCTTTTCAATGAAGATCTGCGTCT 691
DB 719 CCTTCAAGCTTCTTCATCCACATAGGTACTGGGAGAACCTGCTC---AAATCTGTTGCT 775
QY 692 TCAATCTTTGCTTGTGATCCCTGTCTCATCATCATGTCTGCTACACCTGATGATCC 751
DB 776 TCAATCTTGGCTTTCATATGCGGCTCTCATCATCATGTTGTTATGAGACTGATGATCT 835
QY 752 TGCGCTCAAGAGGCTCGGCTCTTCTTGGCTCCGAGAGAAAGATGCAACCTGGGTA 811
DB 836 TAGACATCAAGAGTCTCGCATGCTGTGGGCTCCAAAGAAAGACAGAACTTGGGCA 895
QY 812 GGATACACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 896 GGATACACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTCATCTGCTGAGGCTCTGGGAGACACTCCACAGACAGACGCTCTCTTCCA 931
DB 956 ACATCTATGTCATCAAAAGCACTGATCAAGATTCCAGAAACCACTTTCCAGACTGTTT 1015
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QY 932 GCTATTAATTTGATGCGCTTTAGGCTATACCAACAGTAGCTGAATCCATTCTACG 991
DB 1016 CCGGCACTTCTGATGCTCTTGGGTTTACCAAAACAGCTGCTGAACCCAGTCTTTATG 1075
QY 992 CTTTCTTGATGAAACCTTCAAGGCGTGTTCGGGAGCTTCTGCTTCCACTGAAGATGA 1051
DB 1076 GCTTCTGATGAAACCTTCAAGGCGTGTTCGGGAGCTTCTGCTTCCACTGAAGATGA 1135
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGAGTCCGAAATTAAGTTGACAGATC 1099
DB 1136 CAATGAAACAGCAAAACCTGCTCGAATCCGTCAAAACACTAGGGAAC 1183

RESULT 52
US-10-283-300-1
; Sequence 1, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-283-300-1

Query Match      37.5%; Score 432.4; DB 15; Length 1423;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAACGGGCGGCGCTCGGAGGACGGGCGAGCTGGAGC 151
DB 185 CCGAGCCATGCGGTCTTAACCGGAGGGGCTTGGCGGAGCCAGCAGCTGCTCCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCATCAACGGCGGTCTTACTCCGTAAGTTGG 211
DB 245 CCGGCGAGCCCTTCCATGCTCAGGCAATCAACCATATGAGCCCTTATTCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCAACTCGCTGCTCATTTGCTATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCCGTCGTGATGATATGTATGAATATCCAAAGATGA 364
QY 272 AGACAGCAACCAACATTTTACATATTTAACTGGCTTTGGAGAGTCTTTAGTACTACA 331
DB 365 AGACTGCCACCAACATCAATTTTCAACCTTGTCTGGAGATGCTCTTACGACTACGA 424
QY 332 CCATGCCCTTTGAGATAGGTCTTACTGATGATTTCTGCTGCTTTGGGAGATGCTGT 391
DB 425 CGCTGCCCTTTGAGATGTTAATCTAGATGGAGACGTGGCCCTTTGGAAACATCTCT 484
QY 392 GCAAGATGATATTTCCATGATTTACTAACAATGTTTCAACGAGATCTTCACTTTGACA 451
DB 485 GCAAGATGATATTTCAATTAAGCTAATCAACATGTTTCAACGATATCTTCACTTTGCA 544
QY 452 TGATAGGCTGGACCGGTACATTTGCGTGGCAACCCCGTGAAGCTTTGGACTTCCGA 511
DB 545 CCATAGGTGAGACCGGTACATTTGCGTGGCAACCCCGTGAAGCTTTGCGTGA 604
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGCTGCTCATCTGTTGCA 571
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Db      605 CCCCCGAATGCCAAATTTGTCAATGTCTGCAACTGCATCCTCTTCTTGCCATTTGTC 664
Qy      572 TCTTGCAATAGTCTTGTGAGGACCAAGTCAAGGAAAGAGCTGCATGTGATGAGTGT 631
Db      665 TCCCGGTAATGTTCAATGCGAACCAAAATPACAGGACGAGGTC-----CATAGATTGCA 718
Qy      632 CTTTCAGTTCCTCAAGTATGACTACTCTGTTGGGACCTTTTCATGAAAGATGAGTGT 691
Db      719 CCTTCACGTTCTCTCATCCACATGTAATGGAAGAACTGCTC---AAATCTGTGTC 775
Qy      692 TCATTTTTCCTTCTGTATCCTGTCTCATCATCATGTCTGTACACCTGTATGATCC 751
Db      776 TCATCTTGCGCTTTCATCATGCGGTCCTCATCATCATGTGTATGAGACTGATGATCT 835
Qy      752 TGCCTCTCAAGAGCTCCGCTCTTCTTGCTCCGAGAAAGATGCGAACCTTGCGTA 811
Db      836 TACGACTCAAGAGTGTCCGACATGTCGCGGCTCCAAAGAAAGACAGAACTTCGCGA 895
Qy      812 GGATCAGCAGATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      896 GGATCAGCAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
Qy      872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
Db      956 ACATCTATGTCTATCATCAAGACATGATCAGATTCCAGAAACACTTTCAGACTGTT 1015
Qy      932 GCTATTACTTCTGCAATCGCTTAAAGCTATACCAACAGTACCTGAAATCCATTTCTAC 991
Db      1016 CTGGACATTTCTGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
Qy      992 CTTTCTTGTAATAAATCTCAAGCGGTGTTCGCGGACTTTCGCTTTCACATGAAAGTA 1051
Db      1076 CTTTCTTGTAATAAATCTCAAGCGGTGTTCGCGGACTTTCGCTTTCACATGAAAGTA 1135
Qy      1052 GGATGAGCGGACAGCACTAGCAGAGTCCGAATATACATTGAGATC 1099
Db      1136 CAATCGAACAGCAAACTCTGCTCGATCTGTCAAAACACTAGGGAC 1183

RESULT 53
US-10-185-083-15
; Sequence 15, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-15

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```

Query Match      37.5%; Score 432.4; DB 15; Length 1440;
Best Local Similarity 65.8%; Pred. No. 13e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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Qy      92 CCGGCTGGGCGGACCCGACAGCAGCGCGGCTCGGAGGAGCGCGAGCTGAGAC 151
Db      348 CCGAGCCATGCGCTCTTAACCGCAGGGCTTGGGGAGGACCAAGCCTGTGCTCTCAGA 407
Qy      152 CCGGCAATCTCCCGGCGCATCCGGTATCATACAGCGCGGTACTTCCGTAGTGTTC 211
Db      408 CCGGAGCCCTTCCATGTGTCAAGCAATCAATCATATGACCTTATCTATCTGTGTG 467

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Qy      212 TGTGGGCTGTGGGCAACTCGTGTGATGTTCGTATCATCCGATACAAAGATGA 271
Db      468 TAGTGGGCTCTTTGGAAATCTTCTGTATATATATATATATATATATATATATATAT 527
Qy      272 AGACAGCAACCAATTTACATATTTAACTGGCTTTTGGCAGATCTTTAGTACTACAA 331
Db      528 AGACTGCCACCAATCTACATTTTCAACCTTGTCTGGCAGATCTTACCACTAGCA 587
Qy      332 CCATCCCTTTTCAAGTACGGTCTTCTGTAATTTCTGGCTTTTGGGATGTGCT 391
Db      588 CGCTCCCTTTTCAAGTATTTAATCTGATGGGAACGGGCTTTGGAAACATCTCT 647
Qy      392 GCAAGATGTAATTTTCAATGATTTACTTCAACATGTTCCAGCATCTTCACTTGAACA 451
Db      648 GCAAGATGTAATTTTCAATGATTTACTTCAACATGTTCCAGCATCTTCACTTGAACA 707
Qy      452 TGATAGGCTGACCGCTACATTTGCGTGTGCAACCCGATGAAGGCTTTGACCTTCGCA 511
Db      708 CCATAGTGTAGACCGGTACATTTGCGTGTGCAACCCGATGAAGGCTTTGACCTTCGTA 767
Qy      512 CACCTTTGAAGCAAAATCATCAATATCTGATCTGCTGTCTGTCTATCTGTGGA 571
Db      768 CCCCCGAAATGCGCAAAATGTCTCAATGTCTGCACTGATCTCTTCTTGTCCATTTGTC 827
Qy      572 TCTTGCAATATGCTTGTGAGGCAACCAAGTCAAGGAAAGAGCTGATGATGATGATG 631
Db      828 TGCCTGTAATGTTCTATGCGAACACCAAAATACAGGAGGTC-----CATAGATTGCA 881
Qy      632 CTTTCAGTTCCTCAAGTATGATCTCTGTGTGGGACCTTTTCATGAAAGATCTGCTGT 691
Db      882 CCTTCAGTTCCTCATCTCCACATGATGTACGGGAAACCTGTCTC---AAATCTGTGTC 938
Qy      692 TCATTTTTCCTTCTGTATTCCTGTCTCATATATATGTCTGTCTACACCTGATGATCC 751
Db      939 TCATCTTTCCTTCTCATATGCGGTCCTCATCATCATCTGTGTATGAGACTGATGATCT 998
Qy      752 TGCCTGTAAGGCTTCGGGCTCTTTCGCTCCGAGAGAAATATGAGCAACCTGCGTA 811
Db      999 TACGACTCAAGATGTCTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAACTTCGCGA 1058
Qy      812 GGATCAGCAGATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1059 GGATCAGCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1118
Qy      872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
Db      1119 ACATCTATGTATCATCAACACATGATCAGATTCCGAACCACTTTCAGACTGTT 1178
Qy      932 GCTATTACTTCTGCAATGCGCTTAAAGCTATACCAACAGTACCTGAAATCCATTTCTAC 991
Db      1179 CTTGCACTTCTGCAATGCGCTTAAAGCTATACCAACAGTACCTGAAATCCATTTCTAC 1238
Qy      992 CTTTCTTGTAATAAATCTCAAGCGGTGTTCGCGGACTTTCGCTTTCACATGAAAGTA 1051
Db      1239 CTTTCTTGTAATAAATCTCAAGCGGTGTTCGCGGACTTTCGCTTTCACATGAAAGTA 1298
Qy      1052 GGATGAGCGGACAGCACTAGCAGAGTCCGAATATACATTGAGATC 1099
Db      1299 CAATCGAACAGCAAACTCTGCTCGAATCCGTCAAAACACTAGGGAC 1346

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RESULT 54
US-10-194-595-15
; Sequence 15, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; CURRENT FILING DATE: 2002-07-11

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; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-16
```

Query Match	37.5%	Score 432.4;	DB 9;	Length 1610;
Best Local Similarity	65.8%;	Pred. No. 1.4e-114;		
Matches 663; Conservative	0;	Mismatches 336;	Indels 9;	Gaps 2

QY	92	CCGGCTGGGGCCGAGCCCGCAGACGAGAGCGCGGCGCTCGGAGAGCGCGCAGCTGGAGC	151
Db	401	CCGACCCACATGCGGGTCTTAACCGCAGCGGGGCTTGGGGGAGGCCACAGCCCTGTCAGAA	460
QY	152	CCGCGCACATCTCCCCCGGCATCCCGGTCATCATCAGGCGGGTCTACTCCGTAAGTTCG	211
Db	461	CCGGGAGGCCCTTCATGGTCAACAGCATTACATCATATGAGCCCTCTATTCTATCGTGTG	520
QY	212	TCGTGGGCTTGGTGGGCACTCGCTGTGTATGTTGTGTATCTCCGATACACAAAGATGA	271
Db	521	TATGTGGGCTCTTTGGAAACTTCCGTGCATGTATGTATGTATGAATATACAAATGA	580
QY	272	AGATGCAACCAACATTTACATATTTAACCCTGGCTTTGGCAGATGCTTATGTTACTACAA	331
Db	581	AGACTGCCACCAACATCTTACATTTTCAACCTGTCTGTGGCAGATGCTTTAGCCACTTGCA	640
QY	332	CCATGCCCCCTTACAGATACGGCTCTACTGTATGATATTCGTGGCCCTTTGGGAGTGTGCT	391
Db	641	CGTGCCTTTACAGTGTATTACTACCTGATGGAAACGTGGCCCTTTGGAAACATCTCT	700
QY	392	GCAAGATGTATTTTCCATTGTATTACTTACAACTGTTTCAACAGCATTTTACCTTGACCA	451
Db	701	GCAAGATGTATCTCAATTAAGACTTACAACTATTTACAGATATCTTCAACCCCTTGCA	760
QY	452	TGATAGCGGTGAGCCGCTACATTTGCGATGGCCACCCGCTGAAGGCTTTGACCTTCGCA	511
Db	761	CCATAGAGTGAACCGCTACATTTGCCGCTCTGCCACCCGCTCAAGGCCCTTGATTTCCGTA	820
QY	512	CACCTTTGAAGCAAAAGATCAATCAATATCTGCATCTGGCTGTGTGTCTATCTGTGGCA	571
Db	821	CCCCCCCCAAATGTCATATGTCTGCAATGTGATCTCTCTTCTGTGCATTGTGTC	880
QY	572	TCCTGCAATAGTCCTTGGAGGACCAAGTCAGGGAAGAGCTGCATGTCTTAGTGTCT	631
Db	881	TGCCGTAATGTTCAATGSCAACCAAAATACAGGCAAGGCTC-----CATAGATTGCA	934
QY	632	CTTTGCAATTCACAGATGATGACTACTCTGTGGTGGAACCTCTTTCATGAAATCTGCTCT	691
Db	935	CCCTCAGTTCTCTCATCCCACTATGTAATCTGGAGAACTGTCTC---AAATCTGTGTCT	991
QY	692	TCATCTTTGCTTGTGTATCCCTGTCTCTATCATCATCTGTCTGTCTACACCTGATGATCC	751
Db	992	TCATCTTTCGCTTATCATATGCGGGTCTCTCATCATCATCATGTGTGTATGATGATGATCT	1051
QY	752	TGCGTCTCAAGCGTCCGGCTCCCTTCTGTGGCTCCGAGAAAGATGAGCAACGTGGCTA	811
Db	1052	TACATCTCAAGATGTCCGATGCTGTGTGGCTTCCAAAGAAAGACAGAACTGTGGCA	1111
QY	812	GGATCACCAAGCTGTCTGTGTGTGTGTGAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	871
Db	1112	GGATCACCGGATGT	1171
QY	872	ACATATTCATCTGT	931
Db	1172	ACATCTATGTCTATCATCAAAAGACATGTATCAAGATTCAGAAACCATTTTCCAGACTGTTT	1231
QY	932	GCTATTTACTTGTGATCGCTTTAGGCTTACCAAGATGAGCTGAATCCATTTCTTACG	991
Db	1232	CTGTGCACTTGTGATGTCTTGT	1291
QY	992	CTTTCTTGTATGAAAACCTTCAAGCGGTGTCTTCCGGACCTTGTGTGTGTGTGTGTGTGTGT	1051

Db 1292 CGTTCGGATGAAAACTTCAACGATGTTTTAGAGAGTTGCACTCCAACTTCTCCCA 1351

Qy 1052 GGATGAGCGGACAGACACTAGCAGAGTCCGAAATACAGTTCCGATC 1099

Db 1352 CAATCGAACAGCAAAACTCTGCTCGAATCCCTCAAAACACATAGGGAAC 1399

RESULT 58
US-10-283-300-16
; Sequence 16, Application US/10283300
; Publication No. US20030103972A1

```

; ORGANISM: Mus musculus
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICED VARIANTS
; TITLE OF INVENTION: OF THE MU-OPIOID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-283-300-16

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Query Match	37.5%;	Score 432.4;	DB 15;	Length 1610;
Best Local Similarity	65.8%;	Pred. No. 1.4e-114;		
Matches 663: Conservative	0;	Mismatches 336;	Indels 9;	Gaps 2

QY	92	CCGGCTGGGCGGAGCCCGACAGCAACGGCAGCGCCGCTCGGAGAGACGGCAGCTGGAGC	151
Db	401	CCGACCCCATGTGGGCTCTAAACCGGCACGGGGAGCTTGGCGGGAGCCACAGCTCGTGCCCTTCAGA	460
QY	152	CCGGGCAACATCTCCCGCGCCATCCCGGATCATCAACGGCGGTCTACTCCGTAGTTCG	211
Db	461	CCGGCAGCCCTTCCATGATCAACAGCCATCAACATCAAGCCCTCTATTCATCGGTGTG	520
QY	212	TCGTGGGCTTGTTGGGGCAACTCGTGGTCATGTTCGTATCATCCGATACCAAAATGTA	271
Db	521	TATGGGCGCTTCTTGGAAACTTCTGTGTCATGTATGTATTTAAGATATACAAAATGA	580
QY	272	AGACAGAACCAACATTTAACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAA	331
Db	581	AGACTGCACCAACATCTACTATTTCAACCTTGTCTGGCAGATGCTTTAGCCACTACGA	640
QY	332	CCATGCCCCCTTCAAGATACGGTCTACTTGTGAAATTCCTGGCCCTTTGGGAGATGTGCTGT	391
Db	641	CGCGCCCCCTTCAAGTGTAACTACTCGTGAAGGAAAGTGGCCCTTTGGAAAACATCTCT	700
QY	392	GCAAGATAGTAATTTCCATTGATTTACTACAAACATGTTCAACAGCATCTTCACTTGACCA	451
Db	701	GCAAGATCGTATCTCAATAGACTACTACACAAATGTTTCAACAGATATCTTCAACCTCTGCA	760
QY	452	TGATGACCGTGAACCGCTACATTCGCGTGTGCCACCCCGTAAAGGCTTTGGACTTCCGCA	511
Db	761	CCATGATGTATGAACCGCTACATTCGCGTGTGCCACCCCGTAAAGGCTTTGGACTTCCGCA	820
QY	512	CACCTTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTGCTGTCATCTGTTGCA	571
Db	821	CCCCCGCAAAATGCCAAATGTCTCAATGTCTGCAACTGGAATCTCTCTTCTGCCAATGGTTC	880
QY	572	TCTCTGGAATAGTCTTTGGAGGCAACCAAGCAGGGAAGACGTGATGTCAATTAGTACT	631
Db	881	TGCCCCGAATGTTCTATGGCAACCAAAATTAACGGCAGGGGCTC-----CATTAATTTGCA	934
QY	632	CTTTGACGTTCCAGATGATGACTACTCTCGTGTGGAGCTTTCATGAAAGATCTGGCCT	691

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Db 935 CCTCAGCTTCTCTCATCCACATGCTAGTGGAGAACCTGCTC--AAATCTGTCT 991
Qy 632 TCATCTTGGCTTCCTGGATCCCTGCTCTCATCATCTCTGCTACACCTGATGATCC 751
Db 992 TCATCTTGGCTTCCTGGATCCCTGCTCTCATCATCTCTGCTACACCTGATGATCC 1051
Qy 752 TCCGCTCTCAAGACGCTCCGCTCTCTTCTGCTCCCGAGAGAAAGATCGCACTGCGTA 811
Db 1052 TACGACTCAAGAGTGTCCGCTCTCTGCTCCGCTCCAAAGAAAAGACAGAACTGCGCA 1111
Qy 812 GGATCACAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 1112 GGATCACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
Qy 872 ACATCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 1172 ACATCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
Qy 932 GCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 1232 CTTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
Qy 992 CTTTCTTGTGTAAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Db 1292 CTTTCTTGTGTAAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
Qy 1052 GGATGAGCGGCAAGCACTAGCAAGAGTCCGAATATACAGTTCAGATC 1099
Db 1352 CAATCGAACAGCAAACTCTGCTCGAATCCGTAACAAACACTAGGGAC 1399
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RESULT 59

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US-10-185-083-16
; Sequence 16, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Paeternek, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-16
```

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Query Match 37.5%; Score 432.4; DB 15; Length 1614;
Best Local Similarity 65.8%; Pred. No. 1.4e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;
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```
Qy 92 CCGGCTGGGCGAGCCGCAAGCAACGAGCGCGCTCGAGAGACGCGCAGCTGAGC 151
Db 522 CGGACCCAGTGGGTCTTAACGCGACGGGGCTTGGGGGAGCCAGCCGTGCTCAGA 581
Qy 152 CCGGCAATCTTCCCGGCGATCCGGGTCTATCATCAGCGCGGTCTTACTCCGATGTTG 211
Db 582 CCGGAGCCCTTCAATGTCACAGCATCATCATATGCCCCCTTATCTTATCTGCTG 641
Qy 212 TCGTGGGCTTGGTGGCAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
Db 642 TAGTGGGCTCTTTGGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
Qy 272 AGACAGCAACCAATTTACATATTTAACTGCTTGGCAGATGCTTATGTTACTACA 331
Db 702 AGACTGCCACCAATTTACATATTTAACTGCTTGGCAGATGCTTATGCTTACCTAGCA 761
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Qy 332 CCATGCCCTTTAGAGTACGCTCTACTGATGAAATTCCTGAGCTTTGGGAGATGCTCT 391
Db 762 CGCTCCCTTTAGAGTGTATCTACCTGATGAGAACTGAGCTTTGGAAATCTCTT 821
Qy 392 GCAAGATGATATTTTCAATGATTAATAACATGTTCAACGATCTTCACTTGAACCA 451
Db 822 GCAAGATGATATTTCAATGATTAATAACATGTTCAACGATCTTCACTTGAACCA 881
Qy 452 TGATAGGCTGAGACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511
Db 882 CCATAGATGATGACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
Qy 512 CACCTTGAAGCAAGATCAATCAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571
Db 942 CCCCCCAATGCAAAATTTGCAATGCTGCAATGATCTTCTTCTGCTGCTGCTGCT 1001
Qy 572 TCTTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATCATTTAGATGCT 631
Db 1002 TCCCGGTATGTTCAATGCAACCAAAATACAGGCAAGGGTCT-----CATGATTTGA 1055
Qy 632 CTTGCACTTCCAGATGATGATCTACTCTGCTGAGACCTTTCATGAAAGATCTGCT 691
Db 1056 CCTCAGCTTCTCTCATCCACATGATGTACTGGGAAACCTGCTC--AAATCTGTCT 1112
Qy 692 TCATCTTGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
Db 1113 TCATCTTGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
Qy 752 TCCGCTCTCAAGACGCTCCGCTCTTCTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
Db 1173 TACGACTCAAGAGTGTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
Qy 812 GGATCACAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 1233 GGATCACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
Qy 872 ACATCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db 1293 ACATCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
Qy 932 GCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 1353 CTTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1412
Qy 992 CTTTCTTGTGTAAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Db 1413 CTTTCTTGTGTAAGAACTTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1472
Qy 1052 GGATGAGCGGCAAGCACTAGCAAGAGTCCGAATATACAGTTCAGATC 1099
Db 1473 CAATCGAACAGCAAACTCTGCTCGAATCCGTAACAAACACTAGGGAC 1520
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RESULT 60

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US-10-194-595-16
; Sequence 16, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Paeternek, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
```

LENGTH: 1614
TYPE: DNA
ORGANISM: Mus Sp.
US-10-194-595-16

Query Match 37.5%; Score 432.4; DB 15; Length 1614;
Best Local Similarity 65.8%; Pred. No. 1.4e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCCGGACGAGCAGGAGCGCGGCTCGGAGAGCGCGCAGCTGGAGC 151
DB 522 CCGACCCATGCGGCTCTTAACCGGACGCGGCTTGGCGGAGCCACAGCCTGTGCTCCAGCA 581
QY 152 CCGGACGACATCTCCCGGCGCATCCGCGTATCATGACGCGGCGGTACTCGTAGTGTTCG 211
DB 582 CCGGAGCCCTTCCATGATGATGACAGGCGATCATGAGCCCTCTATTTATTCGTGTG 641
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTATGTCGTATCATCCGATACAGAAAGATGA 271
DB 642 TAGTGGGCTCTTTGGAACTTCTGTGTCATGATGATGATTAAGATATACCAAAATGA 701
QY 272 AAGACGAAACCAACATTTATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACA 331
DB 702 AAGCTGCCACCAACATTTATATTTCACTTGTCTGTGACAGATGCTTACGACACTAGCA 761
QY 332 CCATGCGCTTTGAGAGTACGATCTACTGATGAATTCCTGGCCTTTGGGAGATGTGCT 391
DB 762 CGCTGCGCTTTGAGAGTGTAACTACTATGAGAGAGCGGCGCTTTGGAAACATCTCT 821
QY 392 GCAAGATAGTAATTTTCATTTATTTACTACACATGTTCCAGCATCTTCACTTGACCA 451
DB 822 GCAAGATGCTGATCTCAATAGACTACTACACATGTTCCAGTATCTTCACTTGACCA 881
QY 452 TGATAGGCTGAGACCGCTACTATGTCGCTGCGCACCCGCTGAAGCTTTGGACTTCGCA 511
DB 882 CCATAGTGTAGACCGCTACATTTGCGTGTGCGACCGCGCTGAAGCGCTTGATTCGCA 941
QY 512 CACCTTGAAGCAAGATCATTAATTCGATCTGCGTGTGTCATCTGTTGACA 571
DB 942 CCCCCGAAATGCCAAATGTCAATGTGTCAGATGCTCTCTTGTGCAATGGTTC 1001
QY 572 TCTGTCAATAGTCTTGGAGGCGCAAAAGTCAAGGAAAGCGTCGATGTCATGAGTCT 631
DB 1002 TGCCGCTGATGTTCATGCGCAACCAAAATACAGCAGGAGTCTC-----CATAGATTGCA 1055
QY 632 CTTGACGTTCCCAATGATGATCTCTCTGCTGGAGCCTCTTATGAAATCTGCGCT 691
DB 1056 CCTTACGTTCTCTATCCCATGATGATCTGAGGAAACCTGCTC---AAATCTGTGTCT 1112
QY 692 TCATCTTTGCTTGGTATCCCTGTCTCATCATGATGATGATGATGATGATGATGATGATG 751
DB 1113 TCATCTTGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1172
QY 752 TGCGTCTAAGAGCGCTCGGCTCTTCTTGGCTCCGAGAGAAAGATGCAACTGTGCTA 811
DB 1173 TACGACTAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGAGAGCAAGCACTGCGCA 1232
QY 812 GGATACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 1233 GGATACACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 1293 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
QY 932 GCTATTTATCTTGCATGCTGCTTGAAGCTATACCAACAGTACCTGATATCTTCTTACG 991
DB 1353 CCTGACCTTCTGCAATGCTTGGGTATACAAACAGTGTGCTGCAACCACTGATCTTTATG 1412
QY 992 CTTTCTTGAAGAACTTCAAGCGGTGTTCCGGAATTCGCTTCCATGGAAGTGA 1051
DB 1413 GCTTCTGAGTGAATACTTCAACGATGTTTGAAGATGCTGCAATCCCACTTCTTCCA 1472

QY 1052 GGATGAGCGGAGAGCACTAGCAGATCCGAAATATACGTTCAAGATC 1099
DB 1473 CAATGAAACAGCAAACTGTCTGCAATCTGTCAAAACATTAAGGAGAC 1520

RESULT 61
US-10-185-083-24
Sequence 24, Application US/10185083
Publication No. US20030050467A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan Kettering Cancer Center
APPLICANT: Pasternak, Gavril
APPLICANT: Pan, Ying-Xian
TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
FILE REFERENCE: 830002-2007.1
CURRENT APPLICATION NUMBER: US/10/185,083
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/302,072
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 1695
TYPE: DNA
ORGANISM: Mus Sp.
US-10-185-083-24

Query Match 37.5%; Score 432.4; DB 15; Length 1695;
Best Local Similarity 65.8%; Pred. No. 1.4e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCCGGACGAGCAGGAGCGCGGCTGGAGAGCGCGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGACGCGGCTTGGCGGAGCCACAGCCTGTGCTCAGA 244
QY 152 CCGGACATCTCCCGGCGCATCCGCGTATCATGACGCGGCTCTACTCGTAGTGTTCG 211
DB 245 CCGGAGCCCTTCCATGATGATGATGACAGCAGCATCAACATGAGCGCTCTATTTATGATGTG 304
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTATGTCGTATCATCCGATACAGAAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAACTTCTGTGTCATGATGATGATTAAGATATACCAAAATGA 364
QY 272 AAGACGAAACCAACATTTATATTTAACTGGCTTTGGAGATGCTTTAGTTACTACA 331
DB 365 AAGCTGCCACCAACATTTATATTTTCACTTGTCTGCGAGATGCTTGAAGCACTAGCA 424
QY 425 CGTGCCTTTCAAGATGTTAACTACTAGTGGAGAGTGGCGCTTTGGAAACATCTCT 484
QY 392 GCAAGATAGTAATTTCCATGATTTACTACAAATGTTCCAGCATTTTCACTTGACCA 451
DB 485 GCAAGATGCTGATCTCAATGATCTACTACAAATGTTCCAGCATTTTCACTTGACCA 544
QY 452 TGATAGCGTGGACCGCTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511
DB 545 CCAATGATGAGACCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
QY 512 CACCTTGAAGCAAGATCATTAATTCGATCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 571
DB 605 CCCCCGAAATGCAAAATTTGTCAATGTGTGCAAGTGAATGCTCTGCTGCTGCTGCTGCTGCT 664
QY 572 TCTGTCAATAGTCTTGGAGGCAACCAAGTCAAGGAAAGCGTATGATGATGATGATGATG 631
DB 665 TGCCCGTAATGTTTCAAGGCAACCAAAATACAGGAGGAGTCTC-----CATAGATTGCA 718
QY 632 CTTGACGTTCCCAAGATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
DB 719 CCTTCACTTCTCTCATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 692 TCATCTTTGCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751

Db 776 TCATCTCGCTTCATCATCATGCGGCTCCATCATCATCTGTGTATGAGACTGATGATCT 835
 Qy 752 TCGCTCTCAAGAGCGCTCCGGCTCTTTCTGGCTCCCGAAGAAAGATGCCAATCTGGCTA 811
 Db 836 TACGACTCAAGAGTGTCCGACATGCTGTGCGGCTCCAAAGAAAGACAGAAACCTGGCGA 895
 Qy 812 GGATACACGAGATGCTGCTGT 871
 Db 896 GGATACACCGAGATGCTGT 955
 Qy 872 ACATATTCATCTGT 931
 Db 956 ACATCATGTATCATCATCAAGACATGATCAGCATTCAGAAACCATTTCCAGACTGT 1015
 Qy 932 GCTATTACTTCTGCATCGCTTAAAGCTATACCAACAGTAGCTGAATCCCATCTCTACG 991
 Db 1016 CTTGCACTCTTGTGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
 Qy 992 CTTTCTTGAATAAATTCAGACGGGTGTTTCCGGGACTTGTCTTCCACTGAAGATGA 1051
 Db 1076 CTTTCTGATGATAAATTCAGACATGATGTTTGAAGAGTTCTGCAATCCCACTTCTCCA 1135
 Qy 1052 GGATGAGCGGACAGACACTAGACAGTCCGAATACAGTTCAAGATC 1099
 Db 1136 CAATGAAACAGCAAACTCTGCTCGAATCCGTCAAAACACTAGGGAC 1183

RESULT 62

US-10-194-595-24
 ; Sequence 24, Application US/10194595
 ; Publication No. US20030068805A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Memorial Sloan Kettering Cancer Center
 ; APPLICANT: Pasteurmak, Gavril
 ; APPLICANT: Pan, Yang-Xian
 ; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
 ; FILE REFERENCE: 830002-2007.1
 ; CURRENT APPLICATION NUMBER: US/10/194,595
 ; CURRENT FILING DATE: 2002-07-11
 ; PRIOR APPLICATION NUMBER: US/09/561,523
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: 60/302,072
 ; PRIOR FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 24
 ; LENGTH: 1695
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 US-10-194-595-24

Query Match 37.5%; Score 432.4; DB 15; Length 1695;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

Qy 92 CCGGCTGGGCGGACCCGACAGCAACGAGCGCGGCTCCGAGAGACGGGACGCTGGAGC 151
 Db 185 CCGACCCATGCGCTCTTAACCGACGCGGCTTGGGGAGCCACAGCCCTGCTCCAGA 244
 Qy 152 CCGGACACATCTCCCGGCGCATCCGAGTATCATCAGCGGCTTACTCGTAGTGTG 211
 Db 245 CCGGAGCCCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
 Qy 212 TCGGAGGCTTGGTGGGCAATCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 271
 Db 305 TAGTGGGCTCTTGGAAATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 364
 Qy 272 AGACGCAACCAATTTATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
 Db 365 AGACTGCCACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 424
 Qy 332 CCATGCCCTTTCAGAGTACGCTCTACTGATGAATTCCTGGGCTTTTGGGGATGTGCTGT 391

Db 425 CGCTCCCTTTTCAGAGTGTAACTACTAGTGAAGCGGCTTTGGAAATCTCTCT 484
 Qy 332 GGAATATGTAATTTCCATTTATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 451
 Db 485 GCAATATGTAATTTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 544
 Qy 452 TGATAGGCTGGAACCGCTACATTTGCGGTGCGCAACCCCGTGAAGGCTTTGACTCCGA 511
 Db 545 CCATAGGTGTAGACCGCTACATTTGCGGTGCGCAACCCCGTGAAGGCTTTGACTCCGA 604
 Qy 512 CACCTTGAAGGCAAAATTCATCAATTTATCTGATCTGCTGTGTGTGTGTGTGTGTGTGT 571
 Db 605 CCCCCGAAATGCCAAATTTGTCAATTTGTCAATTTGTCAATTTGTCAATTTGTCAATTTGT 664
 Qy 572 TCTGTCAATGTCTTGTGAGGACCAAAATGTAGGAAAGACGTGCAATGTCAATGTGTGT 631
 Db 665 TCCCGGTATGTCTTGTGCAACCAAAATGTAGGAAAGACGTGCAATGTGTGTGTGTGTGT 718
 Qy 632 CTTGCAATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 Db 719 CCTTACGTTCTCTATCCACATGTATCTGAGAACTGCTC--AAATCTGTGTCT 775
 Qy 692 TCATCTTGTGCTTGT 751
 Db 776 TCATCTTGTGCTTGT 835
 Qy 752 TCGCTCTAAGAGCTCCGGCTCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
 Db 836 TACGACTCAAGAGTGTCCGACATGCTGTGCGGCTCCAAAGAAAGACAGAACTGGCGA 895
 Qy 812 GGATACACGAGATGCTGCTGT 871
 Db 896 GGATACACCGAGATGCTGT 955
 Qy 872 ACATATTCATCTGT 931
 Db 956 ACATCATGTATCATCATCAAGACATGATCAGCATTCAGAAACCATTTCCAGACTGT 1015
 Qy 932 GCTATTACTTCTGCATCGCTTAAAGCTATACCAACAGTAGCTGAATCCCATCTCTACG 991
 Db 1016 CTTGCACTCTTGTGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
 Qy 992 CTTTCTTGAATAAATTCAGACGGGTGTTTCCGGGACTTGTCTTCCACTGAAGATGA 1051
 Db 1076 CTTTCTGATGATAAATTCAGACATGATGTTTGAAGAGTTCTGCAATCCCACTTCTCCA 1135
 Qy 1052 GGATGAGCGGACAGACACTAGACAGTCCGAATACAGTTCAAGATC 1099
 Db 1136 CAATGAAACAGCAAACTCTGCTCGAATCCGTCAAAACACTAGGGAC 1183

RESULT 63

US-09-761-962-9
 ; Sequence 9, Application US/09761962
 ; Patent No. US2002007285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Memorial Sloan-Kettering Cancer Center
 ; APPLICANT: Identification and Characterization of Multiple Splice
 ; TITLE OF INVENTION: Variants of Mu-
 ; TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
 ; FILE REFERENCE: 830002-2000.1
 ; CURRENT APPLICATION NUMBER: US/09/761,962
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/743,872
 ; PRIOR FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 1729
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-761-962-9

Query Match 37.5%: Score 432.4; DB 9; Length 1729;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

OY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCCCGCTCGAGAGACGCGAGCTGGAGC 151
DB 185 CCGAGCCCAATGGCGGTCTTAACCGCAGCGGGGCTTGGGGGAGCCACAGCCTGTGCTCAG 244
OY 152 CCGGCAACATCTCCCGGCGCATCCGGGTATATACAGCGGGGTCTACTCCGATGTTG 211
DB 245 CCGGAGCCCTTTCAGGTGACAGCAGCATCACATATGCCCCCTTAATCTAATCGTGTG 304
OY 212 TCGTGGGCTTGGTGGGCAACTCGTGTATGTTGATCATCCGATACACAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAATTCCTGGTATGTATGTATTTAGATATACAAATGA 364
OY 272 AGACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGATCTTTAGTTACTACA 331
DB 365 AGACTGCCAACCACTACATTTTCAACCTTGTCTGGCAGATGCTTAGCCACTAGCA 424
OY 332 CCATGCCCTTTCAAGTACGTCTACTTATGTAATTCCTGGCTTTTGGGAGTGTCT 391
DB 425 CGCTGCCCTTTCAAGTGTAACTACCTGATGGAACGTGGCCCTTTGGAAACATCTCT 484
OY 392 GCAAGATAGTAATTTCCATGTATCTACCAACATGTTCAACGACATCTTCACTTGACA 451
DB 485 GCAAGATGTATCTCATATAGACTATACACATGTTCAACGATCTTCAACCTCTGCA 544
OY 452 TGATAGCGGTGACCGGTACATTTGCGGTGCAACCCCGTGAAGGCTTTGGA 511
DB 545 CCATAGAGTGTAGACCGGTACATTTGCGGTGCAACCCCGTGAAGGCTTTGGA 604
OY 512 CAACCTTGAAGCAAGATCATATCTATCTGATCTGTGTCGATCTGTGGA 571
DB 605 CCCCCGAAATGCAAAATGTGCAATGTGCAACTGGAATCTCTCTTCTGCAATGTGTC 664
OY 572 TCTCTGAATAGTCTTGGAGGACCAAAAGTCAAGGGAAGACGTGATCTATTAGTCT 631
DB 665 TGCCGTATATGTTATGCGACACCAAAATACAGGCAAGGCTC-----CATAGTTGA 718
OY 632 CTTTCAGTTCAGATGATGACTAATCTCGTGTGGGACCTTTCATGGAAGATCTGCT 691
DB 719 CCGTCACTTCTCTCATCCACATGATGTAAGTGGGAACCTGCTC---AAATCTGTGCT 775
OY 692 TCATTTTGGCTTGGTATCCCTGTCTCATCATATGATGTCTGTACACCTGATGATCC 751
DB 776 TCATTTTGGCTTCAATGACCGGTCTCATCATCTGTGTGTATGAGACTGATGATCT 835
OY 752 TGCGTCTGAAGAGCGTCCGGGCTCTTTCGTGGCTCCGAGAGAAAGATGCAACCTGCGTA 811
DB 836 TAGCATCAAGAGTGTCCGCAATGCTGTGGGCTCCAAAGAAAGAGACAGAAACCTGGCA 895
OY 812 GATATCAAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GATATCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
OY 872 ACATATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 956 ACATATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
OY 932 GCTATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
DB 1016 CCGTCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
OY 992 CTTTCTTGTATGAAATCTTCAAGCGGTGTTCCTGGGACTTCTGTTTCCATGGAATGA 1051
DB 1076 CGTTCCTGATGAAATCTTCAAGCGGTGTTCCTGGGACTTCTGTTTCCATGGAATGA 1135
OY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATACAGTTGAGATC 1099
DB 1136 CAATGGAACGCAAAATCTGTCTGGAATCCGTCAAAACATAGGGAAC 1183

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RESULT 64
 US-10-283-300-9
 ; Sequence 9, Application US/10283300
 ; Publication No. US20030103972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Memorial Sloan-Kettering Cancer Center
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICED VARIANTS
 ; FILE REFERENCE: 830002-2000.3
 ; CURRENT APPLICATION NUMBER: US/10/283.300
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 09/761,962
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/743,872
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/15974
 ; PRIOR FILING DATE: 1999-07-15
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 1729
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-283-300-9

Query Match 37.5%: Score 432.4; DB 15; Length 1729;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

OY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCCCGCTCGAGAGACGCGAGCTGGAGC 151
DB 185 CCGAGCCCAATGGCGGTCTTAACCGCAGCGGGGCTTGGGGGAGCCACAGCCTGTGCTCAG 244
OY 152 CCGGCAACATCTCCCGGCGCATCCGGGTATATACAGCGGGGTCTACTCCGATGTTG 211
DB 245 CCGGAGCCCTTTCAGGTGACAGCAGCATCACATATGCCCCCTTAATCTAATCGTGTG 304
OY 212 TCGTGGGCTTGGTGGGCAACTCGTGTATGTTGATCATCCGATACACAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAATTCCTGGTATGTATGTATTTAGATATACAAATGA 364
OY 272 AGACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGATCTTTAGTTACTACA 331
DB 365 AGATGCGCAACCAATTTACATATTTAACTGGCTTTGGCAGATCTTTAGTTACTACA 424
OY 332 CCATGCCCTTTCAAGTACGTCTACTTATGTAATTCCTGGCTTTTGGGAGTGTCT 391
DB 425 CGCTGCCCTTTCAAGTGTAACTACCTGATGGAACGTGGCCCTTTGGAACATCTCTCT 484
OY 392 GCAAGATAGTAATTTCCATGTATCTACCAACATGTTCAACGACATCTTCACTTGACA 451
DB 485 GCAAGATGTATCTCATATAGACTATACACATGTTCAACGATCTTCAACCTCTGCA 544
OY 452 TGATAGCGGTGACCGGTACATTTGCGGTGCAACCCCGTGAAGGCTTTGGA 511
DB 545 CCATGAGTGTAGACCGGTACATTTGCGGTGCAACCCCGTGAAGGCTTTGGA 604
OY 512 CAACCTTGAAGCAAGATCATATCTATCTGATCTGTGTCGTCATCTGTGGA 571
DB 605 CCCCCGAAATGCAAAATGTGCAATGTGCAACTGGAATCTCTCTTCTGCAATGTGTC 664
OY 572 TCTGTGAATAGTCTTGGAGGACCAAAAGTCAAGGGAAGACGTGATGATGAGTGT 631
DB 665 TGCCGTATATGTTATGAGCAACCAAAATACAGGCGGGGCTC-----CATAGATTGCA 718
OY 632 CTTTCAGTTCAGATGATGACTCTGTGTGGGACCTTTCATGGAAGATCTGCTCT 691
DB 719 CCGTCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 775
OY 692 TCATCTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 751
DB 776 TCATCTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 835

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Best Local Similarity 65.8%; Pred. No. 1.6e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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OY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGGAGGACGCGCAGCTGGAGC 151
DB 185 CCGAGCCCAATGCGGCTCTTAACCGGACGGGGCTTGGGGAGGCCACGCGCTGTCCAGCA 244
OY 152 CCGGCAACATCTCCCGGCGCATCCCGGTCATCATCAGCGCGGCTCTAATCCGAGTGTTCG 211
DB 245 CCGGAGCGCCCTTCCATGCTCAGGCAACATCAGATGAGCCCTCTAATCTATCGTGTG 304
OY 212 TCGTGGGCTTGGTGGGCAACTCGCTGATCATGTTGATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAACTTCCTGATCATATGTATGTATGAATATACCAAAATGA 364
OY 272 AGACAGCAACCAACTTTATCATATTTAACTGCTTTGGCAGATGCTTATGTTACTACA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACTTGTCTGTGGCAGATGCTTATGCACTAGCA 424
OY 332 CCATGCGCTTTCAGAGTACGGCTCTACTGATGTAATTCGAGGCTTTTGGGGATGTCGT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTAGTATGGAACGTGGCCCTTTGGAAACATCTCT 484
OY 392 GCAAGATGTAATTTCCATTGATTAATCAACATGTTGACAGCATCTTCACTTTGACCA 451
DB 485 GCAAGATGTAATTTCCATTGATTAATCAACATGTTGACAGCATCTTCACTTTGACCA 544
OY 452 TGATGAGGTGGAACGGCTCACTTGGCTGTGCGACCCCGTGAAGGCTTTGACCTCGCA 511
DB 545 CCATGAGTGTGAGACCGGTACATGTCGTCGACCCCGTCAAGGCTTGAATTTCCGTA 604
OY 512 CACCTTTGAAGCAAGAATCAATATCTGATCTGCTGCTGTGTCATCTGTTGCA 571
DB 605 CCCCCGAAATGGCAAAATTTGTCATGTCTGCACTGATCTCTCTTCTGTGCAATGGTC 664
OY 572 TCTGTCAATAGTCTTGGAGGCAACAAAGTCAGGAAAGACGTGATGTCATTTAGTGT 631
DB 665 TGCCGCTATGTTTCAATGCAACCAAAATACAGGCAAGGCTC-----CATAGATTGCA 718
OY 632 CTTTGCAATTTCCCAATGATGATCTCTGCTGTGGACCTCTTCAATGAAGATTCGCT 691
DB 719 CCGTCAAGTCTCTCATCCCATGTAATGTAAGGAAACCTGCTC---AAATCTGTGCT 775
OY 692 TCATCTTGGCTTGTGATCCCTGTCTCATGATGATGTCGTCAGCAACCTGATGATCC 751
DB 776 TCATCTTGGCTTGTGATCCCTGTCTCATGATGATGTCGTCAGCAACCTGATGATCC 835
OY 752 TGCGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAAAGATGCAACCTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGATGCTGTGAGGCTCCAAAGAAAGAGCAAGAACCTGGCA 895
OY 812 GGATACCAAGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGATACCAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
OY 872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 956 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
OY 932 GCTATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
DB 1016 CTTGCACTTCTGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
OY 992 CTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
DB 1076 GCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
OY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATATACAGTTCAGGATC 1099
DB 1136 CAATCGAACAGCAAACTCTGCTGAAATCCGTCAAAACATAGGGAAC 1183
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RESULT 67

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US-10-185-083-23
; Sequence 23, Application US/10185083
; Publication No. US2003050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 2588
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-23
```

Query Match 37.5%; Score 432.4; DB 15; Length 2588;
Best Local Similarity 65.8%; Pred. No. 1.6e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```
OY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGGAGGACGCGCAGCTGGAGC 151
DB 185 CCGAGCCCAATGCGGCTCTTAACCGGACGGGGCTTGGGGAGGCCACGCGCTGTCCAGCA 244
OY 152 CCGGCAACATCTCCCGGCGCATCCCGGTCATCATCAGCGCGCTCTAATCCGAGTGTTCG 211
DB 245 CCGGAGCGCCCTTCCATGCTCAGGCAACATCAGATGAGCCCTCTAATCTATCGTGTG 304
OY 212 TCGTGGGCTTGGTGGGCAACTCGCTGATCATGTTGATCATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAACTTCCTGATCATATGTATGTATGAATATACCAAAATGA 364
OY 272 AGACAGCAACCAACTTTATCATATTTAACTGCTTTGGCAGATGCTTATGTTACTACA 331
DB 365 AGACTGCCACCAACATCTACATTTTCAACTGTGCTGTGCAAGATGCTTATGCACTAGCA 424
OY 332 CCATGCGCTTTCAGAGTACGGCTCTACTGATGTAATTCGAGGCTTTTGGGGATGTCGT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTAGTATGGAACGTGGCCCTTTGGAAACATCTCT 484
OY 392 GCAAGATGTAATTTCCATTGATTAATCAACATGTTGACAGCATCTTCACTTTGACCA 451
DB 485 GCAAGATGTAATTTCCATTGATTAATCAACATGTTGACAGCATCTTCACTTTGACCA 544
OY 452 TGATGAGGTGGAACGGCTCACTTGGCTGTGCGACCCCGTGAAGGCTTTGACCTCGCA 511
DB 545 CCATGAGTGTGAGACCGCTCACTTGGCTGTGCGACCCCGTGAAGGCTTTGACCTCGCA 604
OY 512 CACCTTTGAAGCAAGAATCAATATCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 571
DB 605 CCCCCGAAATGGCAAAATTTGTCATGTCTGCACTGATCTCTCTTCTGTGCAATGGTC 664
OY 572 TCTGTCAATAGTCTTGGAGGCAACAAAGTCAGGAAAGACGTGATGTCATTTAGTGT 631
DB 665 TGCCGCTATGTTTCAATGCAACCAAAATACAGGCAAGGCTC-----CATATATTGCA 718
OY 632 CTTTGCAATTTCCCAATGATGATCTCTGCTGTGGACCTCTTCAATGAAGATTCGCT 691
DB 719 CCGTCAAGTCTCTCATCCCATGTAATGTAAGGAAACCTGCTC---AAATCTGTGCT 775
OY 752 TGCGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAAAGATGCAACCTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGATGCTGTGAGGCTCCAAAGAAAGAGCAAGAACCTGGCA 895
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QY	92	CCGGCTGGGGCCGAGCCCGGACAGCAACGGGAGCGCCGCTCCGAGAGACCGCAGCTGGAGC	151
Db	125	CCGACCCATGCGGCTCGAAGCCGACCAACCTGGGCGGAGAGACAGCCTGTGCTCCCA	184
QY	152	CCGGCACAATCTCCCCGGCCATCCCGGTCATCAACGGCGGTCTACTCCGTAGTGTTCG	211
Db	185	CCGGCAGTCCCTCCATGATCAAGGCATCAACGATCATGGGCCCTCTACTCCATGTGTGGG	244
QY	212	TGCTGGGCTTGGGGGCACTCGCTGGTCATGTCGTATCATCCGATACCAAAATATA	271
Db	245	TGGTGGGCTCTTCGAAACTTTCGTGTATGTATGTGTCATATACCAATATGA	304
QY	272	AGACAGCAACCAACATTTTACATATTTAACCTGGCTTTGGCAGATGCTTAGTTACTACAA	331
Db	305	AGACTGCCACCAACATCTACATTTTCAACTTGGCTCTGGCAGATGCTTAGACCAACAGTA	364
QY	332	CCATGCCCTTTAGAGTACGGTCTACTGTATGTAATTCCTGGCTTTTGGGAGTGTGCTGT	391
Db	365	CCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCTCTT	424
QY	392	GCAAGATAGTAATTTTCCATTTGATTACTACAAAGATGTTCCACAGCATCTTACCTTGACCA	451
Db	425	GCAAGTATGTATCTCCATAGATTACTAATAATGTTACACGACATATTCACCTCTGCA	484
QY	452	TGATAGAGCTGGAACCGCTACATTTGCCGTGTGCCACCCGTTGAAGGCTTTGGACTTCCGA	511
Db	485	CCATAGGTGTATGATACATATGCAATTTGCAAGTCGCCACCTGTCAAGGCTTAGATTTCCGTA	544
QY	512	CACCCCTTGAGGCAAAAGATCATCAATATCTGCATCTGGCTGTGTCATCTGTGTGGCA	571
Db	545	CTCCCCGAAATCCAAAAATTAATCAATGTCTGGCACTGGATCTCTCTTAGCACTTGGTTC	604
QY	572	TCTCTGCAATAGTCTCTTGGAGGACCAAAAGTCAGGGAACAGTCGATGTCAATTGAGTCT	631
Db	605	TTCTGTATGTTCATGTGGCTACACAAATTAAGGCAAGG-----TTCCATAGATTGTA	658
QY	632	CCCTTCAGTTCCCAATGATGACTACTCCGTGTGGGACCTCTTCATGAGATCTGCGTCT	691
Db	659	CACTAACATTTCTCTCATCCAACCTGTGACTGTGGAAACCTCG---TGAAGATCTGTGTT	715
QY	682	TGATCTTTGGCTTCGTGATCCCTGTCTCATATCATGTCGTCTGCTACACCTGTAGTATCC	751
Db	716	TCATCTTGCCCTTCAATTATGCGCAGTGTCTATATTAACGTGTGCTATGAGACGTAGTATCT	775
QY	752	TGCGTCTCAAGAGCGATCCGAGTCTCTTTTGTGCTCCGAGAGAAAGATCCCACTGCGTA	811
Db	776	TGCGCTCAAGAGTGTCCGCAATGCTCTCTGGCTCCAAAGAAAGAGACAGGAATCTTCGA	835
QY	812	GGATACACAGACTGGTCTGTGTGTGTGTGGCACTTTCGTGCTGTCTGCTGGACTCCATTC	871
Db	836	GGATCAAGAGATGGTGTGTGTGTGTGGCTGTGTTCATCTGTCTGTGACTCCCATTC	895
QY	872	ACATATTCATCTGTGTGAGGCTCTGGGGAAGCACTCCACAGCAACAGCTGCTCTCTCCA	931
Db	896	ACATTTAGCTATCATTTAAAGCTTGTGTTCATATCCGAAACTAGCTTCAGAGCTGTT	955
QY	932	GCTATTACTTTGCACTGGCTTAGGCTATACCAACAGTACCTGTAATCCATTTCTCTACG	991
Db	956	CTTGGCACTTTCGCAATGCTCTAGGTTTACAAACAGCTGCTTCAACCCAGTCTTTTAGG	1011
QY	992	CCTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTTCGCTTTCACATGAAGATGA	105
Db	1016	CATTTCTGTGATGAAAACTTCAACCATGCTTTAGAGAGTTCTGTATCCCACTCTTCCA	1077
QY	1052	GGATGAGCGGCAAGCACTAGCAGAGTCCGAATA	1087
Db	1076	ACATTGAGCAACAAAACCTCACTCCAAATTCGTCCAGA	1111

RESULT 70
US-09-826-509-544
; Sequence 544, Application US/09826509

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; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 544
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-544

Query Match      37.4%      Score 431.6; DB 11; Length 1203;
Best Local Similarity 66.1%;      Pred. No. 2.1e-114;
Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;

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Query Match	37.4%	Score 431.6	DB 11	Length 1203	
Best Local Similarity	66.1%	Pred. No. 21e-114			
Matches	658	Conservative	0	Mismatches 329	Indels 9
				Gaps	2
QY	92	CCGGCTGGGGCCGAGCCCGACAGCAACGGCAGCGCCGGCTCGGAGGACGGCGACCTGGAGC	151		
Db	125	CCGACCCATGGGGGTCCGACCGGACCAACCTGGGGGGGAGACAGAGCCGTGTCCCTCCGA	184		
QY	152	CCGGCGACATCTCCCCGGCCATCCCGGTATCATACGAGCGGTCTTACTTCGGATGTTCG	211		
Db	185	CCGGCAGTCCCTCCATGTATCAACGGCCATCAAGATCATGGCCCTTACTTCATCGTGTGCG	244		
QY	212	TCGTGGGCTTGGTGGGCACTCGCTGTGCATGTTGGTATCATCCGATTAACAAGAATA	271		
Db	245	TGGTGGGGCTCTTGGGAACCTTCCGTGTATGTATGTATGTCCAGATTAACAACAAGATTA	304		
QY	272	AGACAGCAACAACATTACATATTAACTGGCTTTGGCAGATGCTTATGTACTACA	331		
Db	305	AGACTGCCAACAAACATCTACATTTTCAACCTTGTCTGTGGCAGATGCTTATGGCACCA	364		
QY	332	CCATGCCCTTTCAAGATACGGTCTTACTGTATGAATTCCTGGCCTTTTGGGGATGTGCTGT	391		
Db	365	CCCTGCCCTTCCAGATGTGAATTAACCTAAATGGGAACATGGCCATTGGAAACATCTCTT	424		
QY	392	GCAAGATATGTAATTTCCATTTATTACTACACATGTTTACACAGCATCTTCACTTGAACA	451		
Db	425	GCAAGATATGTAATCTCCATATGATTAATTAATTAATGTTTACACAGCATATTCACCCCTGTGA	484		
QY	452	TGATGAGCGTGAACCGCTACATTTGGCGGTGACACCCCGTGAAAGGCTTTGGACTTCCGA	511		
Db	485	CCATGAGTGTGATTCGATACATTTGACAGTCTGCCACCCCTGTCAAGGCTTTAGATTTCCGTA	544		
QY	512	CACCCCTTGAAGGCAAAAGATCATATATCTGCATCTGGCTGTGCTGTGTATCTGTTGGCA	571		
Db	545	CTCCCCGAAATGCAAAATTAATCAATGTCTGCACTGGATCCTGTCTTCAGGCATTTGGTC	604		
QY	572	TCTCTGCATATGTCCTTTGGAGGCAACAAAGTCAGGGAAGAGTGCATGTCAATTAGTGCT	631		
Db	605	TTCTCTGTAATGTTATGGCTTCAACAACAATAACAGGCAAGG-----TTCCATATGATTTGTA	658		
QY	632	CCTTGACGTTCCGAGATGATGATCACTCTGTGGTGGGACCTCTTCAATGAAGATCTGCGTCT	691		
Db	659	CATTAACATTTCTTCATCCAACTTGTGTACTGGAAAACTGTG--TGAAGATCTGTGTTT	715		
QY	692	TCATCTTTTGCCTTGTGATCCCTGTGCTCATATCATCTGCTGTGTACACCCGTATGATTC	751		
Db	716	TCATCTTGTGCTTCAATATATGCAATGTGTCAATCAATTAACGTGTGTCTATATGACATGATCT	775		
QY	752	TGCGTCTCAAGAGCGTCCGCTCTTCTTGGCTCCCGAGAAAGATGCAACTTGCCTA	811		
Db	776	TGCGCTCTCAAGAGTGTCCGATGTCTCTGTGCTCCAAAGAAAGACAGGAATCTTTCGAA	835		

NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 10
LENGTH: 1149
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide sequence of MOR-V2R chimera
US-09-993-844-10

Query Match 37.3%; Score 430.4; DB 9; Length 1149;
Best Local Similarity 68.1%; Pred. No. 4,5e-114;
Matches 631; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 110 ACAGACGCGGACCGCGCTGGAGAGACGCGACCTGGAGCCCGCGACATCTCCCGG 169
DB ACCGACCGGCGCTTGGCGGAAAGACAGCTGTGCCCTCAGACCGGACCGCTTCATGG 196
QY 170 CCATCCCGGTCACTACACGCGGCTCTACTCCGTAGTGTCTGCGGCTTGGTGGCA 229
DB 197 TCACAGGCATTACCATCAGTGGCCCTCTACTCTATGCTGTGTAGTGGCCCTTCGGAA 256
QY 230 ACTCGCTGTGATGTTCTGTATCATCCGATACCAAAAGATGAAGACAGCAACCAATTT 289
DB 257 ACTTCCTGTCATGTATGTATGTATGATTAACCAAAATGAAGACTGCCACCAATCT 316
QY 290 ACATTTTAACCTGGCTTGGAGATGCTTATTAACAACATGCCCTTTCAGATTA 349
DB 317 ACATTTCAACTTCTCTGCGAGACGCTTACGACCACTACCTGCGCTTCAGATG 376
QY 350 CGGTCTACTGTATGATTCCTGGCCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCA 409
DB 377 TCAACTTACCTGATGGAAACATGGCCCTTCGGAACATCTCTGCAAGATCTGATCTAA 436
QY 410 TTGATTACTACAACTGTTTACCAAGATCTTCACTTGAACATGATGAGCGTCT 469
DB 437 TAGATTACTACAACTGTTTACCAAGATCTTCACTTGAACATGAGCGTCTGACCCCT 496
QY 470 ACATGGCGGTGGACCGCGGTAAGGCTTGGACTTCGCGACACCTTGAAGGAAAGA 529
DB 497 ACATTTGCTGTCTGCGACCAAGTCAAGCCCTGATTTCCGTACCCCGAAATGCAAAA 556
QY 530 TCATCAATATCTGATCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 589
DB 557 TCGTCAAGCTGTGCAAGTGAATCTCTCTGTGCAATGCTGTGCTGTGTATGTTCAAG 616
QY 590 GAGGACCAAAAGTCAAGGAAAGCTGATGTATGATGAGTCTCTTGAAGTTCCAGATG 649
DB 617 CAACCAAAAATACAGGCA-----GGGATCCATGATGCACTCTCAAGTTCTCCACC 670
QY 650 ATGACTACTCTCGTGGGACCTCTTCATGAGATCTGGGTCTTCACTTGGCTTCGGA 709
DB 671 CAACCTGTATCTGGAGAACTGCTC---AAATCTGTGTCTTATCTTGGCTTTCATCA 727
QY 710 TCCCTGTCTGATCATCTGCTGTCTGCTACACCTGTATGATCTGTGCTCAAGAGCTGC 769
DB 728 TGGCATCTCATCATCTGCTGTGTGTTACGGCTGTATGATCTTACGATCAAGAGCGTTC 787
QY 770 GCGTCTTCTGTGCTCTCCGAGAGAAAGATCGCAACTGTGTGATGATCAACGAGTGGTCC 829
DB 788 GCATGCTATCGGGCTCCAAAAGAAAGACAGAAATCTCGAGATGATCAACCGGATGGTGC 847
QY 830 TGGTGTGTGTGAGAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
DB 848 TGGT 907
QY 890 AGGCTCTGGGAGCACTCCACAGACAGAGTGTCTCTCAAGATTAATCTTGTGATG 949
DB 908 AAGGCTGTATCATCATCTCAAGAAACACATTTCAAGACGTTTCGGGACCTTGTGATG 967
QY 950 CCTTAGGCTATACCAAGATGAGCTGATTCATCTCTTACGCTTTTGTGATGAAACT 1009
DB 968 CTTTGGGTTTACAGAAAGCTGCTGATTCAGTTCTTTACGCTTCTGTGATGAAACT 1027

QY 1010 TCAAGCGGTGTTCCGGGACTTCTGC 1035
DB 1028 TCAAGCGATGCTTCAAGAGTTCTGC 1053

RESULT 73
US-09-761-962-4
Sequence 4, Application US/09761962
Patent No. US2002007285A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization of Multiple Splice
TITLE OF INVENTION: Variants of Mu-
FILE REFERENCE: 83002-2000.1
CURRENT APPLICATION NUMBER: US/09/761,962
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1542
TYPE: DNA
ORGANISM: Mus musculus
US-09-761-962-4

Query Match 37.2%; Score 429.2; DB 9; Length 1542;
Best Local Similarity 65.6%; Pred. No. 1.2e-113;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGACCGGACGCAACGCGCGGCTGGAGAGCGGAGCTGAGC 151
DB 185 CCGACCATGTGGCTCTTAAACGACGCGGCTTGGCGGAGCAAGCTGTGCTTCA 244
QY 152 CCGGACATCTCCCGGACATCCGGTATCATCAGCGGATCTACCTGATGTTG 211
DB 245 CCGGACCGCTTGCATGATGATCAGCCATCAACATGAGGCGCTTATCTATGCTGTG 304
QY 212 TCGTGGCTTGTGGGCACTCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 271
DB 305 TAGTGGGCTCTTGGAACTCTGCTGATGTATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
DB 365 AGATGCGACCAATCTTCAATTTTCAACTTGTCTGTGAGATGCTTGTGCACTGCA 424
QY 332 CCATGCCCTTTCAGAGTACGCTCTACTTGTATGATTCCTGCGCTTTTGGGATGTGCT 391
DB 425 CCGTGGCTTTCAGAGTATTAATCTGATGAGGAGTGGGCGCTTTGAAACATCTCT 484
QY 392 GCAAGATGATTAATTTCCATGATTAATTTCAACAATGTTCAACAGATTTTCACTTGA 451
DB 485 GCAAGATGATGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 544
QY 452 TGAAGAGGAGACCGTCAATGTCGCTGTGCAACCGCGTGAAGGCTTGGACTTCCGA 511
DB 545 CCAATGATGATGACCGCTTCAATGTCGCTGTGCAACCGCGTGAAGGCTTGGACTTCCGA 604
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGCTGTCTGTCTGTCTGTGGA 571
DB 605 CCGCGGAAATGCAAAATTTGTCAATGTCTGCAAGTGGATCTCTCTTCTGCAATTTG 664
QY 572 TCTGTCAATGATCTTGTGAGGACCAAGTCAAGGAAAGCTGTGATGATGATGATG 631
DB 665 TGCCTGTAATGTTTCAATGCAACCAAAATACAGGAGGAGTCT-----CATGATG 718
QY 632 CTTGAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 719 CCTTCAAGTCTCTCACTCCCAATGATGATGATGATGATGATGATGATGATGATGATG 775
QY 692 TCATCTTGTGCTGTGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 751

[illegible]

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RESULT 74
US-10-283-300-4
Sequence 4, Application US/10283300
Publication No. US20030103972A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICED VARIANTS
FILE REFERENCE: 830002-2000.3
CURRENT APPLICATION NUMBER: US/10/283,300
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/761,962
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US99/15974
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1542
TYPE: DNA
ORGANISM: Mus musculus
US-10-283-300-4

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	Query Match	Similarity	Score	429.2	DB 15	Length	1542
	Best Local	Similarity	65.6%	Pred.	No. 1.2e-113		
	Matches	661	Conservative	0	Mismatches	338	Indels 9; Gaps 2
QY	92	CCGCGTGGGGCCGAGCCCGACAGCAACGGCAGGCCCGCGCTCGAGAGACGCGCAGCTGGAGC	151				
DB	185	CCGAGCCCATGCGGCTCTTAACCCGACGGGGCTTGGCGGGAGCCACAGCCTGTGCTCCCTCAGA	244				
QY	152	CCGGGCCACATCTCCCGCGGCATCCGGTCATATACCGGGGGCTTACTCCGATAGTTCG	211				
DB	245	CCGGCAGCCCTTCCATGGTCACAGCCATATACCATCATGGCCCCCTTAATTTCGTGTGTG	304				
QY	212	TCTGTGGGCTTGGTGGGCACTCGCTGTCATGCTTCGTGATCATCCGATACACAAAATGA	271				
DB	305	TAGTGGGCTCTTTGGAAACTTCGTGTCATGATGATGATGATGAAATATATACCAAAATGA	364				
QY	212	AGACAGCAACCAACATTTATCATATTTAACTGTGCTTTGGCAATGCTTTAGTATCTACAA	331				
DB	365	AGACTGCCACCAACATCTAATATTTTCAACTTGTCTGTGCAATGCTTTAGCCACTACGA	424				

OY	332	CCATGCCCTTTCAGAGTGAACGGTCTACCTGGATGAATTCCTGGCCCTTTTGGGGAGTGTGCT	331
OY	332	CCATGCCCTTTCAGAGTGAACGGTCTACCTGGATGAATTCCTGGCCCTTTTGGGGAGTGTGCT	331
Db	425	CGTGCCTTTCAGAGTGTAACTACCTGATGGAAAGTGGCCCTTTGGAAACATCTCT	484
OY	392	GCAAGATAGTAAATTCATTTGATTTACTACAAAGATGTTCAACGACATCTTCAACCTTGACCA	451
Db	485	GCAAGATGTGTATCTCAATAGACTCTAACAAGATGTTCAACGATCTTCACTCCCTGTGCA	544
OY	452	TGATGAGCGTGGACCGCTACATTGGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCA	511
Db	545	CCATGAGGTGAGACCGCTACATTTGCCGTCTGCCACCCCGGTCAAGGCCCTGGATTTCCGTA	604
OY	512	CACCCCTTAAAGCAAAAGATTCATCAATATTCGATCTGGCTGTCGTGATCTGTTGGCA	571
Db	605	CCCCCGAAATGCCAAAAATTTGAAATGTTGCAATGTGCAACTGGAATCTCTTTTGCCACTTGTGC	664
OY	572	TCTGTCAATAGTCCCTTGGAGGACCAAAAGTCAGGGAAACGTGATGATTAAGTGCT	631
Db	665	TGCCCGTATGTTTATGGCAACCAAAATTAAGGAGGGGATC-----CATAGATTTGCA	718
OY	632	CCTTGCAAGTTCACAGATGAATCACTCTCTGTGGAGCTCTTTCAATGAAGATCTGCTCT	691
Db	719	CCCTCACGTTCTCTATCCCAATGGTAAGTGGAGAACTGCTC-----AAATCTGTGTCT	779
OY	692	TCATCTTGGCCTTGGTGAATCCCTGTCTCATCATCATATGCTGTCTACACCTGATGATCC	751
Db	776	TCATCTTGGCCTTCAATCAATCCGGTCTCTATCACTGTGTGTTATGCACTATGATCT	835
OY	752	TGCGTCTCAAGACGCTCCGCGCTCTCTTTCGAGCTCCGAGAGAAAGATTCGCAACTGTGTA	811
Db	836	TACGACTCAAGAGTGTCCGCAATGCTGTGGGGCTCCAAAGAAAGACAGGAACCTGGCA	895
OY	812	GGATCAACAGACTGGTCTGTGTGTGTGTGTGGCACTTTCGTCTGTCTGTGAATCCCATTC	871
Db	896	GGATCAACCCGATGTGTGTGTGTGTGTGTGTGTATTTATGTCTGTGTGAACCCCATTC	955
OY	872	ACATATTCATCCGTGGTGGAGGCTCTGGGGAGACCTCCACAGACAGCTGTCTCTCCA	931
Db	956	ACATTTATGTCACTCAAGACACTGATACGAATTCAGAAACCACTTTCAGACATGTTT	1011
OY	932	GCTATTACTTTCGATTCGCTTGGCTTATATCCAAAGTACCGCTGAATTCCTTACG	991
Db	1016	CCTGGCACTTTCGATTCGCTTGGGTTTACAAAGACGCTCGCAACCCAGTCTTTATG	1070
OY	992	CCTTTCTTGATGAATACTTCAAGCGGTGTTTCCGGGACTTTCGCTTTCCACTGAAGTGA	1059
Db	1076	CGTTCCTGGATGAATACTTCAAGCGATGTTTAAAGAGTCTTGCAATCCCACTTCTCCA	1131
OY	1052	GGATGGAACGGACAGCACTACACAGTCCGAATCAATTCAGATGATC	1099
Db	1136	CAATGAACAGCAAACTCTGCTCGATCCGTCTAAACACTAGGGAAC	1183

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-823-114-15

Query Match 37.2%; Score 429.2; DB 9; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.3e-113;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;
Qy 92 CCGGCTGGGCGGAGCCGACAGCAAGCGGCGGCTCGAGAGGACCGAGCTGAGC 151
Db 374 CCGAGCCATGGGCTCTTAACCGAGGCGCTTGGGGAAGACGCGCTGCGCCCTGACA 433
Qy 152 CCGGACATCTCCCGGCGATCCGGTCATCATCGCGGCTTACTCTCGTAGTTCG 211
Db 434 CCGGAGCCCTTCCATGCTCAAGCAGCATCACCATCATGCGCTTATCTATCGTGTG 493
Qy 212 TCGGCGGTGGTGGGCAACTCGCGTCATGTCGTGATCATCCGATACCAAGATGA 271
Db 494 TAGTGGGCTCTTGGAACTTCCTGGTCATGATGATGATGATGAATTAACCAAAATGA 553
Qy 272 AGACAGCAACCAATTTACATATTAACTGCTTGGCAGAGTCTTAACTTACTACA 331
Db 554 AGACGCGCAACCACTACATTTTCAACTGCTCTGCGAGATCCCTTAAGCACTACA 613
Qy 332 CCATGCCCTTCAAGTACGCTTACTGATGAATTCCTGGCTTTGGGATGCTGT 391
Db 614 CGTGCCTTTCAGAGTGTAACTACGATGGGAACGTGGCCCTTGGAAACATCTCT 673
Qy 392 GCAAGATGTAATTCATGATTTAATACTAACAATGTCACAGACATCTTCACTGACA 451
Db 674 GCAAGATGTAATTCATGATTTAATACTAACAATGTCACAGATCTTCACTGACA 733
Qy 452 TGATGAGCGTGAACCGTACATGCGGTGCGCAACCGGTGAAGGCTTGAATTCGCA 511
Db 734 CCATGAGTGAACCGCTACATGCGGTGCGCAACCGGTGAAGGCTTGAATTCGCTA 793
Qy 512 CACCTTGAAGGCAAAATCATCAATATCTGATCTGCTGTCTGTCATCTGTTGCA 571
Db 794 CCCCCGAAATGCCAAATGTCAATGCTGCAATGATCCTCTCTTCCCATGCTGC 853
Qy 572 TCTCTGCAATAGTCTTGAAGGCAACCAAGTCAGGGAAGAGCTGATCTATGAGTCT 631
Db 854 TGCCGTAATGTTCAATGCAACCAAAATACAGGCAAGGCTC-----CATGATGCA 907
Qy 632 CTTGCACTTCCAGATGATGATCTCTGCTGGGAGCCTCTTCAATGAAGATCTGCTCT 691
Db 908 CCGTCACTTCTCTCATCCCATGATGATGAGGAAACCTGCTC---AAATCTGCTCT 964
Qy 692 TCATCTTTCCTTCTGATCCCTGTCTCATCATCATGCTGCTCAACCTGATGATCC 751
Db 965 TCATCTTTCCTTCTGATCCCTGTCTCATCATCATGCTGCTCAACCTGATGATCT 1024

Qy 752 TGGCTCAAGAGCGCTCGGCTCTTCTGAGCTCCCGAGAGAAAGATCGCAACCTGCTA 811
Db 1025 TACAGCTCAAGAGCTCGGCTCTTCTGAGCTCCCGAGAGAAAGATCGCAACCTGCTA 1084
Qy 812 GAATCACCAGACTGCTCTGAGTGGTGGGCAAGTCTTCTGCTGCTGCACTCCATTC 871
Db 1085 GGATCACCAGAGTGTCTGAGTGGTGGGCAAGTCTTCTGCTGCTGCACTCCATTC 1144
Qy 872 ACATATTCATCCTGAGAGCTCTGAGGAGCACTCCCAAGACAGCTGCTCTCA 931
Db 1145 ACATATTCATCCTGAGAGCTCTGAGGAGCACTCCCAAGACAGCTGCTCTCA 1204
Qy 932 GCTATTCCTTCTGATGCGCTTGAAGCTATACCAAGTGGCTGATTCCTTCAAG 991
Db 1205 CTTGCACTTCTGATGCGCTTGAAGCTATACCAAGTGGCTGATTCCTTCAAG 1264
Qy 992 CTTTCTTGAATGAATCTCAAGCGGTGTTCCGGAATCTGCTTCTCACTGAAGATGA 1051
Db 1265 CGTTCCTGATGAATGAATCTCAAGCGGTGTTCCGGAATCTGCTTCTCACTGAAGATGA 1324
Qy 1052 GGATGAGCGGCGAGACATGACAGATCCGAATTAAGTTCAAGTTC 1099
Db 1325 CAATCGAAGCAAGCAAACTCTGCTGATCGGTCAAAACACTAGGGAAC 1372

RESULT 76
US-10-290-748-15
Sequence 15, Application US/10290748
Publication No. US20030124672A1
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,748
FILING DATE: 07-No. US20030124672A1-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-290-748-15
Query Match 37.2%; Score 429.2; DB 15; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.3e-113;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGAGCCCGACAGCAACGCGAGCGCGGCTCGAGGACGCGCAGCTGGAGC 151
DB 374 CCGAGCCCATCGGCTCTTAACCCGACGGGCGCTGGGGGAGACAGACGCTGCTCCCTCACA 433
QY 152 CCGGCGACATCTCCCGGCGCATCCGCGTATCATCAAGCGGCTTACTCCGAGTGTTCG 211
DB 434 CCGGAGCGCTTCCATGATGACAGGCATCACCATATGCGCCTCTATTCTATCGGTGTG 493
QY 212 TCGTGGGCTTGGTGGGCACTCGCTGTGTATGTTGTGATCATCCGATACACAAAGATGA 271
DB 494 TAGTGGGCTCTTGTGAAACCTTCGTGTATGTATGTATGATTAAGATATACCAAAATGA 553
QY 272 AGACGCAACCAACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
DB 554 AGACGCAACCAACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 613
QY 332 CCATGCGCTTTCAGAGTACGCTCTACTTGTATGAATTTCTGCGCTTTTGGGAGTGTCTGT 391
DB 614 CGCTGCGCTTTCAGAGTGTATTAATCTATGTATGGAACGCGCTTTTGGAAACATCTCT 673
QY 392 GCAAGATAGTAATTTTCATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 451
DB 674 GCAAGATAGTATTTCAATTAAGTACTAATTAATTTAATTTAATTTAATTTAATTTA 733
QY 452 TGATAGAGGTGACCGGCTTACTTGTGCGGTGCGACCCCGTGAAGGCTTTGGACTTCCGA 511
DB 734 CCATAGAGGTGACCGGCTTACTTGTGCGGTGCGACCCCGTGAAGGCTTTGGACTTCCGA 793
QY 512 CACCGCTGAAGGCAAGATCATCAATATCTGATCTGCGTGTCTGATCTGTTGGCA 571
DB 794 CCGCGCGAAATCCCAAAATTTGATGTGTGCACTGATCTCTCTCTTCTGCGATTTGGTC 853
QY 572 TCTGTCAATAGTCTTGTGAGGACCAAAAGTCAAGGAGACGTCGATGTAGTGTCT 631
DB 854 TGCCGCTATATGTTCAATGAGCAACCAAAATTAACAGGAGGAGTCTC-----CATAGATTGA 907
QY 632 CTTTGACGTTCCCAATGATGATCTCTGCTGGGACCTTTTCATGAAGATCTGCTCT 691
DB 908 CCGTACGCTTCTCTATCCACATGATGATGATGATGATGATGATGATGATGATGATGAT 964
QY 692 TCATCTTGTGCGTGTGATCCCTGTCTGATCATGATGATGATGATGATGATGATGATGAT 751
DB 965 TCATCTTGTGCGTGTGATCCCTGTCTGATCATGATGATGATGATGATGATGATGATGAT 1024
QY 752 TCGCTCTCAAGACGCTCGGCTCTTCTGTGCTCCGAGAGAAAGATCGCAACTGCGTA 811
DB 1025 TACAGCTCAAGAGTGTCCGCGATGCTGTGCGGCTCCAAAGAAAGACAGGAACCTGCGCA 1084
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QY 872 ACATATTATCTCTGAGGAGGCTCTGGGAGAGACCTCCACAGCAAGTGTCTCTCTCA 931
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QY 932 GCTATTACTTCTGATCGCTTATAGGCTATATCAACAGTAGCTGATCCCATTTCTTCA 991
DB 1205 CCGTGCACCTTCTGATGCTGCTTGGGTACAAACAGAGCTGAAACCAAGTTCTTTATG 1264
QY 992 CTTTCTTGTATGAAAACTTCAAGCGGCTTTCGCGGACTTGTCTTTTCACTGAAGATGA 1051
DB 1265 CTTTCTTGTATGAAAACTTCAAGCGGCTTTCGCGGACTTGTCTTTTCACTGAAGATGA 1324
QY 1052 GATAGAGGAGGAGAGCACTAGCAGAGTCCGAATTAAGTTGAGATC 1099
DB 1325 CAATGAGAGGAGAGCACTAGCAGAGTCCGAATTAAGTTGAGATC 1372

RESULT 77
US-09-823-114-7
; Sequence 7, Application US/09823114

Patent No. US200206154A1
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
ZIP: 20006-1888
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFORSWSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 29..1144
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-823-114-7
Query Match 36.6%; Score 422.6; DB 9; Length 1829;
Best Local Similarity 67.1%; Pred. No. 1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
QY 93 CCGGCTGGGCGAGCCCGACAGCAACGCGAGCGCGGCTCGAGGACGCGCAGCTGGAGCC 152
DB 91 CCGCTTTCAGCGCGCTTCCCGACGCGCGCGCAATGTGTGTGTGTGTGTGTGTGTGTGTGT 150
QY 153 CCGGCAATCTCCCGGCGCATCCGGTATCATCAAGGCGGTCTACTCGTATGTGTGTGT 212
DB 151 TAGT 210
QY 213 CCGTGGGCTTGTGGGCAACTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
DB 211 AGTGGGCTTGTGGGCAACTGT 270
QY 273 GACAGCAACCAACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 332
DB 271 GACCGCGCAACCAACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 330
QY 333 CATGCGCTTTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392
DB 331 GCTGCGCTTTCAGAGCGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 390
QY 393 CAAGATAGTAATTTTCATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 452
DB 391 CAGGCTGT 450

QY 453 GATGAGCGTGAACGGCTACATTCGCGTGGGACACCCCGGAGCGTTTGAATTCGAC 512
 DB 451 GATGAGCGTGAACGGCTACATTCGCGTGGGACACCCCGGAGCGTTTGAATTCGAC 510
 QY 513 ACCCTTGAAGGCAAGATCATATATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 DB 511 ACCGACCAAGGCAAGCTGATCATATATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
 QY 573 CTCTGCAATAGTCTCTGAGGACCAAAAGTCAAGGAGAGCTGATGTCATTAGTCTC 632
 DB 571 CCCCATCATAGTCAAGGAGTGAACCCCGGAGATGATGAGTATGATCATCTCA 630
 QY 633 CTGGAAGTTCCCAATGATGATCACTACCTCGGAGGACCTTCATGAGATCTGAGTCT 692
 DB 631 GTTCCCAAGTCC-----CAGCTGTTACTGGAACACTGACCAAGATCTGAGTCT 681
 QY 693 CATCTTTGCTTCTGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 DB 682 CTTCTTTGCTTCTGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
 QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 DB 742 GCGCTGAGGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801
 QY 813 GATCAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 DB 802 CATCAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
 QY 873 CATATTCATCTCTGATGAGGCTCTGAGG---AGCACTCCCAACAGCAGCTGCTCTC 929
 DB 862 CATCTTCATCTCTGATGAGGCTCTGAGG---AGCACTCCCAACAGCAGCTGCTCTC 921
 QY 930 CAGCTATTAATCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
 DB 922 CGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
 QY 990 GCGCTTCTGATGAAGAACTTCAAGCGGCTTCCGGGACTCTG 1034
 DB 982 GCGCTTCTGAGAGAACTTCAAGCGGCTTCCGGGACTCTG 1026

RESULT 78
 US-10-290-748-7
 Sequence 7, Application US/10290748
 Publication No. US20030124672A1
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 KEITH, DUANE E.
 TITLE OF INVENTION: OPIOID RECEPTOR GENES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/290,748
 FILING DATE: 07-No. US20030124672A1-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/405,271A
 FILING DATE: 14-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20526.22

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030 MRSNFORSMW
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1829 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 29..1144
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-290-748-7
 Query Match 36.6%; Score 422.6; DB 15; Length 1829;
 Best Local Similarity 67.1%; Pred. No. 1e-111;
 Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
 QY 93 GCGCTGAGGCGAAGCCGACAGCAACGAGCGCGCTCGGAGAGACGGGAGCTGGAGCC 152
 DB 91 GCGCTTTCCAGCGCTTCCAGCGCGGCGCAATGCTCGGAGGCGGAGACCGG 150
 QY 153 GCGGACATCTCCCGGCGCATCCGATCATCAAGCGGCTCTACTCGTAGTCTTGT 212
 DB 151 TAGTCTCTGCTCTCTGCGCTTACGATGCGATCAAGCGGCTCTACTCGGCTGTGCGC 210
 QY 213 GGTGGGCTTGTGGGCAACTGCGTGTGATGCTGATGATCCGATACCAAGATGAA 272
 DB 211 AGTGGGCTTGTGGGCAACTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270
 QY 273 GACAGCAACCAATTTACATTTAACTGCGCTTGGCAGATGTTAGTTACTACAC 332
 DB 271 GACGCGCAACCAATTTACATTTAACTGCGCTTGGCAGATGTTAGTTACTACAC 330
 QY 333 CATGCGCTTGTGAGTACGCTCTACTGATGATTAATTCCTGCGCTTGGGAGTGTGCTG 392
 DB 331 GCTGCGCTTGTGAGTACGCTCTACTGATGATTAATTCCTGCGCTTGGGAGTGTGCTG 390
 QY 393 CAAGATGATTAATTTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 452
 DB 391 CAAGCTGCTGCTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 450
 QY 453 GATGAGCGTGAACGGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
 DB 451 GATGAGCGTGAACGGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 510
 QY 513 ACCCTTGAAGGCAAGATCATATATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 DB 511 ACCGACCAAGGCAAGCTGATCATATATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
 QY 573 CTCTGCAATAGTCTCTGAGGACCAAAAGTCAAGGAGAGCTGATGTCATTAGTCTC 632
 DB 571 CCCCATCATAGTCAAGGAGTGAACCCCGGAGATGATGAGTATGATCATCTCA 630
 QY 633 CTGGAAGTTCCCAATGATGATCACTACCTCGGAGGACCTTCATGAGATCTGAGTCT 692
 DB 631 GTTCCCAAGTCC-----CAGCTGTTACTGGAACACTGACCAAGATCTGAGTCT 681
 QY 693 CATCTTTGCTTCTGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 DB 682 CTTCTTTGCTTCTGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
 QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 DB 742 GCGCTGAGGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801
 QY 813 GATCAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 DB 802 CATCAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
 QY 873 CATATTCATCTCTGATGAGGCTCTGAGG---AGCACTCCCAACAGCAGCTGCTCTC 929

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Db      862 CATCTTCGTCATCGCTGGAGCGCTGTGGACATCAATGGCGCGACCACTTGTGTGGC 921
Qy      930 CAGCTATTACTTCTGCATCGCTTGGGCTATACCAACAGTACCTGAATCCATTCTCTA 989
Db      922 CGCACTGCACCTGTGCATCTGGCTGGGCTACCGCAACGACAGCTTCAACCCGGTCTCTA 981
Qy      990 CGCCTTCTGTATGAAAACTTCAAGGGGTTTCCGGGACTTCTG 1034
Db      982 CGCCTTCTGTAGAGAACTTCAAGCGCTTCTTCCGCGACGCTCTG 1026

RESULT 79
US-09-214-904-3
; Sequence 3, Application US/09214904
; Patent No. US20010047519A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
; TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/214,904
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR97/01282
; FILING DATE:
; APPLICATION NUMBER: FR 96.08810
; FILING DATE: 15-JUL-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..1173
; US-09-214-904-3

Query Match      36.6%; Score 422.6; DB 9; Length 2218;
Best Local Similarity 67.1%; Pred. No. 1,1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
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Qy      453 GATGAGCGTGGACCGCTACATTTGCGGTGTCACCCCGTGAAGGCTTTGGAATTCCGAC 512
Db      480 GATGAGCGTGGACCGCTACATTTGCTGTGCTGATCTGTCAAGGCCCTGGACTTCGGAC 539
Qy      513 ACCCTTGAAGGCAAGATCATCATATATCTGCATCTGGCTGTGTGTCATCTTTGGCAT 572
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Qy      573 CTGTCAATPATCTCTTGGAGGACCAAGTCAAGGAAAGCTGCATGTCTATGAAGTGTCT 632
Db      600 CCCCATCATGTGTCATGAGGAGTGAACCAACCCCGGATGTGTGATGATGATGATCTCCA 659
Qy      633 CTGTGAGTTCCCAAGATGATGATCTACTCCGTGGGAGACCTTTATGAAGATCTGGGCTT 692
Db      660 GTTCCCAAGTCC-----CAGCTGTGATCTGGGACACTGTGACCAAGATCTGGGCTT 710
Qy      693 CATCTTTCCTTCTGTGATCCCTGTCTCATCATCATCATCTGCTACACCTGATGATCTCT 752
Db      711 CCTCTTTCCTTCTGTGATCCCTGTCTCATCATCATCATCTGCTACACCTGATGATCTCT 770
Qy      753 GCGTCTCAAGAGCGTCCGAGCTCTTCTGTGCTCTCCGAGAAAGATCCGCACTTGGCTAG 812
Db      771 GCGCTGTGGGACGCGCTGTGCTGTGCTCCGGTTCGAAGAGAAAGACCGACGCTCGGG 830
Qy      813 GATCAACGACGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
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Qy      930 CAGCTATTACTTCTGCATCGCTTGGGCTATACCAACAGTACCTGAATCCATTCTCTTA 989
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Qy      990 CGCCTTCTGTATGAAAACTTCAAGCGGTTTCCGGGACTTCTG 1034
Db      1011 CGCCTTCTGTAGAGAACTTCAAGCGCTTCTTCCGCGACGCTCTG 1055

RESULT 80
US-10-112-599A-1
; Sequence 1, Application US/10112599A
; Publication No. US20030005476A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING THERETO
; FILE REFERENCE: R-678
; CURRENT APPLICATION NUMBER: US/10/112,599A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/280,513
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-112-599A-1

Query Match      36.6%; Score 422.6; DB 15; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1,1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
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Db 181 TAGTGCCTGTCCTCGCCCTAGCCATGCGCATCAACCGCGCTCTACTGCGCTGTGTGCGC 240
Qy 213 CGTGGGCTTGGTGGGCACTGCTGTGATGTTGCTGATCATCCGATACAAAGATGAA 272
Db 241 AGTGGGGCTTCTGGGCAACGTGCTGTGATGTTTGGCAGTCGTCGGTACACCAATTGAA 300
Qy 273 GACAGCAACCAACATTTATTAATTTAACTGGCTTTGGCAGATGCTTAACTTACTACAC 332
Db 301 GACCGCCACCAACATCTACATCTTCAATCTGGCTTTGGCTGATGGCGTGGCCACAGAC 360
Qy 333 CATGCCCTTTCAAGATACGCTCTACTTGAATTCCTGGCTTTTGGGAGATGTCTGTG 392
Db 361 GCTGCCCTTCCAGAGCGCCAAAGTACTTGATGGAACGTGGCGCTTGGCGAGCTGTGTG 420
Qy 393 CAAGATTAATTTCCATTTGATTAATAACAATTTTCCAGACATTTCACTTGAACAT 452
Db 421 CAAGCTGTGCTCTCAATTTGACTTACTACAACTGTTCACTAGCATTTTCACTTACAT 480
Qy 453 GATGAGCGTGAACCGCTACATTCGCGTGTGCCACCCCGTGAAGCTTTGSACTTCCGAC 512
Db 481 GATGAGCGTGAACCGCTACATTTGCTGTCTGCATCTGTCAAAAGCCCTGGACTTCCGAC 540
Qy 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGTCTGTCTGTCTGTGAGAT 572
Db 541 ACCAGCCAAAGGCCAAGCTGATCATATATATGATCTGGGCTTGGCTGAGGTGGAGT 600
Qy 573 CTCTGCAATATGCTCTTGGAGGACCAAGTCAAGGAAACGTCGATGTTCATTTAGTGTG 632
Db 601 CCCCATATATGCTCAAGGAGTGAACCAACCCCGGAGTGGTGAAGATATGATGCTCA 660
Qy 633 CTGCAAGTTCCAGATGATGACTACTCTGTGGGAGCTCTTCATGAAGATCTGCTGT 692
Db 661 GTTCCCAAGTCC-----CAGCTGTGATCGGAGCACTGTGACCAAGATCTGTGT 711
Qy 693 CATCTTTCCTTCTGTGATCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 752
Db 712 CCTCTTTCCTTCTGTGATCTGTGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 771
Qy 753 GCGTCTCAAGAGCGCTCGGCTCTTCTGTGCTCCGAGAAAGATTCGCAACCTGTGGT 812
Db 772 GCGCTGCGAGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 831
Qy 813 GATCAACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 872
Db 832 CATCAACGCGCATGT 891
Qy 873 CATATTTATCTGTGTGAGGCTCTGTGGG--AGCACTTCCACAGACAGCTGTCTCTC 929
Db 892 CATCTTTCCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGT 951
Qy 930 CAGCTAATTAATTTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db 952 CGCACTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1011
Qy 990 CGCCTTTCTGTGATGAAAATTCAAGCGGTGTTTCCGGGACTTCTG 1034
Db 1012 CGCCTTCTGTGAGAGAACTTCAAGCGCTGTCTTCCGGCAAGCTCTG 1056

RESULT 81

US-10-435-655-1

; Sequence 1, Application US/10435655

; Publication No. US20040096940A1

; GENERAL INFORMATION:

; APPLICANT: KIEFER, BRIGITTE

; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,

; TITLE OF INVENTION: NUCLEIC ACIDS CODING THEREFOR AND USES THEREOF

; FILE REFERENCE: EX92009-US

; CURRENT APPLICATION NUMBER: US/10/435,655

; CURRENT FILING DATE: 2003-05-12

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59) .. (1174)
US-10-435-655-1
Query Match 36.6%; Score 422.6; DB 17; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1.1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
Qy 93 CGGCTGGGCGAGCCGCAACAGCAACGCGAGCGCGCTCGGAGGACGCGAGCTGAGGCC 152
Db 121 CGCCTTTCAGAGCGCTTCCCAAGCGGAGGCGCAATGCGTGGGAGTGGCGGAGGCCG 180
Qy 153 CGCGCAATCTTCCCGGCGCATCCGGTCAATCAAGCGGCTTACTCTCGTATGTGTGT 212
Db 181 TAGTGCCTGTCCTCTGCGCCCTAGCCATCGCCATCAACGCGCTCTACTCGGCTGTGTG 240
Qy 213 CGTGGGCTTGGTGGGCAACCTGCTGTGATGTTGCTGTGATTCGGAATCAAAAGATGAA 272
Db 241 AGTGGGCTTCTGGGCAACGTGCTGTGATGTTTGGCAGTCGTCGGTACACCAATTGAA 300
Qy 273 GACAGCAACCAACATTTATTAATTTAACTGGCTTTGGCAGATGCTTAACTTACTACAC 332
Db 301 GACCGCCACCAACATCTACATCTTCAATCTGGCTTTGGCTGATGGCGTGGCCACAGAC 360
Qy 333 CATGCCCTTTCAAGATACGCTCTACTTGAATTCCTGGCTTTTGGGAGATGTCTGTG 392
Db 361 GCTGCCCTTCCAGAGCGCCAAAGTACTTGATGGAACGTGGCGCTTGGCGAGCTGTGTG 420
Qy 393 CAAGATTAATTTCCATTTGATTAATAACAATTTTCCAGACATTTCACTTGAACAT 452
Db 421 CAAGCTGTGCTCTCAATTTGACTTACTACAACTGTTCACTAGCATTTTCACTTACAT 480
Qy 453 GATGAGCGTGAACCGCTACATTCGCGTGTGCCACCCCGTGAAGCTTTGSACTTCCGAC 512
Db 481 GATGAGCGTGAACCGCTACATTTGCTGTCTGCATCTGTCAAAAGCCCTGGACTTCCGAC 540
Qy 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGTCTGTCTGTCTGTCTGTGAGAT 572
Db 541 ACCAGCCAAAGGCCAAGCTGATCATATATATGATCTGGGCTTGGCTTCAAGTGTGCGG 600
Qy 573 CTCTGCAATATGCTCTTGGAGGACCAAGTCAAGGAAACGTCGATGTTCATTTAGTGTG 632
Db 601 CCCCATATATGCTCAAGGAGTGAACCAACCCCGGAGTGGTGAAGATATGATGCTCA 660
Qy 633 CTGCAAGTTCCAGATGATGACTACTCTGTGTGGAACCTCTTCAATGAAGATCTGCTGT 692
Db 661 GTTCCCAAGTCC-----CAGCTGTGATCGGAGCACTGTGACCAAGATCTGTGT 711
Qy 693 CATCTTTCCTTCTGTGATCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 752
Db 712 CCTCTTTCCTTCTGTGATCTGTGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 771
Qy 753 GCGTCTCAAGAGCGCTCGGCTCTTCTGTGCTCCGAGAAAGATTCGCAACCTGTGGT 812
Db 772 GCGCTGCGAGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 831
Qy 813 GATCAACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 872
Db 832 CATCAACGCGCATGT 891
Qy 873 CATATTTATCTGTGTGAGGCTCTGTGGG--AGCACTTCCACAGACAGCTGTCTCTC 929
Db 892 CATCTTTCCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGT 951
Qy 930 CAGCTAATTAATTTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db 952 CGCACTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1011
Qy 990 CGCCTTTCTGTGATGAAAATTCAAGCGGTGTTTCCGGGACTTCTG 1034

Db 1012 CGCCTTCCGACGAGACTTCAAGCGCTGCTCCGCCAGCTCTG 1056

RESULT 82
US-09-935-061-13

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Sequence 13, Application US/09935061
Publication NO. US20030129649A1
GENERAL INFORMATION:
APPLICANT: Kobilka, Brian M.
APPLICANT: Ghanouni, Pejman
APPLICANT: Lee, Tae Weon
TITLE OF INVENTION: Conformational assays to detect binding
TITLE OF INVENTION: to G protein-coupled receptors
FILE REFERENCE: STAN213
CURRENT APPLICATION NUMBER: US/09/935,061
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/285,250
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1176
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ' Opioid receptor with TEV site in 2nd
OTHER INFORMATION: intracellular loop
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1176)
US-09-935-061-13

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Query Match	36.0%	Score	415.6	DB	10	Length	1176
Best Local Similarity	65.1%	Pred. No.	9e-110				
Matches	648	Conservative	0	Mismatches	339	Indels	9
						Gaps	2

Qy	92	CCGGCTGGGGCCGAGCCCGACACGACACGGCAGGCGCGGCTCGAGGAGACGGCGACGTGGAGC	157
Db	125	CCGACCCATGCGGTGCGAAACCGGACCGACTGGGGGAGAGACAGCCCTGGGCCCTCCAA	184
Qy	152	CCGCGGACATCTCCCGGCGCATCCGGGTATCATCGAGGCGGTCTACCTCGTAGTGTTCG	211
Db	185	CCGGCAGTCCCTTCATGATTCAGGCGCATACGATATGGCCCTTACTTCATCGGTGCG	244
Qy	212	TCGTGGGCTTGGTGGGCAACTCGCTGTCATGTTTGATCATCGATACCAAGATGA	271
Db	245	TGGTGGGGCTCTCGGAACTTCCTGTGATATGATATGTCAATGACCAAGATGA	304
Qy	272	AGACAGCAACCAACATTTACATATTTAACCTTGGCTTTGGCAGATGCTTTAGTACTCA	331
Db	305	AGACTGGACACCAACTCTACATTTTCAACTTGTCTGGCAGATGCTTTAGCACAAGTA	364
Qy	332	CCATGCCCCCTTACAGAGTACGGTCTACTGATGAAATTCCTGGCTTTTGGGGATGTGCTGT	391
Db	365	CCCTGCCCTTCCAGAGTGTGAATTTCCCTATGGGAACTGGCCATTTGGAAACCATCTCTT	424
Qy	392	GCAAGAATGAAATTTTCATTTGATTTCTACAAGTGTACACAGCATCTCTACCTTGACA	451
Db	425	GCAAGATAGTACTCTCATATGATATCTATMACTGTTCACAGCATATTTCCCTCTGCA	484
Qy	452	TGATGAGCGTGAACCGCTCACTATTTCCGTTGTCACCCCGTAGAGGCTTTGGACTTCGCA	511
Db	485	CGATGAGTGTGATTCGATCAATTGCAAGTGTGCAACCTGTCAAGGAAACCTCTACTTCC	544
Qy	512	CACCTTTGAAGGCAAAAGATCATATATCTGCATTTGGCTGTGCTGTCATCTGTGGCA	571
Db	545	AGGGGCGAAATGCGCAAAATTAATCAATGTCTGCACTGATCCTCTTCACCACTTGTGTC	604
Qy	572	TCTCTGCATATGTCCTTTGGAGGCAACCAAGTCAGGAAAGACGTGCATCTTAAGTGTCT	631
Db	605	TTCTCTGAATGTTCATATGCTACACCAAAATACAGGCAAG-----TTCCATMAATTTGA	658

QY	632	CCTTGAGCTGCCAGATGATGATCACTACCTCGGTGGGACCTCTTATGAGAACTCGGCTT	691
Db	659	CACTAACATCTCTCATCCAACTGGTACTGGGAAAACTTC--TGAAGATCTGTGTTT	715
QY	692	TCATCTTTGACCTTGGTATCCCTGTCCTCATCATCATGTCGTGTACACCCGTATGATCC	751
Db	716	TCATCTTGCCCTTATTATATGCCAGAGGTCATCATTAACGTGTGGTATGTAGCTGATGATCT	775
QY	752	TGCGTCTCAAGAGCGTCCGGCTCCTTTTGTGGCTCCCGAGAGAAAGATGCAACTGCGTA	811
Db	776	TGCCGCTCAAGAGTCCGACATGCTCTCTGCTCCAAAGAAAAGACAGGAATCTTCSAA	835
QY	812	GGATCACCAAGCTGATCCTGGTGGGNGGAGGAGCTTGTCGTCTGCTGACTCCATTG	871
Db	836	GGATCACCAAGATGATGCTGATGATGATGAGCTGTGTTTATGTCGTCTGCACTCCATTG	895
QY	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACCTCCACAGACAGACTGCTCTTCCAA	931
Db	896	ACATTTCAGTCATATTAAAGCCTTGTTGTTAACATCCCGAAGAACTACGTTCCAGACTGTT	955
QY	932	GCTATTAATCTTGATGATGCGCTTAGGGCTATACCAACAGTAGGCTTAATCCATTCTCTAG	991
Db	956	CTTGCGCACTTCTGCAATGTGCTTAGGTATACAAACAGCTGCTCAACCAAGTCCTTATG	1015
QY	992	CCTTCTTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTTCCACTGAAGATGA	1051
Db	1016	CATTCTTGATGAAAACTTCAAGAGGCTTCAAGAGAGTTCTGTATCCCAACTCTTCCAA	1075
QY	1052	GGATGAGCGGCAAGACATAGCAGAGTCCGAAATA	1087
Db	1076	ACATTGAGCAACAAACTCCACTCGAATTCGTCTGAA	1111

RESULT 83
US-10-692-071-13
; Sequence 13, Application US/10692071
; Publication No. US20040157268A1

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? GENERAL INFORMATION:
? APPLICANT: Kobilka, Brian K.
? APPLICANT: Ghanouni, Pejman
? APPLICANT: Lee, Tae Weon
? TITLE OF INVENTION: Conformational assays to detect binding
? TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
? FILE REFERENCE: STAN-213CIP
? CURRENT APPLICATION NUMBER: US/10/692,071
? CURRENT FILING DATE: 2003-10-22
? PRIOR APPLICATION NUMBER: PCT/US02/13250
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 09/935,061
? PRIOR FILING DATE: 2001-08-21
? PRIOR APPLICATION NUMBER: 60/286,250
? PRIOR FILING DATE: 2001-04-24
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13
? LENGTH: 1176
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: ' Optoid receptor with TEV site in 2nd
? OTHER INFORMATION: intracellular loop
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(1176)
US-10-692-071-13

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Query Match	36.0%	Score 415.6;	DB: 17;	Length 1176;
Best Local Similarity	65.1%;	Pred. No. 96-110;		
Matches 648;	Conservative	0;	Mismatches 333;	Indels 9;
			Gaps	2
Oy	92	CCGCGCTGGGGCCGAGCCCGACGCAACGGCAGCGCGCTCTCGAGAGACGGCAGCTGGAGC	151	
Oy	125	CCGAGCCCATGCGCGTCCGACCCGACCCGACTCTGGGGGGAGAGACAGCGCTGGCCCTCCCA	184	

Oy 92 CCGGCTGGGCAGACCCGAAGAACAAGCAGGCCGTGCAATCGGCGAAGTGGAGC 151

||| | | | ||| | | |

Db 125 CCAGCCCATTGGTCGAAACCGCACCGACTTGCGCGGAGAACACAGCTTTCCCTCCA 184

||| | | | ||| | | |

Db 955 CACATCTATGTCATCATCAAAAGCACTGATTCAGATTCCAGAAACCACTTTCCAGACTTT 1014

Qy 931 AGCTATTACTTCTGCATGCGCTTAGGCTATACCAACAGTAGCGTGAATCCGATTTCTTAC 990

Db 1015 TCTTGGGCACTTCTGATATTGGCTTGGGTTACACAAACACCTGCTGAACCCAGTTCTTTAT 1074

Qy 991 GCCTTTCTTGATGAAACCTTCAAGCGGTGTTCCGGGACCTTGCTTTCACAGTGAAGATG 1056

Db 1075 GCGTTTCCGTGATGAAACCTTCAACGATGTTTATAGAGAGTTCTGCATCCCAACTTCCTC 1134

Qy 1051 AGAGTGAAGCGGACAGACATAGCAGATCCGGAATACAGTTCCAGATC 1099

Db 1135 ACAATCGAACAGCAAAACTGCTCTCGATCCGCTCAAAACACTGAGGAAC 1183

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RESULT 95
US-10-283-300-12
/ Sequence 12, Application US/10283300
/ Publication No. US20030103972A1
/ GENERAL INFORMATION:
/ APPLICANT: Memorial Sloan-Kettering Cancer Center
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICED VARIANTS
/ TITLE OF INVENTION: OF THE MU-OP10ID RECEPTOR GENE
/ FILE REFERENCE: 830002-2000.3
/ CURRENT FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 09/761,962
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 09/743,872
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: PCT/US99/15974
/ PRIOR FILING DATE: 1999-07-15
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: Patencin version 3.0
/ SEQ ID NO 12
/ LENGTH: 1346
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-283-300-12

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Query Match	35.6%	Score 411;	DB 15;	Length 1346;
Basic Local Similarity	65.7%;	Pred. No. 2.1e-108;		
Matches 663;	Conservative	0;	Matches 335;	Indels 11;
				Gaps 4;
Qy	CCGGCTGGGCGGAGCCCGACAGCAACGGCAGCGCGCTCGGAGGAGCGCGCAGCTGAGGC	151		
Db	185 CCGAACCATGGGGTCTTAACCGCAGCGGGCTTGGGGGAGCGCACAGCTGTGGCTTCAGA	244		
Qy	152 CCGGCGCATCTCCCCGGCCATCCCGGTATCATCAAGCGGGTCTACTCCGTAAGTTTCG	211		
Db	245 CCGGAGCGCTTCATGGTGTCAAGGCAATCACCATATGAGCCCTCATTTCTTCGTGTG	304		
Qy	212 TCGTGGGCTTGGTGGGCAACTCGCTGTGATGTTGATGATCATCCGATACCAAAAGATGA	271		
Db	305 TAGTGGGCTCTTTGGAACTTCCGTGTCAATGTATGTATTTGTAAGATATACAAAATGA	364		
Qy	272 AGACGACAAACAATTACATATTTAACTGGCGTTTGGCAGAGTCTTTAGTTACTACAA	331		
Db	365 AGACTGCCACCAACATCTTACATTTTCAACTGTGCTGTGGCAGATGCCTTTACCACTACAA	424		
Qy	332 CCATGGCCCTTTCAAGATACGGGTCTACCTGATGAATTCCTGGCGTTTGGGAGTGGCGGT	391		
Db	425 CGGTGCCCTTTCAAGGTGTTTAACTACCTGATGGGAGAGTGGCCCTTTGAAACAATCCTCT	484		
Qy	392 GCAGATAGTAAATTTCAATTGATTACTACAAATGTTTACAGCATCTTCACTTGAACA	451		
Db	485 GCAAGATCGTATCTCAATAGACTACTACAAACATGTTTACACGATCTTCAACCTGTGCA	544		
Qy	452 TGATAGGCTGGACCGGCTACATGGCGGTGGCAACCCGTGAAGGCTTTGACACTTCGCA	511		
Db	545 CCATAGGTGTAACCGGTACATGGCGGTGGCAACCGGATCAAGGCGCTTGAAATTTTCGTA	604		
Qy	512 CACCCTTGAAGCAAAAGATCATCATATCTGCATCTGGCTGTGTCATCTGTTGGCA	571		

Db	605	CCCCCGAAAGCCAAATGTGTCAATGTCTCAACTGGATCTCTTCTGCAATTGCTC	664
Oy	572	TCCTGCAAATAGTCCTTGGAGGACACAAAGTCAGGGAAAGCTGCATGTCATTAGTGCCT	631
Db	665	TGCCCCGTAATGTTCAATGACACACCAAAATACAGGACAGGGCTC-----CATAGATTGCA	718
Oy	632	CCTTGCAGTTCACAGATGATGACTACTCTCGTGGGACCTCTTCATGAAAGATCTGCGTCT	691
Db	719	CCCTCAGGTTCTCTCATCCACATGTAATCTGGGAAGACCTGCTC---AAATCTGTGTCT	775
Oy	692	TCATCTTTGCTTGCATGATCCCTGTCTCATCATCATCATGTCGTGCTACACCTGATGATCC	751
Db	776	TCATCTTGCTTGCATCATGCGGAGCTCATCATCATCATGTCGTGTTATGATGATGATGATCT	835
Oy	752	TGCGTCTCAAGAGGCTCCGGCTCTCTTCTTGCGCTCCGAGAGAAAGATGCAACTGCGGTA	811
Db	836	TACACATTCAGAAAGTGTCCGCATGTGTGTGCGGCTCCAAAGAAAGACAGGAACCTGCCCCA	895
Oy	812	GGATCACACAGCTGGTCCCTGGTGGAT--GGTGGACGTCCTGTCGTGTGAGATCCCATTT	870
Db	896	GGATCACCCGGATGGTGTGTGGTGTGCTGGCTGTGATTTATGTGTGCTGGAC--CCATTC	954
Oy	871	CACATATTCATCCTGATGAGGCTCTGTGGGAGACCTCCACAGACAGCTGCTCTGCC	930
Db	955	CACATCTATGTCATCATCAACAGCACTATATCGATTCAGAAACACATTTCCAGACTGTT	1014
Oy	931	AGCTATTACTTCTGCATGCTTAGGCTATACCAACAGTAGCTGAATCCGATTCCTTAC	990
Db	1015	TCTGTGGCACTTCTGCATTTGCTTGGGTTACCAAAACAGCTGCTGGAACCCAGTCTTTAT	1074
Oy	991	GCTTTCTTGATGAAAACCTTCAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATG	1056
Db	1075	GCGTTCTCGATGAAAACCTTCAACAGATGTTTATAGAGAGTTCTGCATCCCAACTTCTCTC	1134
Oy	1051	AGGATGAGCGCGCAGAGACTAGACAGATCCGAAATACATTTACAGATTC	1099
Db	1135	ACAATCGAACGCAAACTCTGCTCGATTCGTCGATCAAAACACTAGGAAAC	1183

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RESULT: 86
US-10-112-599A-3
; Sequence 3, Application US/10112599A
; Publication No. US20030005476A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
; TITILE OF INVENTION: COMPOSITIONS AND METHODS RELATING
; FILE REFERENCE: R-678
; CURRENT APPLICATION NUMBER: US/10/112,599A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/280,513
; FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: fastseq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-599A-3

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Query Match	Similarity	Score	408.6	DB	15	Length	1773
Best Local	Similarity	64.7%	Pred.	No.1-2e-107			
Matches	644	Conservative	0	Mismatches	339	Indels	12
							Gaps
							2
OY	44	CCTGGGCCCGAGCGCCTTGCCTTGCCTCCCAACAGAGAGGCGCTGGTTCCTCCGGCTGGAGCGC	103				
Db	247	CCTCCGCGCGAGCGCGAGAGCTGCAGGCCCTCCGCTTTCGCCAAGCGCTTCGAGCGCTTACCTTA	306				
OY	104	AGCCCGACAGCMAAGCGCAGCGCGCGCTTCGAGAGAAGCGCACTGAAGGCCCGCGACATCT	163				
Db	307	GCGGCTTCCCGAGCGCTGCGCCCATGCGTGTGGGAGCGCCACAGACCGGGAGCGCCTCGT	366				

Db 1078 TCGTGTGAGCGGTGTGATGATGACCGGCGGACCCGGCTGTGTGTGCTGCGCTGACCC 1137

Qy 941 TGTGATGCGCTTGAAGCTTATACCAAGATAGCTGATATCCATTTCTTACGCTTTCTTG 1000

Db 1138 TGTGATGCGCTTGAAGCTTATACCAAGATAGCTGATATCCATTTCTTACGCTTTCTTG 1197

Qy 1001 ATGAAACTTCAAGCGGTGTGCTTCCGGGACTTCTGC 1035

Db 1198 ACGAGACTTCAAGCGGTGTGCTTCCGGGACTTCTGC 1232

RESULT 88

US-10-305-720-1405

/ Sequence 1405, Application US/10305720

/ Publication No. US20040010136A1

/ GENERAL INFORMATION:

/ APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

/ TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio

/ FILE REFERENCE: PA-0002-1 CON

/ CURRENT APPLICATION NUMBER: US/10/305,720

/ PRIORITY FILING DATE: 2002-11-26

/ PRIOR APPLICATION NUMBER: 09/016,434

/ PRIORITY FILING DATE: 1998-01-30

/ NUMBER OF SEQ ID NOS: 1490

/ SOFTWARE: PERL Program

/ SEQ ID NO 1405

/ LENGTH: 1773

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: m18c feature

/ OTHER INFORMATION: GenBank ID No. US20040010136A1 g497313

US-10-305-720-1405

Query Match 35.4%; Score 408.6; DB 16; Length 1773;

Best Local Similarity 64.7%; Pred. No. 1.2e-107;

Matches 644; Conservative 0; Mismatches 339; Indels 12; Gaps 2;

Qy 44 CCTGGGCCCCGAGCGGCTGCTGCTCCCGCCCAAGCAGCGGCTGTTCCCGGCTGGGCGG 103

Db 247 CCTGGGCCCCGAGCGGCTGCTGCTCCCGCCCAAGCAGCGGCTGTTCCCGGCTGGGCGG 306

Qy 104 AGCCGAGCAGCAAGCGGCGGCGGCTGGAGAGCGGAGCTGAGCGGCGGCGGCAATCT 163

Db 307 GCGGCTTCCCGAGCGGCTGGGCGGCAATGCTCGGCGGCGGAGAGCGGCGGCTGCT 366

Qy 164 CCCCGGCGCATCCCGGCTGATCATCAGCGGCTGCTACTCCGTAAGTGTCTGCTGAGGCTTG 223

Db 367 CCTGGGCGGCTGGGAGTCCGCTATCAGCGGCTGCTACTCCGCGGCTGCTGCGGCGGCTGC 426

Qy 224 TGGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283

Db 427 TGGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486

Qy 284 ACATTATCATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343

Db 487 ACATTATCATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546

Qy 344 AGAGTACGCTTACTTATGATGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403

Db 547 AGAGTACGCTTACTTATGATGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606

Qy 404 TTTTCATGATTTATCAACATGTTTCAACAGATTTTCACTTTCATGATGATGAGCTTG 463

Db 607 TTTTCATGATTTATCAACATGTTTCAACAGATTTTCACTTTCATGATGATGAGCTTG 666

Qy 464 ACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523

Db 667 ACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726

Qy 524 CAAGAATCATTAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583

Db 727 CAAGAATCATTAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786

Qy 584 TCTTGAAGGACCAAGTCAAGGAGAGAGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643

Db 787 TATGAGCTGTGACCCGTCCCGGAGCGGTGAGTGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846

Qy 644 CAGATGATGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703

Db 847 C-----CAGCTGTGATCTGGAACAGGTGATCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

Qy 704 TGTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763

Db 898 TGTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957

Qy 764 GGTGCGGCT 823

Db 958 GTGTGCGCT 1017

Qy 824 TGTGCT 883

Db 1018 TGTGCT 1077

Qy 884 TGTGAGAGCT 940

Db 1078 TGTGCTGAGCGCT 1137

Qy 941 TGTGATGCGCTTGAAGCTTATACCAAGATAGCTGATATCCATTTCTTACGCTTTCTTG 1000

Db 1138 TGTGATGCGCTTGAAGCTTATACCAAGATAGCTGATATCCATTTCTTACGCTTTCTTG 1197

Qy 1001 ATGAAACTTCAAGCGGTGTGCTTCCGGGACTTCTGC 1035

Db 1198 ACGAGACTTCAAGCGGTGTGCTTCCGGGACTTCTGC 1232

RESULT 89

US-09-826-509-538

/ Sequence 538, Application US/09826509

/ Publication No. US20030204073A1

/ GENERAL INFORMATION:

/ APPLICANT: Lehmann-Bruhnsma, Karin

/ APPLICANT: Lin, I-Lin

/ APPLICANT: Liaw, Chen W.

/ TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

/ FILE REFERENCE: AREN-207

/ CURRENT APPLICATION NUMBER: US/09/826,509

/ PRIORITY FILING DATE: 2001-04-05

/ PRIOR APPLICATION NUMBER: 60/195,747

/ PRIORITY FILING DATE: 2000-04-07

/ PRIOR APPLICATION NUMBER: 09/170,496

/ NUMBER OF SEQ ID NOS: 589

/ SOFTWARE: PatentIn Version 2.1

/ SEQ ID NO 538

/ LENGTH: 1119

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-09-826-509-538

Query Match 35.3%; Score 407; DB 11; Length 1119;

Best Local Similarity 64.6%; Pred. No. 2.7e-107;

Matches 643; Conservative 0; Mismatches 340; Indels 12; Gaps 2;

Qy 44 CCTGGGCCCCGAGCGGCTGCTGCTCCCGCCCAAGCAGCGGCTGTTCCCGGCTGGGCGG 103

Db 14 CCTGGGCCCCGAGCGGCTGCTGCTCCCGCCCGCTTTCGCGCAAGCGCTTCCGAGCGGCTTACCTTA 73

Qy 104 AGCCGAGCAGCAAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 163

Db 74 GCGGCTTCCCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 133

Qy 164 CCCCGGCGCATCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223

134 CCTTCGCCCCGCAATCCGCAATCACGCGCTTACTCGCCGTGTGCGCCGTGGGCTGC 193
QY TGGGCACTCCGCTGGATCATGTTGATCATCCGATPACCAAGATGAGACAGCAACA 283
Db TGGGCAAGTGTCTGTCAATGTCGATGTCGGATGTCGGATGACATGAGAGAGAGCA 253
QY ACATTATGATATTTTAACTGCTTTGGAGATGATGCTTTAGTACTAACATGACCTTTTC 343
Db ACATCTATCATCTTTAACTGCTTTAGGCGATGCGCTGGCCACAGCAAGCTGCTTCC 313
QY AGAGTACGCTTACTGATGAAATTCCTGCGCTTTTGGGAGATGCTGTGCAAGATGAA 403
Db AGAGTACGCTTACTGATGAAATTCCTGCGCTTTTGGGAGATGCTGTGCAAGATGAA 373
QY TTTTCATTTGATTTACTAACACATGTTACACGAGCATCTTACCTTGACCATGATGAGCGTGG 463
Db TCTTCATGACTTACTAACATGATGTTACACGAGCATCTTACGCTGACCATGATGATGTTG 433
QY ACCGCTACATTTGCTGTCGCAACCCCGTGAAGCTTTGGAATTCGCAACCCCTTGAAG 523
Db ACCGCTACATTTGCTGTCGCAACCCCGTGAAGCTTTGGAATTCGCAACCCCTTGAAG 493
QY CAAGATCATTAATATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db CCAAGCTCATCAACATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
QY TCCCTTGAAGGCAAGCAAGTCAAGGAGAGAGTCAATGATGATGATGATGATGATGATG 643
Db TCATGCTGTGACCGCTGCGGAGAGAGTCAAGTGTGATGATGATGATGATGATGATG 613
QY CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
Db C-----CAGCTGTGATGAGAGAGAGTCAAGTGTGATGATGATGATGATGATGATG 664
QY TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
Db TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 724
QY GCGTCGCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823
Db GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 784
QY TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
Db TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844
QY TGTGAGAGGCTTGTGGGAGACATCTCC---CACAGCAAGCTGCTTCTTCAGCTAATTA 940
Db TGTGCTGAGAGCTGCTGAGACATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
QY TGTGATGAGAGCTTGTAG 940
Db TGTGATGAGAGCTTGTAG 904
QY TGTGATGAGAGCTTGTAG 1000
Db TGTGATGAGAGCTTGTAG 964
QY 1001 ATGAAACTTCAAGCGGTGTTTCCGAGACTTCTGC 1035
Db 965 ACGAAGACTTCAAGCGGTGTTTCCGAGACTTCTGC 999

RESULT 90
US-09-935-061-15

; Sequence 15, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250

; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ' Opioid receptor with TRV site in 3rd
; OTHER INFORMATION: Intracellular loop
; NAME/KEY: CDS
; LOCATION: (1) ... (1197)
US-09-935-061-15

Query Match 34.9%; Score 402.2; DB 10; Length 1197;
Best Local Similarity 64.8%; Pred. No. 7e-106;
Matches 659; Conservative 0; Mismatches 328; Indels 30; Gaps 3;

QY 92 CCGGCTGGGCGGAGCGCGAGCAAGCGAGCGCGCTCGAGAGAGAGCGGAGCTGAGC 151
Db 125 CCGAGCCATGCGGTGTCGAACCGCACCGACTGGGCGGAGAGAGAGAGAGAGAGAG 184
QY 152 CCGGCGACATCTCCCGGCGATCCCGGTCATCATCAGCGCGGTCTACTCGTATGTTG 211
Db 185 CCGGAGTCCCTTCATGATATCAGGCGCATCAGATCATGCGCTCTACTCATCGTGTGCG 244
QY 212 TCGTGGGCTTGTGGGAGCACTGCTGTCATGTTGTCATGATCATCGGATGACCAAGATGA 271
Db 245 TGTGGGGCTTGTGGAACTTCTGTCATGATGATGATGATGATGATGATGATGATGATG 304
QY 272 AGACAGCAACCAACATTTATTAATTTAACTGGCTTTGGAGATGATGATGATGATGATG 331
Db 305 AGATGCGCACCAACATCTACATTTTAACTGCTGTCGAGATGCTTACCGCACAGTA 364
QY 332 CCATGCTTTTCAAGATGAGGTCTATGATGATGATGATGATGATGATGATGATGATG 391
Db 365 CCTGCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
QY 392 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
Db 425 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 484
QY 452 TGATGAGGTGAGACCGGTCATCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 511
Db 485 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
QY 512 CACCTTGAAGCAAGATCATCAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
Db 545 CTCCCGCAATGCGCAAAATTAATTAATGTCGCACTGATCTCTTCAAGCCATGCTG 604
QY 572 TCTGTGCAATGATGCTTGGAGAGCAACCAAGTCAGAGAGAGAGAGAGAGAGAGAG 631
Db 605 TTCTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
QY 632 CCTTGAAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db 659 CACTTAATTTCTCATTCCAACCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
QY 752 TGTGCTTCAAGAGGTGCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Db 776 TGTGCTTCAAGAGGTGCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
QY 798 -----TCGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 850
Db 836 TCGAGGAGAGAGATCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATG 895
QY 851 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 910

Db	896	TGCTGTCTGAGCTCCCATTCACATTTAGCATCATTTAAAGCTTGTTACATCCAG	955
Qy	911	ACAGCAGACGTGCTCTCTCCAGCTATTACTTTCGACATCGCCTTAGGCTATTACCAACAGTA	970
Db	956	AAACTACGTTCCAGACATGTTTCTTGSGACCTCTGCATGTGCTGTAGGTTACAAACAGCT	1011
Qy	971	GCCTGAATCCCATTTCTTACGCTTTTCTTGATGAAACTTCAAGCGGTGTTTCCGGACT	1033
Db	1016	GCTTCACCCCATGCTCTTATGATTTCTGAGTAAACCTTCAACGATCTCTCAGAGAGT	1073
Qy	1031	TCTGCTTTCCACTGAAGATGAGAGTGAAGCGGCAGACCTAGCAGATGCCGAATA	1087
Db	1076	TCTGATATCCCAACCTCTTCCACATTGAGCAACAAATCTCCACTGGAATTTGCTGGA	1132

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RESULT 91
US-10-692-071-15
? Sequence 15, Application US/10692071
? Publication No. US20040157268A1
? GENERAL INFORMATION:
? APPLICANT: Kobalika, Brian K.
? APPLICANT: Ghannoui, Pejman
? APPLICANT: Lee, Tae Weon
? TITLE OF INVENTION: Conformational assays to detect binding
? TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
? PRT REFERENCE: STAN-213CIP
? CURRENT APPLICATION NUMBER: US/10/692,071
? PRIOR FILING DATE: 2003-10-22
? PRIOR APPLICATION NUMBER: PCT/US02/13250
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 09/935,061
? PRIOR FILING DATE: 2001-08-21
? PRIOR APPLICATION NUMBER: 60/286,250
? PRIOR FILING DATE: 2001-04-24
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 15
? LENGTH: 1197
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: ' Opioid receptor with TEV site in 3rd
? OTHER INFORMATION: intracellular loop
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1) ... (1197)
US-10-692-071-15

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	Query Match	34.9%	Score 402.2	DB 17	Length 1197
	Beet Local Similarity	64.8%	Pred. No. 76-106		
	Matches 659	Conservative	0	Mismatches 328	Indels 30
				Gaps	3
Qy	92	CCGGCTGGGGCCGAGCCCGCAGACAACGGCAGCGCCGCTCGAGAGACGGCGACGTGAGAC	151		
Db	125	CCGACCCATCGCGGTCCGAACCGCACCCGACTGGGGGGAGAGACAGCTGTGCTCCAA	184		
Qy	152	CCGGCGACATCTCCCCGGGCATCCGGTCATCATCAGCGCGGTCTACTCCGATGTTTCG	211		
Db	185	CCGGCAGTCCCTCCATGATCAAGGCATCAACATATGGCCCTTACTCATCTGATGTTGG	244		
Qy	212	TCGTGGGCTTGGTGGGCACTCGCTGTCATGTTGTGTCATCCGATACACAAGATCA	271		
Db	245	TGGTGGGGCTCTTCGGAAAACTTCCTGGTCATGTATGTGATTTGTCAGATTCACCAAGATGA	304		
Qy	272	AGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAATGTTAGTTACTACAA	331		
Db	305	AGACTGCCAACCAACATTTACATTTTCAACTTTCCTGGCAATGCTTAAAGCACACAGTA	364		
Qy	332	CCATGCCCTTTCAAGATACGGGTCTACTTGATGAATTTCCGGGCTTTTGGGGATGTGCTGT	391		
Db	365	CCCTGCCCTTCCAGAGTGTGAATTTACTTAATGGAAACATGGCCATTTTGGAAACATCTTT	424		
Qy	392	GCAAGATGATATTTTCCATGTGATTTACTAACACATGTTCACGACATCTTCACCTTGACCA	451		

Db	445	GCAGATATGATCTTCACATAGTACTAATACATATGTTCCACAGCATATTTACCCCTTCGCA	484
Qy	4452	TGATGAGCGTGAGCCGCTACATATGCGGTGTGCAACCCCGTGAAGCTTTGAGCTTCGCA	5111
Db	485	CCATGAGTGTGATGTGATACATTTGCAAGTGTGCAACCTGTCAAGGCTTATGATTTCCGTA	5444
Qy	512	CACCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTGTCTGTCTCATCTGTGGCA	5711
Db	545	CTCCCCGAAATGCGCAAAATTTATCAATATGCTGTGCAACGTGATCTCTCTTTCAGCCATTGGTC	6044
Qy	572	TCTGCAATATGCTCCTTGAGGCGACCAAAAGTCAGGGGAACGTCGATGTCAATGAGTGC	6311
Db	605	TTCTGTATGTTCATATGACTACACAAATATACAGGAA-----GGTTCATATGATTTGA	6588
Qy	632	CTTTCAGTTCACAGATGATGACTACTCCTGTGTGGACCTCTTTCATGAAGATCTGGCTCT	6911
Db	659	CACHTAACATTTCTCTATCCAACTGTGGTACTGGGAAAACTGTGT---GAGATCTGTGTTT	7155
Qy	692	TCATCTTTGCTTGGTGTATCCCTGTCTCTCATCATCATGCTGTCTACACCTGATGATCC	7511
Db	716	TCATCTTGGCTTCAATTAATGCGAGTGCATCATTAACCTGTGTCTATGACATGATATCT	7755
Qy	752	TGCGCTCAAGAGCGATCCGGGCTCTTTCTGTGGCTCCCGAAGAGAAGA-----7977	
Db	776	TGGCGCTCAAGAGTGTCCGATGCTCTCTGTGGCTCCAAAGAAAAGACGAAACCTTACT	8355
Qy	798	-----TCGCAACCTGTGTAGATCACCAAGCTGGTCTGTGTGTGTGTGTGGCAGTCTTG	8500
Db	836	TCCAGGGGAGGAATCTTGGAAAGATCACCAAGATGGTGTGTGTGTGTGTGTGTCTCA	8955
Qy	861	TCGTCTGTGAGCATCTCCCATTTCAATATTTCAATCTGTGTGAGGCTCTGGGAGGACCTCCC	9100
Db	896	TCGTCTGTGAGCATCTCCCATTTCAATTAAGTATCATTAACCTTTGTATCAATCCAG	9555
Qy	911	ACAGCAGCGTGTCTCTCCAGCTATTAATTTCTGCATCGCTTAAAGCTTATTAACAAGTA	9700
Db	956	AAACTACGTTCCAGACTGTTCTTTGGCACTTTGCATTTGCTTAAGTTACACAAACAGCT	1010
Qy	971	GCCTGAATCCCAATTCCTACGCGCTTTCTGTATGAAAACTTCAAGCGGCTTTTCCGGGACT	1033
Db	1016	GGCTCAACCGAGTCTTTATGCAATTTCTGTGATGAAAACTTCAAGCGATCTTCAAGAGT	1077
Qy	1031	TCTGCTTTTCCACTGAAGATGAGAGTGAAGCGGCGACAGCACTTGAAGATGCCAATA	1087
Db	1076	TCTGTATCCCAACTCTTTCACATTTGAGCAAAACCTCACTGCAATTTGTGCAGA	1132

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RESULT 92
US-10-435-655-3
; Sequence 3, Application US/10435655
; Publication No. US20040096940A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, BRIGITTE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING ONE
; TITLE OF INVENTION: NUCLEIC ACIDS CODING THEREFOR
; FILE REFERENCE: EX92009-05
; CURRENT APPLICATION NUMBER: US/10/435,655
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (922)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:

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NAME/KEY: modified_base
LOCATION: (927)
OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (931)..(932)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-435-655-3

Query Match 34.6%; Score 399; DB 17; Length 998;
Best Local Similarity 67.8%; Pred. No. 5.4e-105;
Matches 593; Conservative 0; Mismatches 270; Indels 12; Gaps 2;

163 TCCCGGCGCATCCGCGTATCATCAACGCGGCTCTCCGATGATGTTGCTGCGGCTG 222
13 TCCCTGCGCCTGGCAATGCGCATCAACGCGCTCTACGCGCTGCGCGGCTG 72
223 GTGGGCAATCGCGTGTGATGTTCCGATCATCCGATACCAAAAGATGAGACCAACC 282
73 CTGGGCAACGTGCTGTGATGTTGGGCAATCGTCCGATACCTAAGATGAGACCAACC 132
283 AACATTACATTTTAACTGCGCTTTGGCAATGCTTTAGTTACTTAAACCAATGCCCTTT 342
133 AAGATCTACATCTTCAACCTGGCCTTAGCCGATGCGCTGGCCACGACGCGCTCTTC 192
343 CAGAGTACGCTCTATTTGATGATGAAATTCGCGCTTTTGGGAGATGCTGCAAGATGTA 402
193 CAGAGTACGCTCTATTTGATGATGAAATTCGCGCTTTTGGGAGATGCTGCAAGATGTA 252
403 ATTTCATTGATTTATCAACATGTTTCAACGATCTTCAACCTTACCATGATGAGCTG 462
253 CTCTCATGCACTATCAATATGTTTCAACGATCTTCAACCTTACCATGATGAGCTG 312
463 GACCGCTACATTCGCGTGTGCAACCCGCTGAAAGCTTTGACTTCGCAACCTTTGAG 522
313 GACCGCTACATTCGCGTGTGCAACCCGCTGAAAGCTTTGACTTCGCAACCTTTGAG 372
523 GCAAGATCATCAATATGATGATGCTGCGCTGCTGATCTGTTGGATCTGTCATTA 582
373 GCAAGATCATCAATATGATGATGCTGCGCTGCTGATCTGTTGGATCTGTCATTA 432
583 GTCTTGGAGGCAACCAAGTCAAGGAGACGTCGATGATGATGATGATGATGATGATG 642
433 GTCTTGGAGGCAACCAAGTCAAGGAGACGTCGATGATGATGATGATGATGATGATG 492
643 CCAAGTATGATGATCTCTGCTGCTGCTCTTCAATGAAAGTCTGCTTCAATCTTGGC 702
493 CC-----CAGCTGTACTGAGGACACGCTGACCAAGATCTGCTTCTCTTCCGC 543
703 TTGCGATCCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 762
544 TTGCGATCCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 603
763 AGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
604 AGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
823 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
664 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
883 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
724 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
940 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999
784 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
1000 GATGAAATCTTCAACGCTGCTTCTGCGGAACTTCTG 1034
844 GACGAGACTTCAAGCGCTGCTTCCGCAAGCTCTG 878

RESULT 93

US-09-905-186A-9
Sequence 9, Application US/09905186A
Publication No. US2003008289A1
GENERAL INFORMATION:
APPLICANT: laForce, Mary Jeanne
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US2003008289A1Receptin Receptor Gene, Diagnostic Methods
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905.186A
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1829
TYPE: DNA
ORGANISM: homo sapiens
US-09-905-186A-9

Query Match 34.2%; Score 395; DB 10; Length 1829;
Best Local Similarity 65.2%; Pred. No. 1.1e-103;
Matches 616; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

153 GCGGCAATCTCCCGGCGCATCCGCTCATCAACGCGGCTTACTCCGATGTTCTG 212
162 GCGCTTCCGCTCCGCGCTCAAGTCAACATGCGGCTTACTCCGCTGCTGCTGCTG 221
213 CCGGCGCTTGGTGGCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
222 CGAGGCGCTCCGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 281
273 GACAGCAACCAATTTATCATATTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
282 GACAGCAACCAATTTATCATATTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 341
333 CATGCCCTTTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
342 GCTGCCCTTCAAGGCAAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 401
393 CAAGTATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAAT 452
402 CAAGTATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAAT 461
453 GATGAGCGTGAACGCTACATTTGCGGTGCGCAACCGGTAAGGCTTTGACTTCCGAC 512
462 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 521
513 ACCCTTGAAGCAAAAGATCATCAATTTCTGATCTGCTGCTGCTGCTGCTGCTGCTG 572
522 GTCCAGCAAAACCGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 581
573 CTGCTGATGATCTTCTGAGGCAACCAAGTCAAGGAAAGTCAATGATGATGATGATG 632
582 TCCCGTTCATCATGAGGCTGCGCAAGTCT-----GAGATTAAGGAAATGAGTGGCT 635
633 CTGCAATGATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
636 GGTGAGATCCCTTACCCCTCAGATTTAC---TGGGGCCCGGTGTTTGCAATCTGATCTT 692
693 CATCTTGGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
693 CCTCTTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
753 GCGTCTCAAGAGGCTCGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
753 GCGGCTCCGTGAGATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
813 GATCACCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,748
FILING DATE: 07-Mar-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-Mar-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 10..1119
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-290-748-18
Query Match 34.1%; Score 393.4; DB 15; Length 1805;
Best Local Similarity 65.1%; Pred. No. 3.1e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
QY 153 GCGGCATCTCCCGGCGCATCCCGGTGATCATCAAGCGGGGTCTACCGTGAAGTTCGT 212
DB 138 GCGCTTCTGCGCCCTCGGGCTCAAGGTACCATCGTGGGCTCTACCGCGCGTGTGT 197
QY 213 CGTGGCTTGTGGGCACTCGCTGTATCTTCTGTATCATCCGATACACAAAGATGAA 272
DB 198 CGAGGGCTCTCGGGGAAGTGGCTGTGATGACGTACCTCTCAGGACACCAAAATGAA 257
QY 273 GACGACCAACAATTTACATTTTAACTGCTTGGCAATGCTTTAGTTACTACAAAC 332
DB 258 GACGACCAACAATTTTACATTTTAACTGCTTGGCAATGCTTTAGTTACTACAAAC 317
QY 333 CATGCCCTTTCAGAGTACGCTCTACTATGATGAATCTTGCGCTTTTGGGAAATGTCGTG 392
DB 318 GCTGCCCTTTCAGAGGACGACATCTCTGCGCTTTCGCGCTTTTGGGAAATGCGCTGTG 377
QY 393 CAAGATGATTAATTTTCATGATTTACTACAAAGTTCACAGCATCTTACCTTGACCAT 452
DB 378 CAAGCATGATTTGCTATGACTACTACAAAGTTCACAGCATCTTACCTTGACCAT 437
QY 453 GATGAGCTGACGCTTACATTTGCGGTGTGCAACCGCGTGAAGGCTTTGACTTCGAGAC 512
DB 438 CATAGGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
QY 513 ACCCTGAAGGCAAGATCATCATATATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
DB 498 GTCCAGCAAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557
QY 573 CTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGGAAGCTGATGATGATGATGATGATGAT 632

DB 558 TCCCGTTCATCATGAGGCTCGGACAGGTC-----GAGATGAAGATGATGATGCT 611
QY 633 CTTCGATTTCCCAATGATGATCTACTCTGTGTGGACCTCTTCAATGAAGATCTGCTTT 692
DB 612 GGTGAAGATCCCTTACCCCTCAGATTAAC---TGGGGCCCGGTGTTTGGCATCTGATCTT 668
QY 693 CATCTTGGCTTTCGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB 669 CTCTTCTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
QY 753 GCGCTCAAGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
DB 729 GCGGCTCGGTGAAGTCCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
QY 813 GATACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
DB 789 CATCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
QY 873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
DB 849 GGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
QY 933 CTATTAATCTTGCATGCTGCTTGAAGCTTATACCAAGATGACCTGAATCCATTTCTAGC 992
DB 909 TCTGCGCTTCTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY 993 CTCTTCTGATGAATTAATTTCAAGCGGTGTTTCCGGAATCTTCTGCTTCCATGGAATGAG 1052
DB 969 CTCTCTGATGAATGAATTTCAAGCGGTGTTTCCGGAATCTTCTGCTGCTGCTGCTGCTG 1028
QY 1053 GATGAGGCGGACGACGACTAGACAGATCCGAAATACAGTTTCAGGA 1097
DB 1029 CCGGAGCTGAGGTGTGTGACCGCGCTGCGGAGCATTTGCCAAGGA 1073
RESULT 96
US-09-905-186A-10
; Sequence 10, Application US/0905186A
; Publication No. US2003008289A1
; GENERAL INFORMATION:
; APPLICANT: Kretek, Mary Jeanne
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Orphanin
; TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-284N
; CURRENT APPLICATION NUMBER: US/09/905,186A
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/218,205
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-905-186A-10
Query Match 34.1%; Score 393.4; DB 10; Length 1829;
Best Local Similarity 65.1%; Pred. No. 3.1e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
QY 153 GCGGCATCTCCCGGCGCATCCCGGTGATCATCAAGCGGGGTCTACCGTGAAGTTCGT 212
DB 162 GCGCTTCTGCGCCCTCGGGCTCAAGGTACCATGATGATGATGATGATGATGATGATGAT 221
QY 213 CGTGGCTTGTGGGCACTCGCTGTATCTTCTGTATCATCCGATACCAAGATGAA 272
DB 222 CGAGGGCTCTCGGGGAAGTGGCTGTGATGATGATGATGATGATGATGATGATGATGAT 281
QY 273 GACGACCAACAATTTTACATTTTAACTGCTTGGCAATGCTTTAGTTACTACAAAC 332
DB 282 GACGACCAACAATTTTACATTTTAACTGCTTGGCAATGCTTTAGTTACTACAAAC 341

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QY 333 CATGCCCTTTCAGAGAGGCTGTAATTGTAATTCCTGGCCTTTTGGGAGATGTGTG 392
DB 342 GCTGCCCTTTCAGAGGACGAGACATCTCTGGGCTTCTGGCCGTTTGGAAAGCGCTGG 401
QY 393 CAAGAATGTAATTCATGATTAATTAACAAGTTCACAGCATCTTACCTTGACAT 452
DB 402 CAAGAATGTAATTCATGATTAATTAACAAGTTCACAGCATCTTACCTTGACAT 461
QY 453 GATGACGTTGACCGCTACATGTCGGTGTGCAACCCCGTGAAGCTTTGAACTTCCGAC 512
DB 462 CATGAGTGTGATCGCTATGTAGCCATCTGCAACCCCATCGTCCCTGAGAGTCCGAC 521
QY 513 ACCCTTGAAGCAAGATGATCAATATCTGCATCTGGCGCTGTGTCTATCTGTTGGCAT 572
DB 522 GTCCAGCAAGCCACAGCTGTCAATGTGGCCATCTGGGCCCTGTGGCTCTGTTGTGGGT 581
QY 573 CTCTCAATATGCTCTTGGAGGACCAAAAGTCAGGGAAGAGTGTATGATGAGTCTC 632
DB 582 TCCCGTTGCAATATGAGGCTCGGACAGTCTC-----GAGGATGAAGATGAGAGTCT 635
QY 633 CTTCAGATTCCTCAATGATGACTACTCTGTGTGGAGCTCTTCATGAAGATCTCGCTT 692
DB 636 GGTGAGAGATCCCTACCCCTCAGAGATTAC---TGGGGCCCGGTGTGTGTCATCTGATCT 692
QY 693 CATCTTTCCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
DB 693 CCTCTTCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
QY 753 GCGTCTCAAGAGCGTCCGGCTCTTCTTGGCTCCGAGAGAAAGATTCGCACTTGCGT 812
DB 753 GCGGCTCCGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812
QY 813 GATCACTGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 813 CATCACTGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
QY 873 CATATTCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 873 GGTCTTTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
QY 933 CTATATTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 933 TCTGCGCTTCTGCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
QY 993 CTTCCTTGAATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 993 CTTCCTGATGAGATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
QY 1053 GATGAGCGGCAAGACATGACAGAGTCCGAAATACAGTTCCAGGA 1097
DB 1053 CCGGAGTGTGAGGTGTCTGACCGGCTGTGCGAGCATTTGCCAAGGA 1097

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RESULT 97
US-09-905-186A-11

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; Sequence 11, Application US/09905186A
; Publication No. US2003008289A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Orphanin
; TITLE OF INVENTION: Fg/No. US2003008289A1: Opioid Receptor Gene, Diagnostic Methods
; FILE REFERENCE: 600-1-284N
; CURRENT APPLICATION NUMBER: US/09/905,186A
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/218,205
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1829

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TYPE: DNA
ORGANISM: homo sapiens
US-09-905-186A-11

Query Match 34.1%; Score 393.4; DB 10; Length 1829;
Best Local Similarity 65.1%; Pred. No. 3,1e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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QY 153 CCGGACATCTCCCGGCGCATCCGCTCATCTACAGCGGCTTACTCCGTAGTTCGT 212
DB 162 CCGCTTCTCCCGCTCCGCGCTCAGAGTCCATCTGCGGCTCTTACTCGGCGTGTGT 221
QY 223 CGTGGCTTGTGGCACTGCTGTGTATGTTGTGGATCATCCGATACAAAGATGAA 272
DB 222 CGAGGCTCTGGGAACTGCTGTGTATGTTGTGGATCATCCGATACAAAGATGAA 281
QY 273 GACAGCAACCAATTTATATATTTAACTGCTTGTGGAGATGCTTTAGTTACTAAC 332
DB 282 GACAGCAACCAATTTATATTTAACTGCTTGTGGAGATGCTTTAGTTACTAAC 341
QY 333 CATGCCCTTTCAGAGAGGCTGTAATTGTAATTCCTGGCCTTTTGGGAGATGTGTG 392
DB 342 GCTGCCCTTTCAGAGGACGAGACATCTCTGGGCTTCTGGCCGTTTGGAAAGCGCTGG 401
QY 393 CAAGAATGTAATTCATGATTAATTAACAAGTTCACAGCATCTTACCTTGACAT 452
DB 402 CAAGAATGTAATTCATGATTAATTAACAAGTTCACAGCATCTTACCTTGACAT 461
QY 453 GATGACGTTGACCGCTACATGTCGGTGTGCAACCCCGTGAAGCTTTGAACTTCCGAC 512
DB 462 CATGAGTGTGATCGCTATGTAGCCATCTGCAACCCCATCGTCCCTGAGAGTCCGAC 521
QY 513 ACCCTTGAAGCAAGATGATCAATATCTGCATCTGGCGCTGTGTGTGTGTGTGTGT 572
DB 522 GTCCAGCAAGCCACAGCTGTCAATGTGGCCATCTGGGCCCTGTGTGTGTGTGTGT 581
QY 573 CTCTCAATATGCTCTTGGAGGACCAAAAGTCAGGGAAGAGTGTATGAGTCTC 632
DB 582 TCCCGTTGCAATATGAGGCTCGGACAGTCTC-----GAGGATGAAGATGAGAGTCT 635
QY 633 CTTCAGATTCCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
DB 636 GGTGAGAGATCCCTACCCCTCAGAGATTAC---TGGGGCCCGGTGTGTGTCATCTGATCT 692
QY 693 CATCTTTCCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
DB 693 CCTCTTCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
QY 753 GCGTCTCAAGAGCGTCCGGCTCTTCTTGGCTCCGAGAGAAAGATTCGCACTTGCGT 812
DB 753 GCGGCTCCGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812
QY 813 GATCACTGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 813 CATCACTGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
QY 873 CATATTCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 873 GGTCTTTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
QY 933 CTATATTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 933 TCTGCGCTTCTGCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
QY 993 CTTCCTTGAATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 993 CTTCCTGATGAGATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
QY 1053 GATGAGCGGCAAGACATGACAGAGTCCGAAATACAGTTCCAGGA 1097
DB 1053 CCGGAGTGTGAGGTGTCTGACCGGCTGTGCGAGCATTTGCCAAGGA 1097

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RESULT 98
US-10-305-720-1391
; Sequence 1391, Application US/10305720
; Publication No. US20040010136A1
GENERAL INFORMATION:
; APPLICANT: Au-Yang, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO: 1391
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g471316
US-10-305-720-1391

Query Match      34.1%; Score 393.4; DB 16; Length 1973;
Best Local Similarity 65.1%; Pred. No. 3.2e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCCGTATCATCAAGCGCGCTCTACTCTCGTAGTTCGT 212
DB 306 CGCCTTCTCCGCGCTCCGCTCAAGGTCCATCCGCGGGGCTCTACCTGGCCGTGTGT 365
QY 213 CGTGGCTTGTGGGCACTCGCTGTCTATGTTCTGATCCGATACAAAGTAA 272
DB 366 CGAGGCGCTCCGCGGAACTGCTGTCTATGATCGTATCCAGGCAACAAATGA 425
QY 273 GACGACAACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 332
DB 426 GACGACAACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 485
QY 333 CATGCCCTTTCAGAGTACGCTCTATCTTGAATTCCTGGCTTTGGGGAATGTCTGT 392
DB 486 GCTGCTCTCCAGGGGAGGAGATCTCTGCTGGCTTTGCGCGTTGGGAATGCGCTGT 545
QY 393 CAAGATGATTAATTTCCATGATTAATTAATTAATTAATTAATTAATTAATTAAT 452
DB 546 CAAGACAGTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 605
QY 453 GATGACGCTGACCGCTATCATTTGCGCTGACCGCCGTAAGGCTTTGGAATTCGAC 512
DB 606 CATGATGATGATTCGCTATGATGATTCGCTATGATGATTCGCTATGATGATTC 665
QY 513 ACCCTTGAAGGCAAGATCATCATTAATTCGATTCGCTGCTGTCTGATTCGTTGCA 572
DB 666 GTTCAGCAAGCCGAGGCTGTCAATGTGACATCTGGGCTTGGCTTGTGTGTGTGT 725
QY 573 CTCTGCAATGATCTTGGAGGACCAAAATCAAGGAAAGCTGATGATGAGGCTC 632
DB 726 TCCCGTTGGCATATGAGGCTCGGACAGGTC-----GAGGATGAAGAGATGAGGCT 779
QY 633 CTTCGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
DB 780 GGTGAGATTCCTTACCCCTCAGGATTAAC---TGGGGCCGGGTGTTTGCATTCGATCT 836
QY 693 CATCTTGGCTTGTGATTCCTGTCTCTCATCATCATCATCATCATCATCATCATCAT 752
DB 837 CCTCTCTCTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 896
QY 753 GGTCTCAAGAGGTCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 812
DB 897 GGGGCTCCGCTGAGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 956
QY 813 GATCAACCAAGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
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DB 957 CATCACTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1017 GATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
QY 933 CTATTAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1077 TCTGGCTTCTGACCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
QY 993 CTTCCTGATGAAACTTCAAGCGGTGTTTCCGGAATCTTGTCTTTCATGAAATGAG 1052
DB 1137 CTTCCTGATGAAACTTCAAGCGGTGTTTCCGGAATCTTGTCTTTCATGAAATGAG 1196
QY 1053 GATGAGCGGACAGACACTAGACAGATCCGAAATACGTTAGGA 1097
DB 1197 CGGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

RESULT 99
US-10-641-643-1417
; Sequence 1417, Application US/10641643
; Publication No. US20040077003A1
GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1417:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g471316
; SEQUENCE DESCRIPTION: SEQ ID NO: 1417 :
US-10-641-643-1417

Query Match      34.1%; Score 393.4; DB 17; Length 1973;
Best Local Similarity 65.1%; Pred. No. 3.2e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCCGTATCATCAAGCGGCTCTACTCTCGTAGTTCGT 212
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Db      306 CGCCTTCGCCCCCGGGCTCAAGGTCAACATCGGGGGCTTACCTGGCGGTGTGT 365
Qy      213 CGTGGGCTTGGTGGGCACTCGGTGTATGTTCGTGATCATCCGATACAAAGATGA 272
Db      366 CGAGGGCTCCCTGGGGAACTGGCTTGTCAATGACATCCACGACACCAAAATGA 425
Qy      273 GACAGCAACCAATTTATATATTTAACTGGCTTGGGAGATGGCTTTAGTTACTACAAC 332
Db      426 GACAGCCACCAATTTATATTTAACTGGCTTGGGAGATGGCTTTAGTTACTACAAC 485
Qy      333 CATGCCCTTTCAGAGTACGGTCTACTTGAATTCCTGGCGCTTTGGGGATGTCTGTG 392
Db      486 GTGCGCTTTCAGGGGACGAGATCTCTCGGGCTTTCGGCGCTTTGGGAAATGGCTGTG 545
Qy      393 CAAGATAGTAAATTTCCATTGATTACTACAACATGTTACACAGACTTTCACTTGAACAT 452
Db      546 CAAGACAGTCAATGGCATTTGACTACTACAACATGTTACACAGACTTTCACTTGAACAT 605
Qy      453 GATGAGCGTGAACGGCTACATTCGGTGTGCAACCCCGGAAGGCTTTGGACTTTCGAC 512
Db      606 CATGAGTGTGATCGCTATGTAGCAATCGCAACCCCATCGTGCCTTCGACGTCCGAC 665
Qy      513 ACCCTTGAAGGCAAGATCATCAATATCGCATCTGGCTGTGTGTCATCTGTGGCAT 572
Db      666 GTCCAGCAAAAGCCAGGCTGTCAATGTGGCCATCTGGGCCCTGGCTGTGTGTGCTGT 725
Qy      573 CTCTCAATAGTCTCTTGAAGGCAACCAAGTCAAGGAAAGATGTCATTTAGTGTCTC 632
Db      726 TCCCGTTCGATCATGAGGCTCGGCAAGGTCTC-----GAGGATGAAGATGAGTGTCT 779
Qy      633 CTGAGATTCGCAATGATGACTACTCTCGTGGGAGCTCTTCAATGAATGTGGTCTT 692
Db      780 GGTGAGATTCCTTACCCCTCAGGATTAAC---TGGGGCCGGGTGTTGCCATTTGATCTT 836
Qy      693 CATCTTTCGCTCGTATGATCCCTGTCTCATCTCAATCGCTCTTCAACCCGATGATCT 752
Db      837 CCTCTTCTTCTTCAATGATCCCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 896
Qy      753 GCGTCTCAAGAGCGTCCGGCTCTCTTCTGAGCTCCGAGAAAGATTCGCAACTGCTGTAG 812
Db      897 GCGGCTCCGTGAGATCCGCTGTCTCTCGGGCTCCGAGAGAGAACCGGAACCTCGGGG 956
Qy      813 GATCACAGACTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      957 CATCACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
Qy      873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
Db      1017 GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
Qy      933 CTATTAATCTTGTGATCGCTTGTAGGCTATACCAACAGTACCTGAAATCCCATTTCTTACGC 992
Db      1077 TCTGGCTTCTGTGCAACGGCCCTGGGGCTAGGTCAACAGCTGTCTCAACCCCATCTTACGC 1136
Qy      993 CTTTCTTGTATGAAAATTTCAACGGGTGTTTCCGGGACTTTCCTTTCCACTGAAGATGAG 1052
Db      1137 CTTCTGTGATGAAATTTCAACGGCTGTCTTCCGCAAGTTCGTGTGATCTGACCTGTG 1196
Qy      1053 GATGAGCGGAGAGACACTGAGAGATCCGAATACATTTCACTTCACTTCACTTCACT 1097
Db      1197 CCGGACGCTGACGTGTCTGTACCGGCTGTGGGCACTTGCACAGGA 1241

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RESULT 100
US-10-087-345A-22
; Sequence 22, Application US/10087345A
; Publication No. US20030045696A1
; GENERAL INFORMATION:
; APPLICANT: Ouyang, Chung
; TITLE OF INVENTION: ORPHANIN FQ RECEPTOR NUCLEIC ACIDS
; FILE REFERENCE: UM-06962
; CURRENT APPLICATION NUMBER: US/10/087,345A

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; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-345A-22

Query Match      34.1%; Score 393.4; DB 15; Length 2534;
Best Local Similarity 65.1%; Pred. No. 3.6e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

Qy      153 CGCGCAATCTCCCGGCAATCCGGTATATATCAACGGCGGTCTTCCGTAGTGTGT 212
Db      246 CGCCTTCTGCCCCCTGGGCTCAAGGTCAACATCTGGGGCTTCTACCTGGCGGTGTGT 305
Qy      213 CGTGGGCTTGGTGGGCACTCGCTGTGTATGTTCTGTATCTCGATATCCGATACAAAGATGA 272
Db      306 CGAGGGCTCCCTGGGGAACTGGCTTGTCAATGACATCCCTCAAGGACACCAAAATGA 365
Qy      273 GACAGCAACCAATTTATATTTAACTGGCTTGGGAGATGGCTTTAGTTACTACAAC 332
Db      366 GACAGCCACCAATTTATATTTAACTGGCTTGGGAGATGGCTTTAGTTACTACAAC 425
Qy      333 CATGCCCTTTCAGAGTACGGTCTACTTGAATTCCTGGCGCTTTGGGGATGTCTGTG 392
Db      426 GTGCGCTTTCAGGGGACGAGATCTCTCGGGCTTTCGGCGCTTTGGGAAATGGCTGTG 485
Qy      393 CAAGATAGTAAATTTCCATTGATTACTACAACATGTTACACAGACTTTCACTTGAACAT 452
Db      486 CAAGACAGTCAATGGCATTTGACTACTACAACATGTTACACAGACTTTCACTTGAACAT 605
Qy      453 GATGAGCGTGAACGGCTACATTCGGTGTGCAACCCCGGAAGGCTTTGAGACTTCCGAC 512
Db      546 CATGAGTGTGATCGCTATGTAGCCATCTGCAACCCCATCGTGCCTTCGACGTCCGAC 605
Qy      513 ACCCTTGAAGGCAAGATCATCAATATCGCATCTGGCTGTGTGTGTGTGTGTGTGTGT 572
Db      606 GTCCAGCAAAAGCCAGGCTGTCAATGTGGCCATCTGGGCCCTGTGTGTGTGTGTGT 665
Qy      573 CTCTCAATAGTCTCTTGAAGGCAACCAAGTCAAGGAAAGATGTCATTTAGTGTCTC 632
Db      666 TCCCGTTCGATCATGAGGCTCGGCAAGGTCTC-----GAGGATGAAGATGAGTGTCT 719
Qy      633 CTGCAATTTCCCAATGATGACTACTCTGTGTGGGACTCTTTCATGAAGATGTGCTCTT 692
Db      720 GGTGAGATTCCTTACCCCTCAGGATTAAC---TGGGGCCGGGTGTTGCCATTTGATCTT 776
Qy      693 CATCTTTCGCTCGTATGATCCCTGTCTCATATCATGTGTGTGTGTGTGTGTGTGTGTGT 752
Db      777 CCTCTTCTTCTTCAATGATCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 836
Qy      753 GCGTCTCAAGAGCGTCCGGCTCTTCTGTGCTCCGAGAGAAAGATTCGCAACTGCTGTAG 812
Db      837 GCGGCTCCGTGAGATCCGCTGTCTTCCGGCTCCGAGAGAGAACCGGAACCTCGGGG 896
Qy      813 GATCACAGACTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      897 CATCACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
Qy      873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
Db      957 GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
Qy      933 CTATTAATCTTGTGATCGCTTGTAGGCTATACCAACAGTACCTGAAATCCCATTTCTTACGC 992
Db      1017 TCTGGCTTCTGTGCAACGGCCCTGGGGCTAGGTCAACAGCTGTCTCAACCCCATCTTACGC 1076
Qy      993 CTTTCTTGTATGAAAATTTCAACGGGTGTTTCCGGGACTTTCCTTTCCACTGAAGATGAG 1052
Db      1077 CTTCTGTGATGAAATTTCAACGGCTGTCTTCCGCAAGTTCGTGTGATCTGACCTGTG 1136

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Qy 1053 GATGAGCGGACAGCACTAGCAGAGTCCGAAATACAGTTCAAGA 1097
Db 1137 CCGGAGCGTGCAGGTGTGTGACCGCGGTGGCGCAGCATTTGCCAAGA 1181

Search completed: August 31, 2004, 14:23:26
Job time : 626 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 3490 Seconds
(without alignments)
9874.200 Million cell updates/sec

Title: US-09-904-584-1

Perfect score: 1154

Sequence: 1 atgagctcccgatccagat.....ccagatgactgctgga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*
1: em_eatba:*
2: em_eatbm:*
3: em_eatbn:*
4: em_eatbu:*
5: em_eatbv:*
6: em_eatpl:*
7: em_eatrc:*
8: em_eatrl:*
9: gb_eatcl:*
10: gb_eatcl2:*
11: gb_hlc:*
12: gb_eatc3:*
13: gb_eatc4:*
14: gb_eatc5:*
15: em_eatfun:*
16: em_eatfun:*
17: em_eatfun:*
18: em_gga_lnv:*
19: em_gga_lnv:*
20: em_gga_vrt:*
21: em_gga_fun:*
22: em_gga_mam:*
23: em_gga_mus:*
24: em_gga_pro:*
25: em_gga_rod:*
26: em_gga_phg:*
27: em_gga_vrl:*
28: gb_gga1:*
29: gb_gga2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	805.2	69.8	895	14	CB565888 AGENCOURT
2	470.6	40.8	837	14	CF593603 AGENCOURT
3	468	40.6	480	13	BX092912 AGENCOURT
4	430.8	37.3	2405	11	AK038389 Mus muscu

5	420	36.4	4022	11	AK043873
6	367.8	31.9	2919	11	AK038620
7	367.8	31.9	2959	11	AK079529
8	352	30.5	879	29	AY10745
9	335.6	29.1	2940	11	AK044178
10	327.4	28.4	2974	11	AK043275
11	327	28.3	3101	11	AK031926
12	325.8	28.2	879	29	AY10746
13	311.4	27.0	1053	29	CNS04C2T
14	277.6	24.1	788	13	BX874804
15	271.4	23.5	883	13	BE676176
16	268.6	23.3	917	13	BU219878
17	268.6	20.8	657	13	BM588668
18	231.2	20.0	980	12	BM543468
19	229.6	19.9	1176	29	AY10746
20	227.4	19.7	389	10	BE649947
21	226.6	19.6	1176	29	AY100829
22	226.6	19.6	2014	11	AK046464
23	224.6	19.5	980	12	BM543468
24	223	19.3	632	10	BB641725
25	221.4	19.2	1006	29	AY100676
26	217.6	18.9	784	13	BQ179053
27	214.8	18.6	1006	29	AY100674
28	214	18.5	429	12	BM342951
29	213.8	18.5	2432	11	AK051189
30	213	18.5	836	29	CNS02261
31	213	18.5	866	14	CD246184
32	211	18.3	531	29	CE517843
33	208.6	18.1	877	29	CNS02SC2
34	208.2	18.0	842	29	CNS02SKU
35	207.8	18.0	697	13	BU139251
36	207.8	18.0	757	13	BU614716
37	203.4	17.6	785	12	BT754749
38	202.8	17.3	810	12	BM943972
39	199.2	17.3	849	13	BU219037
40	195.6	16.9	816	13	BQ179148
41	194	16.8	787	29	BX228633
42	192.8	16.7	746	13	BQ571737
43	190.6	16.5	954	29	AY101421
44	189.8	16.4	546	28	A2226406
45	182.2	15.8	2848	11	AK039151
46	181.8	15.8	318	29	CF536117
47	181.2	15.7	776	14	CF550026
48	180.4	15.6	1176	29	AY100828
49	179.2	15.5	735	13	BU366266
50	178.8	15.5	987	29	AY101571
51	178.4	15.5	2724	11	BC033145
52	178.4	15.5	433	10	AM489031
53	178.4	15.5	741	13	BU613017
54	177.8	15.4	720	12	BT753905
55	176	15.3	828	13	BX843850
56	171.6	14.9	1307	11	CNSLRI1BD
57	170.2	14.7	654	10	AM373832
58	170.2	14.7	990	29	AY101573
59	169	14.6	1095	29	AY100986
60	168.4	14.6	627	12	BT919235
61	168.2	14.6	183	14	R81583
62	166.4	14.4	710	29	AY101423
63	165	14.3	945	29	AY101423
64	164	14.2	1257	13	AX400332
65	162.2	14.1	502	29	AX400332
66	162	14.0	798	14	CD559493
67	161.4	14.0	1089	29	AY100988
68	160	13.9	714	10	BF193020
69	159.4	13.8	550	10	BF193020
70	159.4	13.8	987	29	AY101572
71	159.2	13.8	768	13	BU318522
72	158.8	13.7	795	14	CD559491
73	158.4	13.7	910	29	AY101422
74	156.2	13.5	1287	29	AY100334
75	156	13.5	701	14	CF147827
76	155.4	13.5	688	13	BU057593
77	153.4	13.3	916	13	BX433241

370	82.6	7.2	765	14	CF270677	AGENCOURT	443	78.8	6.8	1224	29	AY420419	Mus muscu
371	82.6	7.2	794	29	AY399911	Mus muscu	444	78.8	6.8	4676	11	AK038558	Mus muscu
372	82.6	7.2	1201	9	AL556152	AL556152	445	78.2	6.8	600	12	B1987229	Mus muscu
373	82.4	7.1	550	14	CB354574	CB354574	446	78.2	6.8	646	10	BB615654	BB615654
374	82.4	7.1	723	14	CF147812	AGENCOURT	447	78.2	6.8	650	12	B1837704	BB644135
375	82.4	7.1	1114	12	BM605549	AGENCOURT	448	78.2	6.8	662	10	BB644135	BB644135
376	82.2	7.1	529	10	AM653917	AGENCOURT	449	78.2	6.8	665	10	BB628567	BB628567
377	82.2	7.1	636	14	CF359817	821090 MA	450	78.2	6.8	665	13	BY726917	BY726917
378	82.2	7.1	1201	13	BK421511	BK421511	451	78.2	6.8	787	9	AU080004	AU080004
379	82	7.1	546	14	CB514044	BSa11952	452	78.2	6.8	868	14	CD300887	CD300887
380	82	7.1	558	14	CB287514	CBMD1_G05	453	78.2	6.8	965	13	BQ944555	BQ944555
381	82	7.1	561	10	CB287516	CBMD1_G07	454	78.2	6.8	1029	29	AY399294	AY399294
382	82	7.1	561	10	BF591285	BF591285	455	78.2	6.8	1029	29	AY399295	AY399295
383	81.8	7.1	623	12	BM038875	pnm1c.p0	456	78.2	6.8	1126	12	BM919012	BM919012
384	81.8	7.1	676	14	CA355473	CA355473	457	78.2	6.8	1201	13	EX398107	EX398107
385	81.8	7.1	683	13	BU108682	BU108682	458	78	6.8	709	13	BU611590	BU611590
386	81.6	7.1	750	13	BU335137	BU335137	459	78	6.8	710	9	AL707383	AL707383
387	81.6	7.1	623	14	CD468358	Leukoc3_2	460	78	6.8	932	29	CNS02SIR	CNS02SIR
388	81.6	7.1	710	14	CD218005	CD218005	461	78	6.8	1848	11	AK011967	AK011967
389	81.6	7.1	765	14	CB939088	IPCG1x13_	462	77.8	6.7	600	14	CA530488	CA530488
390	81.6	7.1	807	14	CB939828	IPCG1x13_	463	77.8	6.7	640	14	CD740138	CD740138
391	81.6	7.1	988	13	BK346496	BK346496	464	77.8	6.7	690	14	CAS88153	CAS88153
392	81.6	7.1	1119	12	BM543622	BM543622	465	77.8	6.7	710	13	BU613761	BU613761
393	81.6	7.1	1143	29	AY417250	AY417250	466	77.8	6.7	3338	11	AK085990	AK085990
394	81.6	7.1	1766	11	AK008952	Mus muscu	467	77.6	6.7	480	14	CB018048	CB018048
395	81.4	7.1	500	12	BG395247	602457760	468	77.6	6.7	600	29	CE428488	CE428488
396	81.4	7.1	906	13	BU523025	BU523025	469	77.6	6.7	661	13	BY748200	BY748200
397	81.2	7.0	692	14	CB556541	AMGNNUC:U	470	77.6	6.7	799	14	CF256455	CF256455
398	81.2	7.0	909	13	BK350278	BK350278	471	77.6	6.7	916	13	BX424593	BX424593
399	81.2	7.0	912	14	CD106096	CD106096	472	77.6	6.7	903	29	CNS02EZX	CNS02EZX
400	81.2	7.0	942	13	BQ896389	BQ896389	473	77.6	6.7	1083	29	AY400080	AY400080
401	81.2	7.0	1257	11	BC054346	BC054346	474	77.4	6.7	520	12	BM532324	BM532324
402	81.2	7.0	1990	11	BC040850	BC040850	475	77.4	6.7	593	12	BM191613	BM191613
403	81.2	7.0	2578	11	AK044557	Mus muscu	476	77.4	6.7	623	13	BQ570239	BQ570239
404	81.2	7.0	2938	11	BC045651	BC045651	477	77.4	6.7	1003	13	BY708841	BY708841
405	81.2	7.0	3146	11	AK035902	AK035902	478	77.4	6.7	1008	13	BQ060058	BQ060058
406	81.2	7.0	3159	11	AK045634	Mus muscu	479	77.2	6.7	540	29	CE278936	CE278936
407	81	7.0	723	12	BM951933	UI-M-BH0-	480	77.2	6.7	608	13	BY724644	BY724644
408	81	7.0	729	14	CA373689	647893 NC	481	77.2	6.7	663	12	BM426517	BM426517
409	81	7.0	891	14	CD252626	CD252626	482	77.2	6.7	703	12	BG818103	BG818103
410	81	7.0	949	13	BQ923464	BQ923464	483	77.2	6.7	1440	29	AY404935	AY404935
411	81	7.0	1017	12	BM922807	BM922807	484	77.2	6.7	487	10	BE656336	BE656336
412	80.6	7.0	523	9	AL836006	AL836006	485	77	6.7	512	13	EX873014	EX873014
413	80.6	7.0	535	14	CD492892	CD492892	486	77	6.7	512	13	BX880500	BX880500
414	80.6	7.0	805	14	CD246171	CD246171	487	77	6.7	667	13	BY749844	BY749844
415	80.6	7.0	807	12	BT764263	BT764263	488	77	6.7	671	13	BX298388	BX298388
416	80.4	7.0	768	9	AJ444418	AJ444418	489	77	6.7	1201	9	AL547734	AL547734
417	80.4	7.0	795	10	BF345999	602018720	490	76.8	6.7	514	10	BF732711	BF732711
418	80.4	7.0	863	12	BI661279	BI661279	491	76.8	6.7	921	12	BG913631	BG913631
419	80.4	7.0	899	13	BU484242	BU484242	492	76.6	6.6	946	14	CD246174	CD246174
420	80.2	6.9	620	14	CF181257	818066 MA	493	76.6	6.6	1097	13	BQ057309	BQ057309
421	80.2	6.9	666	10	AM966793	EST378867	494	76.6	6.6	1146	29	AY400451	AY400451
422	80.2	6.9	770	14	CF595894	AGENCOURT	495	76.6	6.6	3335	11	AK049892	AK049892
423	80.2	6.9	1002	29	CNS05CZB	AGENCOURT	496	76.6	6.6	3335	11	AK018543	AK018543
424	80.2	6.9	1188	29	AY416699	AY416699	497	76.4	6.6	504	14	CAS78796	CAS78796
425	80	6.9	80	10	BG018816	dab13b04.	498	76.4	6.6	505	14	CAS578793	CAS578793
426	80	6.9	866	29	CNS02RNL	AGENCOURT	499	76.4	6.6	508	14	CAS577592	CAS577592
427	79.8	6.9	997	13	BU839951	BU839951	500	76.4	6.6	532	14	CAS76608	CAS76608
428	79.6	6.9	664	13	BU838276	BU838276							
429	79.4	6.9	695	28	CC320290	TAM32-33G							
430	79.4	6.9	595	9	AJ452917	AJ452917							
431	79.4	6.9	797	12	BI818742	603037572							
432	79.4	6.9	844	13	BU460828	603269446							
433	79.4	6.9	958	12	BT754621	BT754621							
434	79.4	6.9	1201	9	AL531903	AL531903							
435	79.2	6.9	734	12	BI259114	602973025							
436	79	6.8	544	29	CS9594540	OST252778							
437	79	6.8	721	14	CF147813	AGENCOURT							
438	78.8	6.8	581	14	CF540844	UI-M-GM0-							
439	78.8	6.8	701	14	CA371743	652323 NC							
440	78.8	6.8	756	14	CK142821	AGENCOURT							
441	78.8	6.8	764	14	CF287658	AGENCOURT							
442	78.8	6.8	831	12	BI916060	603184490							

ALIGNMENTS

RESULT 1
LOCUS CB565888
DEFINITION AGENCOURT 12691503 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:6519213 5', mRNA_sequence.
ACCESSION CB565888
VERSION CB565888.1 GI:29485418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 895)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: IRBP001 row: f column: 09
High quality sequence stop: 763.
Location/Qualifiers

FEATURES
source

1..895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:519213"
/tissue_type="mixed"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 146"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
http://image.llnl.gov/image_rearrayed_plates/IRBP.presv.dat
a. Note: this is a NIH_MGC library."

ORIGIN

Query Match 69.8%; Score 805.2; DB 14; Length 895;
Best Local Similarity 97.1%; Pred. No. 2,6e-145;
Matches 841; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

QY 1 ATGAGTCCCGCATCAGATCTTCCGCGGAGACCGGCGCTACCTGCGCCCGAGCGCC 60
DB 2 ATGGAATCCCGATTCATATCTTCCGCGGAGACCGGCGCTACCTGCGCCCGAGCGCC 61
QY 61 TGCCTGCCCGCCCAACAGACGCGCTGTTCCCGGCTGGGCGGAGCCCGACAGCAACGCGC 120
DB 62 TGCCTGCCCGCCCAACAGACGCGCTGTTCCCGGCTGGGCGGAGCCCGACAGCAACGCGC 121
QY 121 AGCGCGGCGCTCGAGAGAGCGCGAGCTGGAGCCCGGCGACATCTCCCGGCGCATCCCGGTC 180
DB 122 AGCGCGGCGCTCGAGAGAGCGCGAGCTGGAGCCCGGCGACATCTCCCGGCGCATCCCGGTC 181
QY 181 ATCATCAGCGCGGCTGTAATCCGTAAGTTCGTCGTGGGCTTGATGGGCAACCTCGCTGGTC 240
DB 182 ATCATCAGCGCGGCTGTAATCCGTAAGTTCGTCGTGGGCTTGATGGGCAACCTCGCTGGTC 241
QY 241 ATGTTGCTGATCATCCGATACCAAGATGAGAGACGCAACCAATTTACATATTTAAC 300
DB 242 ATGTTGCTGATCATCCGATACCAAGATGAGAGACGCAACCAATTTACATATTTAAC 301
QY 301 CTGGCTTTGGCAGATGCTTTAGTACTACCAACCATGCGCTTTCAAGATACGCTTACTTG 360
DB 302 CTGGCTTTGGCAGATGCTTTAGTACTACCAACCATGCGCTTTCAAGATACGCTTACTTG 361
QY 361 ATGAATCTCGGCTTTTGGGAGATGCTGTCAGAGATGTAATTTCCATTGATTACTAC 420
DB 362 ATGAATCTCGGCTTTTGGGAGATGCTGTCAGAGATGTAATTTCCATTGATTACTAC 421
QY 421 AACATGTTCCAGCAGCATCTTCACTTGAACATGATGAGGCGGACCGCTACATTCGCGTG 480
DB 422 AACATGTTCCAGCAGCATCTTCACTTGAACATGATGAGGCGGACCGCTACATTCGCGTG 481

QY 481 TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 540
DB 482 TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 541
QY 541 TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGAGGACCAAA 600
DB 542 TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGAGGACCAAA 601
QY 601 GTCCAGGAAGAGCTGATGTCATTTGAGATGCTCTTGGCACTTCCCAATATGACTATCC 660
DB 602 GTCCAGGAAGAGCTGATGTCATTTGAGATGCTCTTGGCACTTCCCAATATGACTATCC 661
QY 661 TGGTGGAGCCTTTGATGAAGATGTCGCGCTTCATCTTTGCGCTGATGCTGCTGCTC 720
DB 662 TGGTGGAGCCTTTGATGAAGATGTCGCGCTTCATCTTTGCGCTGATGCTGCTGCTC 721
QY 721 ATCATCATCTGCTGTACACCTGTATGATCTGCTGCTCAAGAGCTCC-GGCTCCTTC 779
DB 722 ATCATCATCTGCTGTACACCTGTATGATCTGCTGCTCAAGAGCTCCGGGCTCCTTC 781
QY 780 TGGCTCCGAGAGAAAGATC-GCAACCTGCGTATGATCAGACTGCTGCTGCTG 838
DB 782 TGGCTCCGAGAGAAAGATCAGCTGCGTATGATCAGACTGCTGCTGCTGCTG 841
QY 839 TGGCAGTCTTGGCTGCTGCTGCTGCTGCT 864
DB 842 GTGGCAGGCTTCTGCTGCTGCTGCTGCT 867

RESULT 2
CF593603
LOCUS
DEFINITION
AGENCOURT_15623822 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30531690 5', mRNA sequence.
CF593603
CF593603.1 GI:36347316
EST.
KEYWORDS

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 837)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Haneson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: NDAM622 row: n column: 19
High quality sequence stop: 592.
Location/Qualifiers

FEATURES
source

1..837
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30531690"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
/note="Organ: placenta; Vector: pBluescriptR, site 1:
ali-XhoI; Site 2: BamHI; Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NH&I, National Institutes of Health). Note: This is a NIH_MGC library."

Query Match 40.8%; Score 470.6; DB 14; Length 837;
Best Local Similarity 99.2%; Pred. No. 1.3e-80;
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAGTCTCCCGATCCAGATCTTCCGCGGAGCCGCGCTTACCTGCGCCCGGAGCGCC 60
DB 240 ATGAGTCTCCCGATCCAGATCTTCCGCGGAGCCGCGCTTACCTGCGCCCGGAGCGCC 299
QY 61 TGGCTGCCCCCAACGACGAGCGCTGTTTCCCGGCTGAGCGGCGGCAACGAGCGCC 120
DB 300 TGGCTGCCCCCAACGACGAGCGCTGTTTCCCGGCTGAGCGGCGGCAACGAGCGCC 359
QY 121 AGCGCGGCTCGGAGGAGCGGAGCTGAGCGCGGCGGCAATCTCCCGGCGCATCCCGGCTC 180
DB 360 AGCGCGGCTCGGAGGAGCGGAGCTGAGCGCGGCGGCAATCTCCCGGCGCATCCCGGCTC 419
QY 181 ATCATCAGCGCGCTTACTCTCCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240
DB 420 ATCATCAGCGCGCTTACTCTCCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 479
QY 241 ATGCTGTGATATCATCCGATACCAAGATGAGAGCAACCAATTTTACATTTTAC 300
DB 480 ATGCTGTGATATCATCCGATACCAAGATGAGAGCAACCAATTTTACATTTTAC 539
QY 301 CTGGCTTTGGCAGATCTTAACTTACTAACAACATCCCTTCAAGATGAGTCTGATCTG 360
DB 540 CTGGCTTTGGCAGATCTTAACTTACTAACAACATCCCTTCAAGATGAGTCTGATCTG 599
QY 361 ATGAATCTCTGCTTTTGGGAGATGCTGTCGAAGATGATTAATTTTCAATTTTAC 420
DB 600 ATGAATCTCTGCTTTTGGGAGATGCTGTCGAAGATGATTAATTTTCAATTTTAC 659
QY 421 AACATGTTACAGCATCTTTGACCTTGACATGATGAGGAGCGGCAATTTGCC 477
DB 660 AACATGTTACAGCATCTTTGACCTTGACATGATGAGGAGCGGCAATTTGCC 716

RESULT 3
BX092912 480 bp mRNA linear EST 23-JAN-2003
LOCUS BX092912 Soares placenta ND2HP Homo sapiens cDNA clone
DEFINITION IMAGP998B19190 ; IMAGE:134322, mRNA sequence.
ACCESSION BX092912
VERSION BX092912
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 480)
Ebert, L., Heil, O., Hemig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998B19190.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111

FEATURES

source

www.rzpd.de
This clone is available royalty-free from RZPD.
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M31r, Primer sequence: TTTCACACAGGAAACACCTATGAC.
Location/Qualifiers
1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998B19190 ; IMAGE:134322"
/sex="Female"
/dev_stage="VDH10B (ampicillin resistant)"
/clone_lib="Soares placenta ND2HP"

ORIGIN

Query Match 40.6%; Score 468; DB 13; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.3e-80;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 687 CGTCTTCATCTTCTCCCTGATCCCTGCTCCATCATCATCTGCTGACACCTGAT 746
DB 1 CGTCTTCATCTTCTCCCTGATCCCTGCTCCATCATCATCTGCTGACACCTGAT 60
QY 747 GATCTGCTGCTCAAGAGCGCTCCGCTCTTCTGCTCCGAGAGAAAGATCGCAACT 806
DB 61 GATCTGCTGCTCAAGAGCGCTCCGCTCTTCTGCTCCGAGAGAAAGATCGCAACT 120
QY 807 GCGTAGATCAACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866
DB 121 GCGTAGATCAACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 867 CATTCACATATTCATCTCTGCTGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCT 926
DB 181 CATTCACATATTCATCTCTGCTGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCT 240
QY 927 CTCAGCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
DB 241 CTCAGCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 987 CTACGCTCTTCTGATGAAAACCTCAAGCGGCTGTTTCCGGGACTTCTGCTTTCACATGAA 1046
DB 301 CTACGCTCTTCTGATGAAAACCTCAAGCGGCTGTTTCCGGGACTTCTGCTTTCACATGAA 360
QY 1047 GATGAGATGAGGCGGAGACACTAGCAGAGTCCGAATACAGTTGAGATCTGCTTGA 1106
DB 361 GATGAGATGAGGCGGAGACACTAGCAGAGTCCGAATACAGTTGAGATCTGCTTGA 420
QY 1107 CCTAGGAGCATGATGAGTGAATTAACAGATATGCTAGTGTGGA 1154
DB 421 CCTAGGAGCATGATGAGTGAATTAACAGATATGCTAGTGTGGA 468

RESULT 4

AK038389 2405 bp mRNA linear HTC 19-SEP-2003
LOCUS AK038389
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A23000D02 product:opioid receptor, mu,
full insert sequence.
ACCESSION AK038389
VERSION AK038389.1 GI:26332528
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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99279253

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11042159

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (10), 1617-1630 (2000)

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MEDLINE
PUBMED
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

FEATURES
source

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AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCES

6 (bases 1 to 4022)

Adachi,J., Aizawa,K., Altamura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,U., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kuribara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohashi,N., Ozasaki,Y., Saito,R., Satoh,H., Sakai,K., Sakai,K., Sekazune,N., Seno,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akashi,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE

Direct Submision

JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.go.jp], URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers

FEATURES

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polya_site

ORIGIN

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Matches 632; Conservative 0; Mismatches 301; Indels 12; Gaps 2

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AK038620

LOCUS AK038620 2919 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male hypothalamus cDNA, NIKEN full-length enriched library, clone: A230051A20 product, NIKENICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR), full insert sequence.

ACCESSION AK038620

VERSION AK038620.1 GI:26332698

KEYWORDS HTC; CAP tripper.

SOURCE Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
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Shibata, K., Itoh, M., Aizawa, K., Nagata, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nihei, K., Kitanai, T., Tashiro, H., Itoh, M., Smit, N., Ishii, Y., Nakamura, S., Hazama, M., Nishise, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
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11076861

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Nature 409, 685-690 (2001)

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REFERENCE
AUTHORS
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS
6 (bases 1 to 2919)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kond, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submision
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2959)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirokane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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KEYWORDS GSS.
SOURCE Homo sapiens (human)

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

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ACCESSION AK043275
VERSION AK043275.1 GI:26089596
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P., and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS

3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Sunl,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawa,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
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Kato,H., Kawaji,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaki-Akihira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

TITLE
JOURNAL
COMMENT
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES
SOURCE

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 LOCUS Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
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 (ORPHANIN FQ RECEPTOR), full insert sequence.
 ACCESSION AK031926 GI:26082601
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 KEYWORDS HTC, CAP trapper.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
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 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 JOURNAL PANTOM Consortium.
 MEDLINE Functional annotation of a full-length mouse cDNA collection
 PUBMED Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
 JOURNAL Group Phase I & II Team.
 MEDLINE Analysis of the mouse transcriptome based on functional annotation
 PUBMED of 60,770 full-length cDNAs
 REFERENCE 6
 AUTHORS Nature 420, 563-573 (2002)
 JOURNAL (bases 1 to 3101)
 MEDLINE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
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 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 JOURNAL Direct SubMISSION
 MEDLINE Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
 PUBMED Physical and Chemical Research (RIKEN), Laboratory for Genome
 REFERENCE Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 JOURNAL RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 MEDLINE Kanagawa 230-0045, Japan (E-mail: genome-research@riken.go.jp,
 PUBMED URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 REFERENCE Fax: 81-45-503-9216)
 JOURNAL cDNA library was prepared and sequenced in Mouse Genome
 MEDLINE Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
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VERSION AY410747.1 GI:39766715
KEYWORDS GSS.
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 879)
AUTHORS Clark A.G., Gnanowski S., Nielson R., Thomas P., Kejarival A.,
Todd M.A., Tanenbaum D.M., Civeille D.R., Lu F., Murphy B.,
Ferreira S., Wang G., Zheng X.H., White T.J., Sinsky J.J.,
Adams M.D. and Cargill M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 879)
AUTHORS Clark A.G., Gnanowski S., Nielson R., Thomas P., Kejarival A.,
Todd M.A., Tanenbaum D.M., Civeille D.R., Lu F., Murphy B.,
Ferreira S., Wang G., Zheng X.H., White T.J., Sinsky J.J.,
Adams M.D. and Cargill M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
TITLE This sequence was made by sequencing genomic exons and ordering
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Qy 560 CATCTGTTGSCATCTTGCAATAGTCTTGGAGGACCAAAAGTACAGGAAGACGCTGATG 619
Db 302 CGGTGTGTGTGTTCTGTTGCTCATATGAGCTCAGACAAAGT-----GGAGATGAAAG 355
Qy 620 TCATTGAGTGTCTCTTGGAGTTCACAGATGATGACTCTCTGTTGGGACCTTTCATGA 679
Db 356 AGATCGAGTGTCTGTGATGAGATCCCGCCCTCAGAA---CTATTGGGGCCCTTATTTG 412
Qy 680 AGATCTGCTTCTCATCTTGTGCTTGTGATCCCTGTCCTATCATCATGCTGTCTACA 739
Db 413 CCATCTGATCTTCTTTTTCCTTCATCAATCCGCTTGTGATCATCTGTGCTACA 472
Qy 740 CCTGTGATGATCTCTGCTCAAGAGCTCCGGCTCTTTTGTGATCTCCGAGAGAAATATC 799
Db 473 GCTCATGATTCGACGACTTGTGTGTGCTGCGGCTTTCAGGCTCCGAGAGAAAGACC 532
Qy 800 GCAACTGCGAGGATGACCAAGACTGCTGCTGAGTGTGAGGAGCTTGTGCTGCTGCT 859
Db 533 GGAACCTGCGACGATACACAGCTGTGATGTAATGTGTGCTGTTGTGTGGCTGCT 592
Qy 860 GGAATCCCATTCACATATTCATCTGTGTGAGGCTCTGAGGAGCACTCCACAGCAG 919
Db 593 GGAACCTGCGACGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652
Qy 920 CTGCTCTCTGAGTATTTACTTCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
Db 653 CTGAGTAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Qy 980 CCATTTCTGACGCTTTCTTGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTC 1039
Db 713 CCATTTCTGATGCTTTCTTGTGATGAGAACTTCAAGGCTGCTTGAAGAACTTCTGCTG 772
Qy 1040 CACTGAAGATGAGAGTGAAGCGGACAGCACTAGCAGAGTCCGAAATACAGTTCCAGAT 1098
Db 773 CTCTGCTGCTGACCGGAGATGAGGTTCTGATCTGTGCGCAGCATTCAGAGAT 831

RESULT 13
CNS04C2T/c 1053 bp DNA linear GSS 01-SEP-2000
LOCUS Tetraodon nigroviridis genome survey sequence pUC-ori end of clone
DEFINITION 098B06 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL283934
VERSION AL283934.1 GI:8022304
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Best Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,
Bernot A., Fizesmes C., Wincker P., Brothier P., Quetier F.,
Saurin W. and Weissenbach J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

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MEDLINE      20296633
PUBMED       10835645
REFERENCE    2
AUTHORS      Roest Crolius, H., Jallion, O., Dastiba, C., Ozouf-Costez, C.,
              Fizem, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
              Saulin, M., Bernot, A. and Weissenbach, J.
TITLE        Characterization and repeat analysis of the compact genome of the
              freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      20359837
PUBMED       10899143
REFERENCE    3 (bases 1 to 1053)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
              BP 191 91106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
              - Web : www.genoscope.cns.fr)
              This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/tetraodon.
FEATURES     source
              1..1053
              /organism="Tetraodon nigroviridis"
              /mol_type="genomic DNA"
              /db_xref="taxon:99883"
              /clone="098806"
              /clone_11b="G"
              /note="Genoscope sequence ID : COB098DA03Sp1-end :
              PUC-Or1"
ORIGIN
Query Match      27.0%; Score 311.4; DB 29; Length 1053;
Beet Local Similarity 65.4%; Pred. No. 8.7e-50;
Matches 588; Conservative 8; Mismatches 229; Indels 74; Gaps 7;

QY      257 GATACCAAGAATGAGACGACGACCAACATTATTAACCGGCTTGCGAGATG 316
DB      961 GGTACACCAAGTGAAGAGCCGACACCAATCTTCACTTCACTTGGCTTGCGACG 922
QY      317 CTTTATTACTACCAACATGCGCTTTCAGAGTACGCTTACTTGTATGATTCCTGCGCTT 376
DB      921 CTYTAGCACCAGCAGACCCCTCCCTTCAGAGGCCAAGTACTGATGAAACGTGTGT 862
QY      377 TTGGGAGTGTCTGTGCAAGATGTAATTCATTGATTACTACCAACATGTTACACAGA 436
DB      861 TCGGGAGCTGCTGTGCAAACTGTATGCACTGACTACCAACATGTTCAACAGCA 802
QY      437 TCTTACCTTGA -CGATGATGAGCGTGA -CGGCTACATGCGCGTGCACCCGCT -GA 493
DB      801 TCTTACCCCTCACCCATGATGAGCGTGCACCCGCTACGTTGCTTGGCACCCGCTCC 742
QY      494 AGGCTTTGGACTTCCGACACACCTTTGAAGGCAAAAGATCATCATATCTGCATCTGGTGC 553
DB      741 GGGGCGCTGACTTCCGACACACCCGCGCAAGGCCAAATATCATACGTGTTCACTCGATCC 682
QY      554 TGTGCTCATCTGTGGCATCTCTGCAATATGTCCTTGAAGGCCAACAAAGTCAGGAGAAG 613
DB      681 TCTCTCTAGCCGTCGGAAGTCCCGGTGATGATGATGGCAGCGACGAAGAGACGATTAAG 622
QY      614 TCGA-----
DB      621 GTGAGTACGATCGCGGTGCTCGGCTCGCAGCGCAAGACTGTACTTCTGTTCTTAC 562
QY      618 -----TGTCTGATGAGTGTCTCTTGGCAGTTCCGAGATGATGACTACTCTGTGGAG 669
DB      561 CCGCAGGGAACATGCGGTGATGCTCAGGTTCCCGAAACCGGAGAAGACTGG---GAG 505
QY      670 CTTCTTACGAGATCTGCGCTTCTTCACTTGTGCTTGATGATCCGTGCTCTCATCATC 729
DB      504 ACGACCACTGAAGAGTCTGGCTGTTCATCTTCCCTTGTGGTTCGCCGCTCGGTCAAC 445
QY      730 GTCTGCTACACCTCATATGATCTGTGGTCTCAAGACGTCGCCGCTCTTGTGGCTCCGA 789

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DB      444 ATCTGCTACGGGCTATATAT -CTGGGGCTCAAGACGCTCGGCTGCTCCGGCTCAAA 386
QY      790 GAGAAAGATCGCAACCTGTGATGATCACACAGACTGTCTGTGTGTGTCAGATCTTC 849
DB      385 GAGAAAGACAGAAACCTCGCGGAGATCAACCCCACTGTCTGTGTGTGTCGCGCTTC 326
QY      850 GTCTGCTGTGAGACCTCCATTCATATTCATCCGTGTGAGAGCTCTGGGGAGCACTTC 909
DB      325 ATCTGTGTGATGATCCCAATTCATCTTACATCATGTCAGAGACGATGTCTCCATCGAC 266
QY      910 CAC--ACACAGCTGTCTCTCCAGTATTACTTCTGCATGCGCTTGAAGCTATATCAAC 966
DB      265 CACAAGAACCTGTGTGTGTGTGTCAGCTGCGACCTGTGATGCGCTGGGCTCATGAAAC 206
QY      967 AGTACCTGAATCCCATCTCTTCAAGCTTTCTTATGAAAACTTCAAGCGGTGTTCCG 1026
DB      205 AGCAGCTGAACCCGGTCTCTTACGCTTCCGTGACGAGAACTTCAAAAAGGTGCTTCAAG 146
QY      1027 GACTTCTGCTTCCCACTGAATGATGAGACCGCGCAGACACTAGCAGATCCGAA 1085
DB      145 GACTTGTGCTGTGCGCCGCGCTCCGCTCCGCTGAGAGAAACAGCTTCTCCAGAGCAGARA 87

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RESULT 14
BX874804
LOCUS      BX874804
DEFINITION BX874804 AGENAE Rainbow trout multi-tissues-normalized (cdk)
ACCESSION BX874804
VERSION    BX874804.1 GI:40003349
KEYWORDS   EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
ORGANISM   Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1 (bases 1 to 783)
            Govoroun, M., Guiguen, Y. and Le Gac, F.
            Construction and primary characterization of normalized cDNA
            libraries in rainbow trout, Oncorhynchus mykiss
            Unpublished (2003)
JOURNAL     INRA - SCRIBE
            Campus de Beaulieu, RENNES cedex, 35042, France
            Tel: 02.23.48.50.09
            Fax: 02.23.48.50.20
            Email: Yann.Guiguen@beaulieu.rennes.inra.fr
            Sequence cleaned of vector, adaptor and repetitions. Contact us
            at sigenauporte@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0002 row: 0 column: 24
            Seq primer: MJ3R.
FEATURES     location/Qualifiers
            1..783
            /organism="Oncorhynchus mykiss"
            /mol_type="mRNA"
            /db_xref="taxon:8022"
            /clone="cdk0002c.o.24"
            /tissue_type="multi-tissues"
            /dev_stage="from embryos to adults"
            /lab_host="DH10B"
            /clone_11b="AGENAE Rainbow trout multi-tissues-normalized
            (cdk)"
            /note="Vector: pT7TD-pac; Rainbow trout
            multi-tissues-normalized + 2 subtractions; Clone
            distribution : AGENAE Resource Centre, Francois PIMI,
            Francois.Pimi@jouy.inra.fr, INRA, CERA Radiobiologie et
            Etude du genome (URB), Domaine de Vilvert, 78352,
            Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
            (0) 1.34.65.22.73"
ORIGIN

```

Query Match 24.1%; Score 277.6; DB 13; Length 783;
 Best Local Similarity 78.8%; Pred. No. 2.7e-43;
 Matches 331; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 180 CATCATCAGCGGGCTACTCCGTAGTGTTCGTCTGCGGCTTGCGGCACTCGCTGCT 239
 |||||
 DB 361 CATATACAGCTGTACTCCGTGTGTTTGTGTGGCTGTGTGGCACTGCTGCT 420

QY 240 CATGTCGTGATCATCCGATACACAAAGATGAAAGACAGACACATTATATTTAA 299
 |||||
 DB 421 CATGATGTTATCATCAGATATACAAAGATGAAAGCGGCACCAATTTACATTTCAA 480

QY 300 CCGGCTTTGGCAGATGCTTTAGTACTCAACCATGACCTTTCCAGAGTAGAGTCTACTT 359
 |||||
 DB 481 CCGGCTTTGGCAGACCGCTGCTGACACAGAGATGCTTTCCAGAGACTGATTAAGT 540

QY 360 GATGAATTCCTGCGCTTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATGATTA 419
 |||||
 DB 541 GTTGAACCTGCTGCGCTTTTGGCGAGGTGTGTAAAGTTCATATCATGACTACTA 600

QY 420 CAACATGTTACACAGATCTTACCTTGAACATGATGAGCTGACCGCTTACATTTCCGT 479
 |||||
 DB 601 CAACATGTTACACAGATCTTACCTTGAACATGATGAGCTGACCGCTTATGTGCGCT 660

QY 480 GTGCCACCCCGTGAAGGCTTTGAGTCTTCCGACACCCCTTGAAGGCAAGATCATCAAT 539
 |||||
 DB 661 GTGCCACCCCGTGAAGGCTTTGAGTCTTCCGACACCCCTTGAAGGCAAGATCATCAAGT 720

QY 540 GTGCATCTGCTGCTGTCTGTCTCATCTGTGGCATCTCTGCAATGATCTTTGAGAGCA 599
 |||||
 DB 721 GTGTATCTGATGATGCTGTCTGTGCGGACCGGAGATACAGACATTTACTGCGGGGAC 780

RESULT 15
 BF676176 888 bp mRNA linear EST 21-DEC-2000
 LOCUS 602084171P1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4248400 5',
 DEFINITION mRNA sequence.
 ACCESSION BF676176
 VERSION BF676176.1 GI:11950071
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 888)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at:
 http://image.llnl.gov
 Place: LDCM1066 row: n column: 17
 High quality sequence start: 6
 High quality sequence stop: 380.
 Location/Qualifiers
 1..888
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4248400"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: 5' (ggcgcgtcgcc); Site 2: 5' (ggcgcgtcgcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCATATATGCGC-3'

and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

Query Match 23.5%; Score 271.4; DB 10; Length 888;
 Best Local Similarity 83.3%; Pred. No. 4.4e-42;
 Matches 419; Conservative 0; Mismatches 66; Indels 18; Gaps 9;

ORIGIN

QY 666 GACGCTTTGATGAAGATCGGCTTCATCTTGGCTTGTGATTCCTGCTGCTGCTCATCAT 725
 |||||
 DB 1 GACCTCTTCATGAAGATCGGCTTCATCTTGGCTTGTGATTCCTGCTGCTGCTCATCAT 59

QY 726 C-ATCGTCTGCTAACCCCTGATGATTCCTGCTGCTCAAGAGGCTCCGCTCTTCTGAGCT 784
 |||||
 DB 60 CTATGCTGCTGCTAACCCCTGATGATTCCTGCTGCTCAAGAGGCTCCGCTCTTCTGAGCT 119

QY 785 CCGAGAGAAAGATCGCAACCTGCTGATGATCACAGACTGCTGCTGCTGCTGCTGCTGCT 844
 |||||
 DB 120 CCGAGAGAAAGATCGCAACCTGCTGATGATCACAGACTGCTGCTGCTGCTGCTGCTGCT 178

QY 845 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
 |||||
 DB 179 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237

QY 905 CCTCCACAGACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 |||||
 DB 238 CTCCACAGACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297

QY 962 CCAACAGTACGCTGATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 |||||
 DB 298 CCAACAGTACGCTGATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357

QY 1021 TTCGGGAGCTTCTGCTTCCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1078
 |||||
 DB 358 TCCGGAGACTCTTCTGCTTCCACTGATGATGATGATGATGATGATGATGATGATGATGAT 417

QY 1079 ----TCCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1130
 |||||
 DB 418 GAGCTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477

QY 1131 TAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153
 |||||
 DB 478 AAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500

RESULT 16
 BU219878 917 bp mRNA linear EST 25-NOV-2002
 LOCUS 603749479F1 CSEQCHN04 Gallus gallus CDNA clone CHEST659n20 5', mRNA
 DEFINITION sequence.
 ACCESSION BU219878
 VERSION BU219878.1 GI:25405026
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 917)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE
 12445392
 PUBMED
 COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology

(UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers

FEATURES

source

1. 917
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="ChEST659n20"
 /tissue_type="whole embryo"
 /dev_stage="20-21"
 /lab_host="DH10B"
 /clone_11b="CSEQCHN04"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+);
 Site 1: EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was bluntended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 23.3%; Score 268.6; DB 13; Length 917;

Best Local Similarity 65.7%; Pred. No. 1.6e-41;

Matches 441; Conservative 0; Mismatches 219; Indels 11; Gaps 3;

372 GCCTTTGGGAGTGCCTGCAAGATGATTAATTCATTGATTAACAATGTTGAC 431
 1 GCCATTGGTCAATTCCTTTGTAAGTTTGTATTCATAGACTACTAACAATATGTTAC 60
 432 CAGCATCTTTCACCTTGACCATGATGAGCGCTGACCGCTAATTCGCGTGCACCCCT 491
 61 CAGTATCTTTTACACTGTGACCATGATGATGATGCTAAGCCGTTTGCACCCACT 120
 492 GAAGCTTTGACCTCCGCAACCTTGAAGCAAAAGATCATATATTCATCTGCTGCT 551
 121 CAAGGCCCTTGAATTCGATCCGCAAGAAATGTCATATGTCGCAACTGAT 180
 552 GCTGTCGATCTGTCGATCTGTCATATCTTGGAGGACCAAGATGAGGAGA 611
 181 TCTTCTCTGTCATGTCGTCGTCGCTGATTTATGCACTACTAAATPACAGGCAAG 240
 612 CGTCGATGTCATGATGTCCTTCCGAGTCCCAAGATGATGATCTCTGCTGAGGACCT 671
 241 CTCTATGATGTCGACACCTACATTCCTCCACCTGCT-----TGTATCTGGGAAA 291
 672 CTTCATGAAGATCTGGGCTTCTATCTTTCCTGATCCTGTCCTCATCATCTGCT 731
 292 CCTACTGAAATCTGTGTGTCATCTTTCCTTCATCATGACGATCTGATCATTA 351
 732 CTGCTACACCCGATGATCTGCTGTCAGAGCGCGGCTCTTTCGCTGCTCCGAGA 791
 352 GTGCTATGGGCTGATGATTTTACGGCTTAAAGATGTCGCCATGTTATCTGAGCTCTPAA 411
 792 GAAGATCGCAACTGCTGATGATCAACGAGTGTCTGCTGCTGCTGCTGCTGCT 851
 412 GAAGAGCAAGAACTGCGAAGATCAAGAGATGTTCTTGTATGAGTGTGAGCTGTTAT 471
 852 CGTCTGCTGATCCCATTCACATATTAATCTGCTGAGGCTCTGGGAGAGACCTCCCA 911
 472 CATCTGCTGATCTCTCATCATATTAATTCATTAAGCCCTGCTGCTGCTGCTGCT 531
 912 CAGCAC-AGCTGCTCTCAGCATTTAATTTCTGCAATGCCCTTAGGCTATA-CGAAAGT 969

Db 532 AACTACTTTCAGACATGCTCTCCCTGCACTTTTGTATGCTTTAGATTATATAAATAC 591
 Qy 970 ACCCTGAATCCCATTTCTTACGCCCTTTCTGATGAGAACTTACAGCGGTGTTCCGGAC 1029
 Db 592 TCCCTCAATCCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
 Qy 1030 TTCTGCTTCC 1040
 Db 652 TTCTGATCTCC 662

RESULT 17

BS588668

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BS588668 RIKEN full-length enriched, adult male hypothalamus Mus
 musculus cDNA clone A23002D02 5', mRNA sequence.
 BS588668.2 GI:16449788
 EST
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 657)
 Arikawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takebe, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arikawa, T., et al. 2001)
 Unpublished (2001)
 On Nov 30, 2000 this sequence version replaced gi:11485212.
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp;
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukumishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanka, I.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Db 412 CTTGCGTGTGTCGAAGGGCTGGGGGTTTCAGCCGGCAGAGAGATCGCGTGGCAATTCT 471
Qy 936 TTACTTTCGATCGCTTGGGCTATACCAAGTACCTGATCCATTCTTCAAGCCCTT 995
Db 472 GGGCTTTCGACAGGGCCCTGGCTACGTCACAGCTCCCTCAACCCCATCTCTACCCCTT 531
Qy 996 TCTTATGAAAACTTCAAGCGGTGTTTCGGGACTTCTGCTTTCATGAAATGAGAT 1055
Db 532 CTTGATGAGAACTTTCAGGCTCTTCCGCAAGTCTGCTGTCATCTGCGCTGCGCG 591
Qy 1056 GGAGCGCAGACACTAGCAGAGTCCGAATACATTCAAGGA 1097
Db 592 GGACGTCGAGGTGTGTGACCGGCTGGCAGCATTTGCCAAGGA 633

RESULT 19
AY400827 1176 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens SSTR1 gene, VIRUTUAL TRANSCRIPT, partial sequence.
DEFINITION genomic survey sequence.
ACCESSION AY400827 GI:39756816
VERSION AY400827.1 GI:39756816
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Periera,S., Wang,G., Zheng,X.H., White,T.J., Slinkov,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1176)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Periera,S., Wang,G., Zheng,X.H., White,T.J., Slinkov,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..1176
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1176
/gene="SSTR1"
/locus_tag="HCM0687"

ORIGIN
Query Match 19.9%; Score 229.6; DB 29; Length 1176;
Best Local Similarity 55.1%; Pred.No. 6e-34;
Matches 523; Conservative 0; Mismatches 409; Indels 10; Gaps 3;

Qy 75 CAGCAGCGCTGTTCCCGGCTGGGCGCCAGCCCAACAGCAAGCGGCGGCTCGGA 134
Db 72 CGGCGGACAGAGGGGCCCGGCGGCGCTCGGACGCGATGAGAGAGCGGCGGGA 131
Qy 135 GAGACGCGAGTGAAGCGCGGCGCACATCTCCCGGCGCATCCGGTCATCATCGGCGGT 194
Db 132 TGCCTCCCAAGACGGACCTTGAAGCAAGGCGCAGGCGCATCTCTTTTCT 191
Qy 195 CTACTCCGTAGTGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Db 192 CTACTCCGTAGTGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251

Qy 255 CCGATACCAAGATGAGACAGCAACCAATTATATTTAACTGGCTTGGCAGA 314
Db 252 GCGCTATGCGCAAGATGAGACAGCGCCACCAACTATATATCTTAAATCTGGCACTTGTCTGA 311
Qy 315 TGCCTTATGTTACTAACAACCATGCCCTTTGAGAGTACGCTCTACTGATGAATTCCTGGCC 374
Db 312 TGAGCTGCTCATGCTCAGCGTGCCTCTTCTAGTCACTCCAGGTTGTGGCCACTGGCC 371
Qy 375 TTTTGGGATGTCCTGTGTAAGATAGTAATTTTCATTAATTTACTAACAATGTTACCG 434
Db 372 CTTGCGTGGCTGCTCTGCGGCTGCGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 431
Qy 435 CATCTTCACTTGAACCATATGAGCGTGAAGCGCTATATTCGCGTGGCAACCCCGTGA 494
Db 432 CATCTACTGTGACCTGCTCAGCGTGAACCGCTACGTCGCGCTGCTGCTGCTGCTGCT 491
Qy 495 GCGCTTGAACCTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGATCTGCTGCT 554
Db 492 GCGGCGCGCTACCGCGGCGCCACCGTGGCCAAAGTATTAACCTGGCGTGTGGTGGCT 551
Qy 555 GTCCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGCAACCAAGTACAGGAAGACT 614
Db 552 ATCGCTGCTGTCATCTGCGCCATCGTGTGCTTCTCTGCAACCGCGCCAAACGCAACG 611
Qy 615 CGATGTCATTTAGTGTCTCTGCAATGTCAGATGATGATGATGATGATGATGATGATGAT 674
Db 612 CACGG---TGGCTTGCACATGCTCTATGCCAAGCCGCTCAACGCTGCTGCTGCTGCT 668
Qy 675 CATGAAGATCTGCTGCTTCTATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
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Qy 735 CTACACCTGATGATCTCGGCTCAAGAGCTCCGCTCTTCTGCTGCTGCTGCTGCTGCT 794
Db 726 CTACGTCATCATCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 785
Qy 795 AGATGCCAACCTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854
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Qy 855 CTGCTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 914
Db 846 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 905
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Db 906 CACGCTGATGCT-----AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
Qy 975 GAATCCCATTTCTAGGCTTCTTATGATGAATCAAGGCTGCTGCTGCTGCTGCTGCTGCT 1024
Db 954 CAACCCCATCTCTATGCTTCTCTGACACACTTCAAGCGCTCTTCTC 1003

RESULT 20
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LOCUS UI-M-BH3-asd-d-09-0-UI-r1 NIH_BMAP_M_S4 Mus musculus cDNA clone
DEFINITION UI-M-BH3-asd-d-09-0-UI 5', mRNA sequence.
ACCESSION BE649947
VERSION BE649947.1 GI:9975771
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 389)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H


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Db      315 GCTGCTCATGCTCAGAGTCCCTTTCTGTGCTACCTTCACAGCTGTTGGCCACATGGCCCTT 374
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Db      729 TGTGCTCATCATTTGCCAAGATGCGCATGCTGCGCCCTCAAGGCTGGGTGACAGAGGCA 788
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Qy      858 CTGAGTCCCATTCATCATATTCATCTGTTGAGGCTCTGGGAGAGACCTCCACAGCAG 917
Db      849 CTGAGTCCCTTCTAAGTGTGACAGTGTGTCACGTTGTCGCCAGCAAGAGAGAGCCGC 908
Qy      918 AGCTCTCTCTCAGCTATTAATCTTCTGATGCTGCTTGAAGCTTATACCAAGTACCTGA 977
Db      909 CGTGAAGC-----AGTGTCTGTCTATCTGAGGCTATGCAACAGCTGTGCCAA 956
Qy      978 TCCCATTTCTTAAGCCTTCTTGTGATGAAGAACTTCAAGCGGTGTTTCCGGGACTTC 1032
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LOCUS AK046464
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN
RECEPTOR TYPE 1, full insert sequence.
ACCESSION AK046464.1 GI:26338112
VERSION AK046464.1
KEYWORDS HTC; Cap trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subcloning of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

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MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
AUTHORS Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsura, S., Kawai, J.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-Format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the
AUTHORS FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 The FANTOM Consortium and the RIKEN Genome Exploration Research
AUTHORS Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL of 60,770 full-length cDNAs
PUBMED Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2014)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, K., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyu, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submision
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-researc.riken.go.jp,
URL:htp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse libraries.
Please visit our web site for further details.
URL:htp://genome.gsc.riken.go.jp/
URL:htp://fantom.gsc.riken.go.jp/
FEATURES
source location/Qualifiers
1. 2014
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CDS

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ORIGIN

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Query Match      19.6%; Score 226.6; DB 11; Length 2014;
Best Local Similarity 54.8%; Pred. No. 2.8e-33;
Matches 523; Conservative 0; Mismatches 414; Indels 18; Gaps 3;

QY 78 CAGCCGCTGTTCCCGCTGGGCGAGCCGACGCAAGCAGCGCGCGCTCGAAGA 137
DB 500 CTGACGACGAGGGGTCCGGGGTCCGGGCTGCGGACGCGACGGAAGAGCCCTGGAAGAGC 559
QY 138 CGCGAGCTGAGCGCCGCGACACATCTCCCGGCATCCCGGTCAATCAGCGCGGTCTA 197
DB 560 TTCCAGAGATGGAGACTTAAGGAGGAGACAGGATAGCCCATCTCATCTCTTTATCTTA 619
QY 198 CTCCTAGTGTTCGTGCTGGGCTTGGTGGCACTCGCTGTCAATGTTCTGTATCATCG 257
DB 620 CTCCTGTGTATCTGTGTGGAGCTGTGTGGAACTCTATGTCTATGTATGTATCTCGG 679
QY 258 ATACCAAGATGAAGACGACCAACATTTACATTTAACTGCTTTGGCGATGC 317
DB 680 CTACCCCAAGATGAAGACGCTACCAACATCTTAAACCTGGCTATTTGCGATGA 739
QY 318 TTTAGTTACTAACCAATGCGCTTCAAGATGACGCTTCTGATGAAATCTGCGCTTT 377
DB 740 GGTGCTCATGCTCAGCGGCTCTTCTGTGCTCTTCCACGCTGTGGCGCACTGCGCTT 799
QY 378 TGGGATGTGCTGTGCAAGATAGTAATTTCAATGATTACTAACCATGTTCCAGCAT 437
DB 800 CGGCGCGCTACTTTCGCGCTGTGCTCAGCTGATGGGTCACATGTTCCAGCAT 859
QY 438 CTTCACCTTGACATGATGAGGTGACCGCTACATTTGCGGTGCCACCCGTAAGGC 497
DB 860 CTACTGTCTGACTGTGCTTAAAGTGACCGCTATGTGCTGTGACACCCGATAAAGC 919
QY 498 TTTGACTTCCGACACCTTGAAGCAAAAGATCAATATCTGATCTGGCTCTGTC 557
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QY 558 GTCACTGTGTCATCTCTGCAATAGTCTTGGAGGACCAAAATCAGGGAAGACGTGCA 617
DB 980 ATTACTGTGTTATCTTGCCCATGCTGTGTCTTTCACGACCGGACCAAGGATGGCAC 1039
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DB 1040 GG--TACCCTGCAACATGCTCATGCCCCGAGCCCGACGCGCTGTGGGCTTGTGT 1096
QY 678 GAAAGTGTGCGCTTCATCTTTGACCTGTGATCCCTGCTCATCATCATGCTGTGCTA 737
DB 1097 ---CTTAAACATTTCTCATAGGGCTTCTGCTGCTGTGCGGGGCAATTTGCTGTGTA 1153
QY 738 CACCTGATGATCTGCGCTCTCAAGAGGCTCGGCTCTTTCTGTGCTCCGAGAGAAAGA 797
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DB 1274 CTGAGTGCCTTTCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1333
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DB 1334 CGTGAGCC-----AGTGTCTGTATCTCTGCGGCTATGCCAACACTGTGCCAA 1381
QY 978 TCCCATCTCTACCGCTTTCTTGAAGAACTTCAAGCGGCTTTCCGGGACTTC 1032
DB 1382 CCCCATCTCTTACCGGCTTCTGTGTGACACACTCAAGCGCTCTTTCAGCGCATC 1436

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RESULT 23

BM543468

LOCUS

DEFINITION

BMS43468 980 bp mRNA linear EST 20-FEB-2002

ACCESSION

BMS43468

AGENCOURT 6492534 NIH_MGC_124 Homo sapiens cDNA IMAGE:5726549

VERSION

BMS43468.1

GI:18773888

KEYWORDS

EST.

Homo sapiens (human)

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

NIH-MGC

http://mgc.nci.nih.gov/

AUTHORS

1 (bases 1 to 980)

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cga@bms-remail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation

Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing

by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the

I.M.A.G.E. Consortium/LMNL at:

http://image.llnl.gov

Plate:

LLAM12719

row: d column: 06

High quality sequence

stop: 711.

FEATURES

Location/Qualifiers

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/clone="IMAGE:5726549"

/tissue_type="hippocampus"

/lab_host="DH10B"

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/note="Organ: brain; Vector: pCMV-Sport6; Site 1: EcoRV

(destroyed); Site 2: NotI; RNA source male hippocampus,

age 27. Library is

oligo-dT primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.4 kb,

insert size range 0.9-4 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber

(Invitrogen). Research Genetics

tracking code 012."

ORIGIN

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Query Match      19.5%; Score 224.6; DB 12; Length 980;
Best Local Similarity 64.8%; Pred. No. 5.2e-33;
Matches 383; Conservative 0; Mismatches 199; Indels 9; Gaps 3;

QY 153 CGCGCAATCTCCCCGCGCATCCCGGTCAATATGAGCGGCTCTACTCCGATGTTGCT 212
DB 295 CGCTTCTCTGCGCTTCCGGGCTCAAGGTACCATGTGAGGCTCTTACCTGCGCGGTGTGT 354
QY 213 CGTGGGCTGTGGTGGCAACTGCTGTGATGTTGCTGATCATCCGATACCAAGATGAA 272
DB 355 CGAGGGGCTCTTGGGGAATGCTCTGTGATGATGATGATGATGATGATGATGATGATG 414
QY 273 GACAGCAACCAACATTTACATTTTAACTGCGCTTTGGCAGATGCTTTAGTTACTAAC 332
DB 415 GACAGCAACCAATTTTAACTTTTAACTGCGCGCTTGGCGACACTCTGCTCTGTGAC 474
QY 333 CATGCCCTTTCAAGATACGCTTCACTTGAATGAATTCCTGCGCTTTGGGAGATGCTGTG 392
DB 475 GCTGCCCTTCCAGGCGACGACATCTCTGCGCTTCTGCGCGCTTGGGAGATGGCGTGTG 534

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QY 393 CAAGATAGTAATTTCATTGATTACTACACATGTTACACAGATCTTACCTGACAT 452
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 QY 453 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGGCTTGGATCTCGCAC 512
 DB 595 CATGAGTGTGATTCCTTATGTAAGCCATCTGCCACCCCATCCGCTGCCCTGAGAGTCCGAC 654
 QY 513 ACCCTTGAAGGCAAGATCATCATATCTGCATCTGGCTGCTGCTCATCTGTTGGCAT 572
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 QY 573 CTCTGCATATAGTCTTGAAGGACCAAAATGACGGAAGACGTCGATGTCTAGATGCTC 632
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 QY 693 CATCTTTCCTTTCGT-GATCCCTGTCCTCATCATCATGCTGTGCTACACCC 742
 DB 827 CCTCTTCTCCTTCATCTGTCCTCCCGGCTGCTGTCATCTGTCTGCTACAGCC 877

RESULT 24
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 LOCUS BB641725 RIKEN full-length enriched, 10 days neonate cortex Mus
 DEFINITION musculus cDNA clone A830044L10 5', mRNA sequence.
 ACCESSION BB641725
 VERSION BB641725.1 GI:15401708
 KEYWORDS EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 632)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
 Hara, A., Hizamoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shitaki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-ree@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A.,
 Arakawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.,
 Arakawa, T., Ishii, Y. and Hayashizaki, Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Func. Genomics 2 pre, 172-186 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.
 FEATURES
 source
 Location/Qualifiers
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 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'-
 GAGAGAGAGAGATCCAAAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5'-GAGAGAGATTCGAGTAAATTAATTCCTCCCTCCCTCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FLX I."

ORIGIN
 Query Match 19.3%; Score 223; DB 10; Length 632;
 Best Local Similarity 69.4%; Pred. No. 8.8e-33;
 Matches 301; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
 QY 93 CGGCTGGGCGGAGCCGACAGCAAGCGGCGGCTCGAGAGACGGGAGCTGAGGC 152
 DB 162 CGCCTTCCGAGCGGCTTCCCGAGCGCGGCGGCGGCGGAGTGGGCGGAGCCGG 221
 QY 153 CGCGACATCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212
 DB 222 TAGTCCCTGTCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 281
 QY 213 CGTGGCTTGGTGGGCAACTCGCTGCTGATGTTCTGTATCATCCGATACACAAAGATGA 272
 DB 282 AGTGGGCTTCTGGGCAAGTGTGCTGATGTTTGGCAGTCGTCGGTACCAAAATTGA 341
 QY 273 GACAGCAACCAATTATCATATTTAACTGCGCTTGGCAGATGCTTTAGTTACTACAAC 332
 DB 342 GACCGCCACCAACATCTACATCTTCATCTGCTTGGCTGATGCGGCGGCGGCGGCGG 401
 QY 333 CATGCGCTTTCAGAGTACGCTGCTACTGATGAATCTCGGCGGCGGCGGCGGCGGCGG 392
 DB 402 GCTGCGCTTTCAGAGCGGCAAGTACTTATGAGAAAGTGGCGGCGGCGGCGGCGGCGG 461
 QY 393 CAAGATAGTAATTTCATTGATTACTACACATGTTACACAGATCTTACCTGACAT 452
 DB 462 CAAGCGTNGCTCTCCATGATGACTACTACAAATGTTCACTGACATCTTACCCCTACCAT 521
 QY 453 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGGCTTGGATCTCGCAC 512
 DB 522 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGGCTTGGATCTCGCAC 581
 QY 513 ACCCTTGAAGGCA 526

Db 582 ACCAGCCAGGCA 595

RESULT 25
AY400676 1006 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus SSTR2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY400676
VERSION AY400676.1 GI:39756665
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1006)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferierra, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.D.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

TITLE
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1006)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferierra, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.D.,
Adams, M.D. and Cargill, M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
1..1006
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1006
/gene="SSTR2"
/locus_tag="HMC0636"

ORIGIN
Query Match 19.2%; Score 221.4; DB 29; Length 1006;
Best Local Similarity 54.0%; Pred. No. 2.2e-32;
Matches 478; Conservative 0; Mismatches 401; Indels 6; Gaps 1;

QY 168 GGCATCCCGTCATCATCGCGGCTCTACTCCGTAGTTCGTGCGGCTTGGTGGG 227
Db 120 GACAAGCAACGCCGCTCCACGCTTCACTTCGCGTGTGTGTGTCGGGCTGTGGG 179
QY 228 CAACCTGCGTCATGTTCTGATCATCCGATACCAAGATGAGACAGCAACCAAT 287
Db 180 CAACACGCTGTCATTTATGATATCCCGCTATGCCAAGAGAACATCAACCAAT 239
QY 288 TTACATATTTAATCTGCTTGGAGATGCTTTAGTTACTACCAACCATGCCCTTACAG 347
Db 240 CTACATCTCTTAACCTGGCATTCGAGATGAATCTTCACTGCTAGGGGCTCCCTTTGGC 299
QY 348 TAGCGTCTACTGATGAATTCCTGCGCTTTGGGAGATGCTGTGCAAGATATGATTTTC 407
Db 300 CATGAGGTGGCGGTAGTCACTGCGCTTTGGCAAGCCATCTGCGGGTGTGATAC 359
QY 408 CATGATTAATCAACATGTTCAACAGATCTTCACTTACCATGATGAGCGTGAACCG 467
Db 360 TGTATAGGCAATCAATCAAGTTACCAATATCTTGTGCTGACGTCATGACATGACCG 419
QY 468 CTACATTCGCTGTGTCACCCCGTGAAGGCTTTGACTTCGACACCCCTTGAAGGCAAA 527
Db 420 CTACCTGGCCGTGTGTCACCCCATTAATGTCACCCAAATGAGAGGCAACCCCGACGCCAA 479
QY 528 GATCATCAATATCTGCACTGTGCTGTGCTGATCTGTGGCATCTCTGCAATATGTCCT 587

Db 480 GATGATCAATATGTCGCTGTGTGTGTGTG-----TCTGTGCTGTGCTATTTGGCCATCAT 533
QY 588 TGGAGCAACCAAGTCAGGAAAGACGTGATGATCATTTAGTCTCTTTCAGATTCACGA 647
Db 534 GATATACCCCGGCTCCGAGAACCAAGTGGGGAGAGACAGCTGTATCATCAATCACTGGCC 593
QY 648 TGATACATCTCTGTGTGGACCTTTATGAAGATCTGCGCTTTTCATCTTTGCCCTTGT 707
Db 594 AGCGCAATCCGGGGGCTGTACACAGATTTTCAATATCAACCCCTTCACTCCGGGGTTCCT 653
QY 708 GATCCCTGCTCCATCATCATGCTGTGTACACCCGTATGATTCGCGGCTTCAGAGCGT 767
Db 654 GGTATCCCTTACATCATTTTGTCTGTCTTACTGTTATCATCAAGGTGAAGTCTTC 713
QY 768 CCGGCTCTTTCTGTGCTCCGAGAAAGATGCAACCTGCGTGAATCAACAGACTGT 827
Db 714 TGAATCCGAGTGGGATCATCCAGAGAAAGTCAGAAAGAGTGAACCCGATGCT 773
QY 828 CCGTGTGTGTGTGTCAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 887
Db 774 GTCAATGTATGT 833
QY 888 GAGAGCTGTGGGAGCACTCCACAGACAGCTGTCTCTCCAGTATTAATCTTCGAT 947
Db 834 TTCGT 893
QY 948 GCGCTTGT 1007
Db 894 GATCCTCACCTATGCCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY 1008 CTTCAGAGGCTGT 1052
Db 954 CTTCAGAGAGCTTCCAGATGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 998

RESULT 26
B0179053 784 bp mRNA linear EST 30-APR-2002
LOCUS UI-M-EV0-bwt-j-18-0-UI.r1 NIH BMAP-EV0 Mus musculus cDNA clone
DEFINITION IMAGE:5701745 5', mRNA sequence.
ACCESSION B0179053
VERSION B0179053.1 GI:20354545
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 784)
NIH-MGC <http://imgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
FEATURES
source
1..784
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5701745"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"

```

/lab host="DH10B (71b phage resistant)"
/clone lib="N1H BMAP EV0"
/notes="Organ: brain; Vector: pXy-Aac; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldi, Lemon and Scaree, Genome Research, 6:791-806,
1996. Denatured mRNAs was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pXy-Aac vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chn, Ph.D., program coordinator."

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ORIGIN

Query Match	18.9%	Score 217.6;	DB 13;	Length 784;
Best Local Similarity	60.6%;	Pred. No. 1.1e-31;		
Matches 396;	Conservative 0;	Mismatches 249;	Indels 9;	Gaps 2

Qy	445	TTGACCAAGATAGAGGTGGACCGCTACATTTGGCGATGGCAACCCCGTAAAGCTTTGAC	504
Db	1	TTGATCGCATAGAGGTAGACCGCTTATGTAGCTATCTGCACCCCTATCCGTCCCTTGAT	60
Qy	505	TTCCGCACACCCCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTGCTGTCATCT	564
Db	61	GTTGGGACATCCAGTAAAGCCAGGACCGCTTATGTAGCCATATGGGCTCTGGCTTGGATG	120
Qy	565	GTTGGGACATCTGCAATAGTCTTTGAGAGCACCAAGTACGGGAAGACGTGCATGTCAT	624
Db	121	GTTGGGTGTTCTGTGGCCATCATGGGCTTCAGACAAGTAGAGATGAAG- ----ATC	174
Qy	625	GAGTGCTCTTGCAGTTCCTCCAGATATGATGACTACTCTCGTGGGACCTCTTCAATGAAGTC	684
Db	175	GAGTGCTCTGTGGAGATCCCGCCCTCAGAGCTAT- --TGGGGCCCTGTATTTTGCATC	231
Qy	685	TGCGTCTTCAATCTTTGGCTTCTGTATTCCTGTCTCATATCATGCTGTCTACACCTTG	744
Db	232	TGCATCTTCTCTTTTCTTCTTCAATCCCGGTTTGTGATCATCTGTCTGTACAGCTTC	291
Qy	745	ATGATCCTGGGCTCTGAAGAGGCTCCGGGCTCTTTGCGTCCGAGAGAAAGATGCGAAC	804
Db	292	ATGATTCACAGACTTCGTGTGTCCGGCTGCTTTAAGGCTCCGAAAGAAAGACCGGAAC	351
Qy	805	CTGGGTAGGATCACACAGACTGCTCCGTGTGTGTGTGGACAGTCTTGTGCTGTCTGGACT	864
Db	352	CTGGGAGGATACACAGCGGTGTACTGTGATGTGTGGCTGTGTTGTGTGGCTGTGGACA	411
Qy	865	CCCATTTCAATTTATCTCTGTGTGAAGGCTCTGGGGAGACCTCCACAGCACAGCTGCT	924
Db	412	CCTGTGCAGGCTTGTCTCTGTGTTCAAGGACTGGGGTTCACGCAAGTATGTAGACTGCA	471
Qy	925	CTCTCCAGCTATTACTTTCGATCGGCTTAAGGCTATTACCAAGTAGACCTGAATCCCAT	984
Db	472	GTAAGCAATTCGCGCTTCTGCACAGCCCTGGGCTATGTACAAGTGTCTCAATCCCAT	531
Qy	985	CTTACGCGCTTCTTGATGAATACTTCAAGCGGCTGTTCCGGGACTTCTGCTTCCACTG	1044
Db	532	CTCTATGCTTCTTGGATGAGAACTTCAAGGCGCTGTTAAGAAAGTTCGTGCTGTCTCT	591
Qy	1045	AAGATGAGAGTAGAGCGCGACAGCACTAGACAAAGTCCGAAATATACGTTAGGAT	1098
Db	592	GCCCTGCACCCGGAGATGACGGTTCATGATCTGTGGCAGGACTTGGCAAGAT	645

RESULT 27				
AY400674				
LOCUS	AY400674	1006 bp	DNA	linear
DEFINITION	Homo sapiens SSTR2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			

ACCESSION	AY400674
VERSION	AY400674.1
KEYWORDS	GI:39756663
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Elkayyoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 1006) Clark,A.G., Glnowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Perrieres,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1006)
AUTHORS	Clark,A.G., Glnowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Perrieres,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submision
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment
FEATURES	Location/Qualifiers

ORIGIN	gene	<1..>1006 /gene="SSTR2" /locus_tag="HCM0636"
Query Match	18.6%;	Score 214.8; DB 29; Length 1006;
Best Local Similarity	54.0%;	Pred. No. 4,1e-31;
Matches 485; Conservative	0;	Mismatches 407; Indels 6; Gaps 2;
QY	155	CGCACATCTCCCGGCGCATCCGGTCAATCATCAGCGGGAGTCTACTCCGTAGTGTTCGCG 21
Db	107	CGTACTATAGCTGACAGACCAATGCAGTCTCTACATTTTGTGTGCTGATCA 166
QY	215	TGGGCTGTGTGGGCAACTGCTGTGATGTTCTGATCATCCGATACAAAGATGAAGA 27
Db	167	TTGGGTGTGTGGGCAACACTTGTCACTTATGTGATCCTCCGGTATGCGCAAGATGAAGA 226
QY	275	CAGCAACCAACATTACATATTAACTGGCTTGGCGAGATGCTTGTGTTACTACAAACA 334
Db	227	CATTCACCAACATTACATCTTCACTTCACTGGCCATGCAAGATGAGCTCTTCAATGCTGGGTC 287
QY	335	TGCGCTTTCAGAGTACGGTCTTACTTGAATTTCTGGCCCTTTTGGGGATGTGCTGCA 394
Db	287	TGCGCTTTCCTGGGCTATGACAGTGGCTCTGGTCCATCTGGCCCTTTGGCAAGCCATTGGCC 346
QY	395	AGATAGTAATTTTCATTGTTACTACAAATGTTTACAGAGATCTTCACTTTGACATGA 455
Db	347	GGGTGTGTCACTGCTGTGATGTGCATCAATCAATTCACAGAGATCTTCTGCTGCAAGTCA 406
QY	455	TGAGCGTGAACCGCTACATTTGCGGTGTGCCAACCCTGTAAGAGCTTTGGACTTCCGACAC 514
Db	407	TGAGCATGCAACCGATACCTGCGTGTGTGTGTCAACCCCATCAATCGGCCCAAGTGAAGAGAC 466
QY	515	CTTTGAAGGCAAAATCATCAATATCTGCATCTGGCTGCTGTCATCTTGTGGCATCT 574
Db	467	CCCGGACGGCCAAAGATGATCAACATGCGTGTGTGTGGGAGT--CTCTCTGTGCTGATCT 522
QY	575	CTGCATATAGTCTTGGAGGCAACAAAGTCAGGGAAGAGTGCAGTGTCTTAGTGTCCT 634
Db	524	TGCGCATCATGATATATGTGTGGGCTCCGAGACCAACAGTGGGGGAGAAGCAAGCTGACACA 588
QY	635	TGCAAGTCCCAAGATGATGACTACTCTGTGTGGAGCTTTCATGAAGATCTTGCTCTTCA 694

AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komno,H., Akiyama,J., Nishi,K., Katsuna,T., Tashiro,H., Itoh,M., Sund,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawa,J., Okazaki,Y., Muramatsu,M., Inoue,K., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2432)
AUTHORS	Adachi,S., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hoti,P., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akihira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
COMMENT	Please visit our web site for further details.
COMMENT	URL: http://genome.gsc.riken.go.jp/
COMMENT	URL: http://fantom.gsc.riken.go.jp/
COMMENT	location/Qualifiers
FEATURES	1..2432
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	/mol_type="mRNA"
	/strain="C57BL/6J"
	/db_xref="FANTOM_DB:DI30013H04"
	/db_xref="MGI:2419395"
	/db_xref="taxon:10090"
	/clone="DI30013H04"
	/tissue_type="spinal ganglion"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="12 days embryo"
CDS	130..1287

Query Match	18.5%	Score 213.8	DB 11	Length 2432
Best Local Similarity	54.0%	Pred. No. 9.1e-31		
Matches 496	Conservative 0	Mismatches 42	Indels 21	Gaps 2
Qy	108	CGACGACGACGCGAGCCGCGCTCGAGAGACGCGACGCTGAGACCCGCGACATCTCC	167	
Db	192	CGCCAGCTGGGCTCCGAGCGAGAGAGAGATGATGGGGGTCGACGCGACAGGAG	251	
Qy	168	GGCATCCCGTCAATCAAGGGGCTACTCCGTAGTGTTCCTCTGGGCTTGGGG	227	
Db	252	AGCGGGACGTGTCATCCAGTGCATCTAGCGCTGTGTGTGGGCGCTGGGG	311	
Qy	228	CACTCGGTGTCAGTTCGTGATCATCCGATACAAAGATGAGACAGACCAACAT	287	
Db	312	AAAGCGCTGTATCTTCGTGATCTCAAGCTATGCAAGATGAGACAGCACCAAT	371	
Qy	288	TTACATATTAACCTGGCTTGGCAGATGCTTATGTTACTACAAACATGCCCTTTCAG	347	
Db	372	CTACCTACTCAACTGGCGCGTCCGATGAGCTCTCATGCTCAGCTGCATTCGAGC	431	
Qy	348	TACGTCCTACTGTAATTCCTGGCTTTGGGGATGTGCTGTGCAAGATGTAATTC	407	
Db	432	CTCGCGCGCTGCCCTGGCGCACTGGCCGCTTGGGGCGGTCTGTGTGCGCAGTCTAG	491	
Qy	408	CATTGATTAACAACAGTTTACACAGCATCTTACCTTGACCAATGATGAGCGTGAACG	467	
Db	492	CGTGAACGCGCTGAGAACATGTTCACTAATGTCTTCTGCTCACCCTGCTCAGCGTGAACG	551	
Qy	468	CTACATGCGCGTGGCCACCCCGTGAAGGGCTTGGACTTCGCGACACCTTGAAGGCAA	527	
Db	552	CTAGTGGCTGTGTGACCCCTCTGGCGCGCCGACACTACCGGGCGCCAGCGTGGCAA	611	
Qy	528	GATCATCAATATCTGCATCTGGCTGTGTGTCTATCTGTTGGCATCTCTGCAATAGTCT	587	
Db	612	GCTATCAACACTGGGAATGTGGCTAAGCATCTTGTCTGTGACCTGCCCATTCGACGCTT	671	
Qy	588	TGAGAGCAACCAATACAGGGAAGACGTCAGATGATGAGATGCTCTTGAAGTTCGAGA	647	
Db	672	CGTGAACCAAGCGCAGCTGTGGGGGCGAGGCGTGTGCAACTGACCTGACCTG	731	
Qy	648	TGATGACTACTCCGTGTGGGACCTCTTCATGAGAGATGTGGCTTCACTTTCCTTCGT	707	
Db	732	CCCGGCTGTGTGCG-----GCTTGTGTGATTAATCTTTTGTGTGGCTTCT	782	
Qy	708	GATCCCTGTCTCATCATTCGTCTGCTACACCTGATGATCTCTGCTTCAAGAGCGT	767	
Db	783	ACTCCCGGTCTGGCCTACGGAATATCTACCTGCTAATGTGGGCAAGATGGCGCTGT	842	
Qy	768	CCGGCTCTTTCGCGCTCCCGAAGAAAGATCCGCAACCTGCGTGAAGATCAACGACGTGT	827	
Db	843	GGCCCTCGGGCTGGCTGGCAACAAGAGGCGCTCAGAAAGAAAGTCACTAGGCTCGT	902	
Qy	828	CTGTGTGTGTGACATCTTTCGTCTGTCTGGACTCCATTCACATATTCATCTCGT	887	
Db	903	GCTAATGTGTGACGCTTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	962	
Qy	888	GGAAGCTCTGGGAGACCTCCACAGACAGCTGTCTCTCGACGTTATTAATCTTGCAT	947	

	Db	965	GNAACGCTTTGGCACAGCGCTGCATGCCACTGT-----CAACCATGTCCTCCTT	1012
Oy	948	GGCCTTAGGCTTTACCACAAGTAGCCCTGATCCATTCTTAAGCCTTTTGATGAATAA	1007	
Db	1011	CATCCTGACCTTAGTGGCAACAGCTGTGGCCATCCATTCCTATAGGCTTCTCTGACAA	1070	
Oy	1008	CTTCAAGCGGTGTTTCGGG	1026	
Db	1071	CTTCCGGCGCCTCTTCCAG	1089	
RESULT 30				
LOCUS	CNS02261	836 bp	DNA	linear
DEFINITION	Tetradodon nigroviridis genome survey sequence T7 end of clone			
ACCESSION	CNS02261			
VERSION	AL177778.1	GI:7815835		
KEYWORDS	GSF; genome survey sequence.			
SOURCE	Tetradodon nigroviridis			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphia; Acanthopterygii; Perciformes; Tetraodontiformes; Tetraodontidae; Tetraodontinae; Tetraodon.			
REFERENCE	1 Roest Crolius,H., Jailion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Wincker,P., Brotier,P., Quetier,F., Saurin,W. and Weissbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)			
AUTHORS	2 Roest Crolius,H., Jailion,O., Dasilva,C., Ozouf-Costaz,C., Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000) 20359637 10899143			
JOURNAL MEDLINE PUBMED	3 (bases 1 to 836) Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end and sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon. Location/Qualifiers 1..836 /organism="Tetradodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="Z27103" /clone_1kb="G" /note="Genoscope sequence ID : C0AG227AE02LP1-end : T7"			
COMMENT				
FEATURES				
source				
ORIGIN				
Query Match	18.5%	Score 213,	DB 29;	Length 836;
Best Local Similarity	74.2%;	Pred. No. 8.5e-31;		
Matches 268;	Conservative 1;	Mismatches 92;	Indels 0;	Gaps 0;
Oy	257	GATACAAAAGATTAAGAAGACAGCAACCAATTCATATTATTAACCTGGCTTTGGACAGATG	316	
Db	270	GGTACACAAAGATTAAGAACCCGCCAACCAATCTTAGATCTTCAACCTGAGCTCTGAGCCAGCG	329	
Oy	317	CTTAGTACTACACCATGCGCTTTCAAGATACGTCATCTTGATGATGATTCCTGGCGCTT	376	

[illegible]

Matches 306; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 153 GCGGACATCTCCCGGCATCCCGTATCATACAGGGGCTACTCCGTAGTGTCT 212
 |||||
 Db 137 GCGCTTCGCGCCCTGGGCTCAAGGTCAACATCGGGGCTCTACCTGGCGTGTGT 196
 |||||
 QY 213 CGTGGGCTTGTGGGCACTCGGTGTCATGTTTCGTATCATCCGATACACAAAGTGA 272
 |||||
 Db 197 CGGAAGGCTCCCTGGGGAATGCTGTGTATGACGTCATCCACAGCACACAAATGA 256
 |||||
 QY 273 GACAGAACCAACATTACATATTAACTCGCTTTGGGACAGATGCTTTAGTTACTAAC 332
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 Db 257 GACACCCACCAATTTATCATCTTTAACTGGCCCGCGCCGACACACTGTGTCTGTGAC 316
 |||||
 QY 333 CATGCCCTTTGAGATACGCTCTACTGTATGAAATTCCTGGCCTTTTGGGAGATGTCTG 392
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 Db 317 GCTGCCCTTCACGGGACGAGACATCTCTGGGCTTTCGGCGTTTGGGAATGCCCTG 376
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 QY 393 CAAAGATAGTAAATTTCCATGATTACTACAAACATGTTACACAGCATCTTACCTGACAT 452
 |||||
 Db 377 CAAGACAGTCATGCTGCTACTGACTACTACAAACATGTTACACACACCTTACCTTAAGC 436
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 QY 453 GATGACGCTGACCGCTACATTCGCTGTCGCAACCCCGTGAAGGCTTTGACTTCGAC 512
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 Db 437 CATGAGTGTGATCGCTATGTAGCCATCTGCCACCCCATCGTCCCTGACGTCCGAC 496
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 QY 513 ACCCTTGAAGGCAAGATCATATATCTGCATCTGGCTGCTGTGTATCTGTGGCAT 572
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 Db 497 GTCCAGCAAGCCACGAGCTGTCAATGTGACCATCTGGGCGCTGTGTGTGTGT 556
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 QY 573 CTCTCAATAGTCTCTTGAGGACCAACAGTCAGGGAAGC 613
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 Db 557 TCCCGTCCGATCATGGCTCGGACAGGTCAAGATGAAG 597
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RESULT 32
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 DEFINITION tigr-gss-dog-17000311696913 Dog library Canis familiaris genomic,
 genomic survey sequence.
 CE517843
 ACCESSION
 CE517843.1 GI:36834624
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 531)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Ruech,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 MEDLINE
 PUBMED
 14512627
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Classes: shotgun.
 Location/Qualifiers
 1..531
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: Bactxi; Libraries were prepared from
 peripheral blood"

FEATURES
 source
 ORIGIN

Query Match 18.3%; Score 211; DB 29; Length 531;
 Best Local Similarity 88.4%; Pred. No. 1.7e-30;
 Matches 229; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 ATGACATCCCGCATCAGATCTTCCGCGGAGCGCGGCTTACCTGCGCCCGACGCC 60
 |||||
 Db 157 ATGAGATCCCGGTCACATCTTTGCGGGAGCGGGGCCACCTGTCTCGGAGAC 216
 |||||
 QY 61 TCCCTGCCCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGGAGCCGACAGCAAGC 120
 |||||
 Db 217 TCCCTGTCTCCCAAGGAGCGGCTGTGCTGCGGCTGGGCGGAGACGGAAGCAAC 276
 |||||
 QY 121 AGCGCGGCTGGAGAGAGCGGAGCTGAGCGCGCGGACATCTCCCGGCAATCCCGG 180
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 Db 277 AGCGCGGCTCGAGAGGCGGAGCTCGAGTCGAGACATCTCTCCGCAATCCCGG 336
 |||||
 QY 181 ATCATCAGCGCGGTCTACTCCGTAGTGTGCTGTGCGGCTTGTGAGGCAACTCGCTG 240
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 Db 337 ATCATCAGCGGCTGTACTCCGTGTGTGTGTCGTGCGGCTTGTGAGGCAACTCCGTG 396
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 QY 241 ATGTTGATGATCATCCGAT 259
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 Db 397 ATGTTGATGATCATCCGAT 415
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RESULT 33
 CDS028C2 877 bp DNA linear GSS 01-SRP-2000
 LOCUS
 DEFINITION Tetrason nigroviridis genome survey sequence PUC-ori end of clone
 16JH06 of library G from Tetrason nigroviridis, genomic survey
 sequence.
 AL211691
 ACCESSION
 AL211691.1 GI:7870510
 VERSION
 GSS; genome survey sequence.
 KEYWORDS
 SOURCE
 ORGANISM
 Tetrason nigroviridis
 Tetrason nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetrason.
 1
 Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brotier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetrason nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 20296633
 MEDLINE
 PUBMED
 10835645
 COMMENT
 Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costez,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetrason nigroviridis
 Genome Res. 10 (7), 939-949 (2000)
 10899143
 MEDLINE
 PUBMED
 3 (bases 1 to 877)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetrason nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetrason.
 Location/Qualifiers
 1..877
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 /mol_type="genomic DNA"

FEATURES
 source
 ORIGIN


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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:5695055"
/issue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="N1H_BMAP_EH0P"
/notes="Organ: Brain; Vector: pYX-Ase; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Ase vector. The library tag
sequence located between the Not I site and the polyA
tail is CAGCCAGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN

Query Match 17.6%; Score 202.8; DB 12; Length 810;
 Best Local Similarity 62.8%; Pred. No. 7, 9e-29;
 Matches 369; Conservative 0; Mismatches 207; Indels 12; Gaps 3;

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154 GGCACATCTCCCGGCGCATCCGCGCATCAGCGCGGTCTACTCCGAGTTCGTC 213
228 GCGTCTCTCCCTTGGAGTCAAGTCAACCATGTGGGCTTACTTGGCTGTGTCATC 287
214 GTGGGCTTGTGGGCACTCGTGTATGTTGTGATCATCGATACCAAGATGAAG 273
288 GGGGGGCTCTGGGAACTGCGTCATGATGTCATCTCGACGACCAAGATGAAG 347
274 AAGCAACCAATTTACATTTTAACTGGCTTTGGCAGATGCTTAACTACTACACC 333
348 ACTGCTACCAATTTACATTTTAACTGGCAGCTGATGATACCTGTGCTTGACACA 407
334 ATGCCCTTCAAGTACGCTACTGATGAATCTCGGCTTTGGGATGTCGTGTC 393
408 CTGCCCTTCAAGGACACATCTCTTGGGCTTTGGCATTGGGATGATGATGTC 467
394 AAGATGATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 453
468 AAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 527
454 ATGAGCGTGGACCGCTACATTTGCGTGGCACCCTGTAAGGCTTTGACCTTGC 513
528 ATGAGTGTAGACCGTATGATGATGATGATGATGATGATGATGATGATGATG 587
514 CCCTTGAAGGCAAGATCATATATCTGATCTGCTGCTGCTGCTGCTGCTGCTG 573
588 TCCAGTAAAGCCAGGCGCTTAATGTGGCATATGGGCGCTTGGTGTGTT 647
574 TCTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGATGATGATGATGATGATG 633
648 CCGTGGTGCATATGGGCTCAGACAAAGT-----GGAAGATGAAGATGATGATG 701
634 TTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGATGATGATGATGATGATG 693
702 GTGGAGATCCCGGCC-----CTCAGGATTAATGGGCGCTGTAATTTGATGAT 756
694 ATCTTGGCTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
757 CTTTCTTT-CTTCAATATCCCGGTTCTGATCATCTCTGTCTGCTACAGC 803

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RESULT 39
 BU219037

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LOCUS BU219037 649 bp mRNA linear EST 25-NOV-2002
DEFINITION 603755443f1 CSEQCHN04 Gallus gallus cDNA clone CHEST65F12 5', mRNA
sequence.
ACCESSION BU219037
VERSION BU219037.1 GI:25402920
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
1 (bases 1 to 649)
AUTHORS Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392

```

COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers

FEATURES

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1..649
location/Qualifiers
  /organism="Gallus gallus"
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  /strain="White Leghorn, H1sex"
  /db_xref="taxon:9031"
  /clone="CHEST65F12"
  /issue_type="whole embryo"
  /dev_stage="20-21"
  /lab_host="DH10B"
  /clone_11b="CSEQCHN04"
  /note="Organ: whole embryo; Vector: pBluescript II KS(+);
  Site 1: EcoRI; Site 2: NotI; This normalized library was
  constructed from 1 million independent clones. cDNA
  synthesis was initiated using an oligo(dT) primer, using
  methylated C in the first strand synthesis reaction.
  Following this first strand reaction, double-stranded cDNA
  was blunted, ligated to NotI adaptors, digested with
  EcoRI, size-selected, and cloned into the NotI and EcoRI
  compatible sites of a custom modified MCS of the
  pBluescript (KS+) vector. The library was normalized in 2
  rounds using conditions adapted from Soares et al., PNAS
  (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6
  (1996): 791, except that a significantly longer
  reannealing hybridization was used."

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ORIGIN

Query Match 17.3%; Score 199.2; DB 13; Length 649;
 Best Local Similarity 65.3%; Pred. No. 3, 6e-28;
 Matches 308; Conservative 0; Mismatches 163; Indels 1; Gaps 1;

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664 TGGACCTTCTCATGAAGATCTGCGTCTTCACTTTGCTGATGCCCTGCTCTCATC 723
24 TGGAAACCTACTGAAATCTGTGTTCACTTTGCTTCAATATGCAAGCTGATC 83
724 ATCATCTGTCTTCAACCTGATGATCTGCGTCTCAAGAGCTCGGCTCTTTTGGC 783
84 ATTACTGTGTGTAAAGGCTGATGATTTTAAACCTTAAGAGTGTCCGATGTTATCT 143
784 TCCGAGAAAGATGCAACTGCGTAGATCACAGACTGCTCGTGGTGGTGGCA 843
144 TCTAAGAGAGAGACAGAACTGCGAAGATCAAGAGATGCTTGTATGTTGGCA 203
844 GTCTTGTCTGTGTGAATCCCATTCATATATTCCTGTTGGAGCTTGGGAGAC 903
204 GTGTTCATCATCTGCTGAGCTCTTATCCACATTTATGTCATATTAAGACCTGTG 263

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QY 904 ACCGCCACGACAGAGCTGCTCTCCAGCATATTCTTCGATCCGCTTAGGCTATACC 963
 Db 264 ATCCGAAATACTATTCTTCAGACTGTCTCTGGACATTTGTATGTAGGTATATA 333
 QY 964 AACAGTAGCTGAATCCCATTTCTTACGCTTTTGTATGAAAACTTCAAGCGGTGTTG 1023
 Db 324 AATAGTGCCTCAATCAGTCTGTATGATTTCTAATGAGAAATTTCAAAAGTGTTC 383
 QY 1024 CGGACCTTCGCTTTCCACTGGAATGAGATGAGCGGACAGCACTAGCAGATCCGA 1083
 Db 384 AGAGAGTTGTGATCTCCACCTCTCAATATGAGAGCAAACTCCACAG-GTCCGA 442
 QY 1084 AATAAGTTAGAGATCTGCTTACCTGAGGACATGATGGATGAATAAC 1135
 Db 443 CAAATACTCTGTACATCTTCTTCACTGCAACACTGTGACAGACTAAC 494

RESULT 40
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 LOCUS UI-M-EMO-bmw-i-19-0-UI.r1 NIH_BMAP_EMO Mus musculus cDNA clone
 DEFINITION IMAGR:5703258 5', mRNA sequence.
 ACCESSION B0179148
 VERSION B0179148.1 GI:20354640
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 816)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

source
 1..816
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
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 /lab_host="DH10B (T1 phage resistant)"
 /clone_id="NIH_BMAP_EMO"
 /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is GTGCGTGAA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 16.9%; Score 195.6; DB 13; Length 816;
 Best Local Similarity 63.9%; Pred. No. 2e-27;
 Matches 294; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 154 GGCACATCTCCCGGCGCATCCGGTCAATCAACGGGGGTCTACTCCGTAGTGTGTC 213
 Db 290 GCTTCCTGCGCCCTTGGACTCAAGGTCAACCATCGTGGGGCTCTACTGGCTGTGTCATC 349
 QY 214 GTGGCTTGTGTGGGCACTCGTGTGATGTTTGTGATCATCCGATACCAAGAATGAAG 273
 Db 350 GGGGGGCTCTGTGGGAACTGCGCTGTATGATGATCATCTTCAGGACACCAAGATGAAG 409
 QY 274 AAGCAACCAATTTAATATTTTAACTGGCTTGGCAGATGCTTTAGTTACTACAACC 333
 Db 410 ACTGTACCAACATTTAATATTTAATGTGACACTGGGTGATATCCCTGTTCCTGAC 469
 QY 334 ATGCCCTTTCAGAGTACGCTACTCTTGAATGAAATCTGTGGCTTTGGGAGTGTGTCG 393
 Db 470 CTGCCCTTCAGGGGACAGACATCTTCTGGGCTTCTGGCCATTGGGAATGCACTGTGC 529
 QY 394 AAGATGATATTTTCCATTGATTACTACAACATGTTTACCAAGCATCTTCACTGACCAT 453
 Db 530 AAGAGGTCATTGTATGACTACTACAACATGTTTACCAAGCATCTTCACTGACCATGCC 589
 QY 454 ATGAGCGTGAACCGTATCATTTGCCGTGTGCCACCCCGGAAGCTTTGACTTCCGACA 513
 Db 590 ATGAGTGTAGACCGTTATGATGATCTATCTGCACCTTATCGGCTCTTGATGTTGAGACA 649
 QY 514 CCTTTGAAGGCAAGATCATCATATCTGCATCTGCTGTGTGATCTGTTGGCATC 573
 Db 650 TCCAGTAAAGCCCAAGGCCGTTATGTGCGCATATGGGCCCTTGCGTGTGTGTGTT 709
 QY 574 TCTGCAATATGCTTTGAGGACCAACCAAGTCAGGGAAGACG 613
 Db 710 CCTGTTCATCATGCGCTCAGCAACAATGAGGAGATGAAG 749

RESULT 41
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 DEFINITION BX228633
 ACCESSION BX228633
 VERSION BX228633.1 GI:28062783
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 787)
 Humphray S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphray@sanger.ac.uk Unpublished
 This sequence was generated from the SP6 end of BAC 244F17. 244F17
 is part of the Daniokey BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

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 /clone="DKEY-244F17"
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ORIGIN
 Query Match 16.8%; Score 194; DB 29; Length 787;
 Best Local Similarity 71.8%; Pred. No. 3.9e-27;
 Matches 254; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment
251				TCATCCGATACCAAGATGGAAGACAGACACCAATTACATATTACCGGGCTTGG				
82				TTGCGAGATACCCCAAGCTGAAATCTGCCACCAATCATCTACATCTTCAATTTGGCCCTGG				
311				CAGATGCTTTAGTTACTACCAACCATGACCCCTTCAGAGTACGGTCTACTTGATGAAATTCCT				
142				CAGATGCACTGGCTCTACTGATACCTTCATCTCCAGAGCAACAGATTTTATGAAACACT				
371				GGCCTTTGGGGATGTGCTGTGCAAGATGATATTTCATTTGATTTACTACCAATGTTCA				
202				GGCCCTTGCGTGAAGCTCTCTTTGGCAAGTGGTATGACCATAGACTACTACATATATGTTTA				
431				CCAGATCTTCACTTGCACATGATGAGAGTGGACCGGTACATTCGCCGTGGCCACCCCG				
262				CCAGATCTTCACTTGCACATGATGAGAGTGGACCGGTACATTCGTGTGGCCACCTGT				
491				TGAAGCTTTGGACTTCCGACACACCCCTTGAAGGCAAAATCATCATATTCGATCTGGC				
322				TGAGAGCACTGGAAGTTTGGTACCCCGATCCAGGCCAAATATATCATGTGTGATCTGGA				
551				TGCTGTGCTCATCTGTGGCATCTCTGTGCAATATGTCCTTGAAGGACCAAGTCA				
382				TCCTCTCTCCGCTGTGGAGTGGACCAATCATGATATGATGCGAGTCACTGAGATGA				
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BO571737								
LOCUS								
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
COMMENT								

sequence located between the Not I site and the poly
tail, is TGACGAGGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemlin Chin, Ph.D., program coordinator."

Query Match	16.7%	Score 192.8	DB 13	Length 746
Best Local Similarity	65.0%	Pred. No. 6.5e-27		
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Db	307	GCCTTCCTGCGCCCTTGGACTCAAGTACCATCGTGGGGGCTTACTTGGCTGTGATC	366	
Qy	214	GTGGGCTTGGTGGGCAACTCGCTGTCTATGTTCTGTATCATCCGATACACAAATGAG	273	
Db	367	GGGGGGGCTCTCCGGGGAACCTGGCTTCGTATGATGTCACTCCAGACACCCAGATAG	426	
Qy	274	ACAGCAACCAACATTTATCATATTTAACTTACCTGGCTTTGGCAGATGCTTAACTACCAAC	333	
Db	427	ACTCTACCAACATTTATCATATTTAACTTGGCACTGCTGTATCTTGGCTTGGCA	486	
Qy	334	ATGCCCTTTGACAGTACGCTCTACTGATGAAATTCCTGCGCTTTTGGGAGATGTGCTGC	393	
Db	487	CTGCCCTTTCCAGGCGCACAGACATCCTTCTGGGCTCTTGGCCATTTGGGAATGACCTGTGC	546	
Qy	394	AAGATAGTAAATTTTCATTTGATTTACTACACATGTTACACGACATTTTCACTTGAACATG	453	
Db	547	AAGACGGTCAATGTGTAATGACCTACTTACAAATGTTTACAGCACTTTTCACTTTGATCGCC	606	
Qy	454	ATGACGCGTGAACGCTCATTTGCGCTGTGACCAACCGCTGAAAGCTTTTGAATTCGCGACA	513	
Db	607	ATGAGTGTAGACCGCTTATGTAGCTATCTGCCACCTTATCCGTCCTTGTATGTTGCGACA	666	
Qy	514	CCCTTGAAGGCAAAAGATCATCATATATCTGCATCTGCTGTGTCATCTGTTGGATC	573	
Db	667	TCCAGTAAAGCCGAGCGCGTTAATGTGGCATATGAGCCCTTGGCTTGGTGTGTGT	726	
Qy	574	TCGTCATATGTCCTTGG	590	
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RESULT 43

AY410421

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

AY410421

Homo sapiens SSTR4 gene, VIRUAL TRANSCRIPT, partial sequence.

AY410421

AY410421.1 GI:39766389

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 954)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejalatal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsny,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 954)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejalatal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsny,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

COMMENT
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source
1. .954
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="SSSTR4"
/locus_tag="HCM3885"

ORIGIN

Query Match 16.5%; Score 190.6; DB 29; Length 954;
Best Local Similarity 55.8%; Pred. No. 1.9e-26;
Matches 436; Conservative 0; Mismatches 324; Indels 21; Gaps 3;

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QY 246 CGTATCATCCGATACAAAGATGAAAGACGACCAACATTATTAATTAACCTGAC 305
DB 1 CGTATCATCCGATACCAAGATGAAAGACGACCAACATTATTAACCTGAC 60
QY 306 TTGGAGATGCTTGTAGTAACTAACAACATGCCCTTTCAGAGTACGCTACTATATGA 365
DB 61 CGTAGCCGACGAGCTTCAATGCTGAGCGGCTTCGTGCGCTGCGCGCCCTGCG 120
QY 366 TTCCCTGGCTTTGGGAGATGCTGTCGAAGATGATTAATTTCCATTGATTAATCAACAT 425
DB 121 CCACTGGCCCTTGGCTCGGCTGCTGCGCGGCGGCTCAGGCTGACGCGCTCAACAT 180
QY 426 GTTACACAGATTTTACCTTGAACATGATGAGCGTGAACCGTACATTCCTGTCGA 485
DB 181 GTTACACAGATTTTCTGCTCACTGCTGACGCGTGAACCGTACATTCCTGTCGA 240
QY 486 CCCCGTGAAGGCTTTGGAATTCGACACACCTTGAAGGCAAGATCATATCTGCAAT 545
DB 241 CCTCTGCGCGCGGCGACCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
QY 546 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
DB 301 GTGGCTGCGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 606 GGAAGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
DB 361 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414
QY 666 GGAACCTTCAATGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
DB 415 GGAACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
QY 726 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
DB 472 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
QY 786 CGGAGAAAGATTCGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
DB 532 GAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591
QY 846 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
DB 592 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
QY 906 CTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965
DB 640 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
QY 966 CAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1025
DB 700 CAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
QY 1026 G 1026
DB 760 G 760

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RESULT 44
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LOCUS RPCI-23-80H6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-80H6,
DEFINITION genomic survey sequence.
ACCESSION AZ226406
VERSION AZ226406.1 GI:8534455
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 546)
Zhao, S., Niemman, W., Feldblum, T., Malek, J., Shateman, S.,
Akinret, B., Levin, M., McGinn, S., Tesgaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-80H6.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html
Plate: 80 row: H column: 6
Seq primer: SP6
Class: BAC ends.

FEATURES
source
location/Qualifiers

1. .546
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="RPCI-23-80H6"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methyase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 16.4%; Score 189.8; DB 28; Length 546;
Best Local Similarity 90.2%; Pred. No. 2.2e-26;
Matches 203; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 386 TGGTGGCAAGATGATGATTTCCATTGATTAATCAACATGTTACAGCATCTTCACT 445
DB 1 TGGTATCAAGATGATGATTTCCATTGATTAATCAACATGTTACAGCATATTCACCT 60
QY 446 TGACATGATGAGGCTGACCGGCTACCTGCGGCGGCGGCGGCGGCGGCGGCTTGGACT 505
DB 61 TGACATGATGAGGCTGACCGGCTACCTGCGGCGGCGGCGGCGGCGGCGGCTTGGACT 120
QY 506 TCGGACACCGCTTGAAGGCAAGATCAATATTCATGCTGCTGCTGCTGCTGCTGCT 565
DB 121 TCGGACACCGCTTGAAGGCAAGATCAATATTCATGCTGCTGCTGCTGCTGCTGCT 180
QY 566 TTGGCATCTGCAATGCTCTTGGAGGCGCAAGTCAAGGAG 610

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Db 181 TTGGTATATACAGCATAGTCTTGGAGGACCAAGTACAGGAG 225

RESULT 45
AK03151 2848 bp mRNA linear HTC 19-SEP-2003
LOCUS Mus musculus adult male hypothalamus cDNA, RIKEN full-length
DEFINITION enriched library clone:A230102K24 product:weakly similar to opioid
receptor, kappa 1, full insert sequence.

ACCESSION
AK03151
VERSION AK03151.1 GI:26086975
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Teshiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Matsubara, S., Kawai, J.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PUBMED 11076861

REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 11076861
PUBMED 11076861

REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haseizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kikuchi, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M.,
Koyama, M., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp,

COMMENT
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>,
location/Qualifiers

FEATURES
source
1..2848
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM:DB:A230102K24"
/db_xref="MGI:2403607"
/db_xref="taxon:10090"
/clone="A230102K24"
/sex="male"
/tissue_type="hypothalamus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

misc_feature
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/note="weakly similar to opioid receptor, kappa 1
(MGI:MGI:97439, GB|L11065, evidence: BLASTN, 100%,
match=273)"

ORIGIN
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Best Local Similarity 81.5%; Pred. No. 1.3e-24;
Matches 211; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
1 ATGAGCTCCCGATCCAGTCTTCCGCGGAGCGGCGCTTACCTGCGCCCGAGCGCC 60
2 585 ATGAGTCCCGCATTCAGATCTTCCGAGAGATCCAGGCGCTTACCTGCTCCAGTCT 644
3 61 TGGCGCCCCCAAGAGAGCGCGCTTTCGCGGCTGCGGCGGAGCGGAGCGGAGCGG 120
4 645 TGGCTTCTCCCAAGAGAGCGCTTTCGCGGCTGCGGAGCGGAGCGGAGCGGAGCGG 704
5 121 AGCGCGGCTCGAGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 180
6 705 AGTGTGGCTCAGAGAGATCAGAGCTGAGTCCGCGCATCTCTCCGCGCATCTCTGT 764
7 181 ATCATCAGCGCGCTTACTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
8 765 ATCATCAGCGCGCTTACTCTGTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
9 241 ATGTTCGATCATTCGAT 259
10 825 ATGTTCGATCATTCGAT 843

RESULT 46
CGS36117 318 bp DNA linear GSS 01-OCT-2003
LOCUS OS1123712 Mus musculus 129SV/5V Mus musculus genomic clone
DEFINITION OS1123712, genomic survey sequence.
ACCESSION
CGS36117
VERSION CGS36117.1 GI:37322689
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richer, L.J.,
Piggott, J., BeltrandelRio, H., Buckton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jai, J.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparkes, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

TITLE	Zhu, Q., Person, C. and Sands, A.T.				
JOURNAL	Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention				
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP OmiBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com gene_trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11) Class: Gene Trap.				
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ORIGIN					
Query Match	15.8%;	Score 181.8;	DB 29;	Length 318;	
Best Local Similarity	77.4%;	Pred. No. 6.2e-25;			
Matches 233;	Conservative 0;	Mismatches 67;	Indels 1;	Gaps 1;	
QY	257	GATACACAAAGATGGAAGACAGACCAACATTATACATTTACACCTGGCTTGGCAATG	316		
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QY	317	CTTTAGTTACTACAAACAATGCCCTTTACAGAGTACGGTCTACTTGTGATTTCTGGCCCTT	376		
Db	67	CGCTGGCCACCGACACGCTGCCCTTCCAGAGGCCAAGTACTGATGGAACGTGGCCGT	126		
QY	377	TTGGGGATGTGCTGTGCAAGATGATGAATTTCCATTGATTACTACAACTTTTACCACGA	436		
Db	127	TTGGGAGCTGTGTGCAAGGCTGTGCTCTCCATTGACTACTACAACTGTTCACCTACGA	186		
QY	437	TCTTCACCTGATCCATGATGAGCGCTGACCCGCTACATTCGCCGTGACCCCGCTGAAG	496		
Db	187	TCTTCACCTGATCCATGATGAGCGGTGACCCGCTACATTCGTCTGCCATCTCTGTCAAG	246		
QY	497	CTTTGAGATTTCCGCACACCCCTTTGAAGGCAAGATCATCATATCTGCATCTGGCTGT	556		
Db	247	CCCTGAGCTTCGGACACACGCAAGCCGAAGCCGATCATATATATGACATCTGGCTTGG	306		
QY	557	C 557			
Db	307	C 307			
RESULT 47					
CF550026	776 bp	mRNA	linear	EST 08-OCT-2003	
LOCUS	AGENCOURT 1559235 NIH_ZGC_4 Danio rerio cDNA clone IMAGE:7014015				
DEFINITION	5', mRNA sequence.				
ACCESSION	CF550026				
VERSION	CF550026.1	GI:3486858			
KEYWORDS	EST.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Bnkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 776)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892				

Query Match	Best Local	Similarity	Score	DB	Length
Matches	403;	Conservative	0;	Mismatches	308;
				Indels	7;
				Gaps	3,
Query Match	15.7%;	Score	181.2;	DB	14;
Best Local	56.1%;	Pred.	No. 1.2e-24;		
Matches	403;	Conservative	0;	Mismatches	308;
				Indels	7;
				Gaps	3,
171	CATCCCGGTCATCATCAGCGGGGCTTACTCCGTCAGTGTTCCTCCGCGGCTTGTGGGCA	230			
40	CAGCGCGATTTCATCTCTTCCTTCACTTACTCCGTCGTGTCTAGTTGACTATGTGGAA	99			
231	CTCGCTGTCATGTTCGTGATCATCCGATACACAAGATGGAAGACAGAACCAACATTTA	290			
100	CTCGATGTGATATATGATGATCTTCAGGTATGCCAAGATGAAGATCGACCAATTCCTA	159			
291	CATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCCAGAGTAC	350			
160	TATTTTGAATCTGGCATCGGGATGAGTTACTATGTGAGCGTCCCTTTCTTGGTAC	219			
351	GATCTACTGATGATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCAT	410			
220	CTCTCTTTTACTTACACACTGGCCGTTTGGTCTCTCTGTGTGCTTGGTTTAAAGT	279			
411	TGATTTACTACAAATGTTACACAGCATCTTTCACCTTACATGATGAGCGTGA	470			
280	TGATGCCATTAATATGTTTCAACAGCATCTACTGTCTCAACGATGTGAGCATCATCTTA	339			
471	CATTGCGGTGGCCACCCCGTGAAGGCTTTTGAATTTCCGACACACCTTTGAAGCAAGAT	530			
340	CATCTCCGTGTGATCCCATCAAGAGTGGCCGCTTACCGGAGACCCACCATGCTTAAT	399			
531	CATCATATATCTGCATCTGGCTGTGTCGTGATCTGTTGGGATCTCTCAATATAGCTTTG	590			
400	GATCAACTTAGCAGTGTGATGTT--CTCATCTGTGTATTTCTCCCATCATCATCTT	456			
591	AGGACACCAAGTCAAGGAAAGCTGCATGTTCATTAAGTCTCTTGCAGTTTCCCAATGA	650			
457	CTCACACACACGCGCCCAACTCTATGAGTCTGTAAGCTGCAACATGACAGATGCAGAGCC	516			
651	TGACTATCTCGGTGGGACCTTCCTTCAATGAAGATCTGTCTTATCTTTTGCCTTCGAT	710			
517	CGAGCCCAAGTGAAGCCGCTGTGTGT--GATTAAGCTCTTTCTGTGATGGGCTTTCTCTT	573			
711	CCCTGTCTCATCATCATCTGTCTGTACACCCGTAAGATCTCTGCTCAAGAGCGTCCG	770			
574	CCCTGTCAATGCGCATGTGATGTGTAACATCTCATCATATGTCAAGATGGAAGTGTGGC	633			
771	GCTCTCTTTTGTGGCTCCCGAAGAAAGTGCAGACTCTGCGATGATCAACAGCTGTCT	830			
634	GCTCAAGCGGGCTGGCAGACAGGCAAAAGTCCGAGAGGAATAATCACTGTATGTGAT	693			
831	GGTGGTGGTGGCAGTCTTGGTGTCTGTGCGATCCCATTCATCATATTCATCTGGTG	888			
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RESULT 48
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LOCUS Pan troglodytes SSTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY400828
VERSION AY400828.1 GI:39756817
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE 1 (bases 1 to 1176)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS 2 (bases 1 to 1176)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1176
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="SSTR1"
/locus_tag="HCM0687"
ORIGIN
Query Match 15.6%; Score 180.4; DB 29; Length 1176;
Best Local Similarity 47.2%; Pred. No. 2e-24;
Matches 448; Conservative 0; Mismatches 484; Indels 18; Gaps 3;
QY 75 CAGCAGCGCTGTTCCCGGCTGGGCGAGCCCGACAGCAAGCGAGCGCGCTCGGA 134
DB 72 CGGCGGACAGAGGGGCGGCGGCGGCGCTGCGAGCGCATGAGAGCCAGGGCGA 131
QY 135 GGACGCGCAGCTGAGAGCGCGCACATCTCCCGGCGCATCCGCGTCATCATCAGCGCGT 194
DB 132 TCGCGTCCGAGACGGGACCTTGAGCGAGGGCCAGGGCAGCGCATCTGATCTTTTAT 191
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QY 315 TGCTTAGTTACTACAAACCATGCCCTTTGAGAGTACGATCTACTTGATGAATTCCTGGCC 374
DB 312 TGAGCTGCTCATGCTCAGCGTCCCTTCTGTTNNCTCACGTTGTTGCGNACCTNNN 371
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DB 372 NNN 431
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DB 432 NNTGTCATCCATCA 491
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QY 615 CGATGTCATGAGTCTCTGCAAGTCCAGATGATGATCTCTGCTGGAGACCTCTT 674
DB 612 CACGG---TGCTTGACATGATCTCATGCAAGCCCGCTCAACGCTGGCTGGTGGCTT 668
QY 675 CATGAAGATCTGCGTCTCATCTTGGCTTGGCTGATCTCTGCTCATCATCTGCTG 734
DB 669 CGT---GCGTTCACATTTCTATGAGGCTCTGCTGCGCGCGGCTATCTGCTGTG 725
QY 735 CTACACCCGTGATGATCTGCGCTCAAGAGCGTCCGCGCTCTTCTGGCTCCGAGAGA 794
DB 726 CTACGCTCATCATCTTCTTAAGATGCGCATGCTGCGCTCAAGCGCGCTGGCAGACGG 785
QY 795 AGATCGCAACTGCGTAGATCAGCAGACTGCTCTGCTGCTGCTGCTGCTGCTGCT 854
DB 786 CAGGCGCTCGAGCGCAAGATCACCTTAATGATGATGATGATGATGATGATGATGAT 845
QY 855 CTGCTGAGTCCCATTCACATTTATCTGCTGAGGCTCTGGGAGACCTCCACAG 914
DB 846 CTGCTGAGTCCCATTCACATTTATCTGCTGAGGCTCTGCTGAGGCTCTGCTGAG 905
QY 915 CACAGCTGCTCTCCAGTATTTACTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
DB 906 CAGGCTGAGC-----ACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
QY 975 GATCCCATCTCTACGCTTCTTCTGATGAAATCTCAAGCGGCTTTCC 1024
DB 954 CAACCCATCTCTATGCTTTCTCTGACAGCAACTTCAAGCGCTTTCC 1003
RESULT 49
BU366266 735 bp mRNA linear EST 28-NOV-2002
LOCUS 603567880P1 CSECHN72 Gallus gallus cDNA clone CHEST523019 5', mRNA
DEFINITION sequence.
ACCESSION BU366266
VERSION BU366266.1 GI:25874267
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 735)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomedical Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 10D, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..735
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"

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/clone="ChEST523019"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSECHN72"
/notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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ORIGIN

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Query Match      15.5%; Score 179.2; DB 13; Length 735;
Best Local Similarity 70.1%; Pred. No. 2.8e-24;
Matches 255; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

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DB 372 GCTTACCGGATTCACCAAGATGAGACGACCAACATTTCATATTAACTGGCTTT 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 GGCAGATGCTTGTACTACAAACATGCTTTGAGAGTACGCTACTATTGATGATTC 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 GGTACACACGCTGTGTGATGACCTTACAGGTTACAGACAGCTTCTGGCTT 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CTGGCTTTGGGAGATGCTGTGCAAGATGATTAATTTTCATGATTAACAACATGTT 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 492 CTGGCTTTGGGAGATGCTGTGCAAGATGCTATCTATATGACTACTACACATGTT 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 CACGAGATCTTACAGATGAGATGAGCGGTGA-CGGCTACATTCGCGTGGCCACG 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 CACAGACACTTACGCTGACATATGAGCGTGAACCGGTACATCGCTATCTGCCATTC 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 488 CCGTGAAGGCTTTGACCTCCGACACCTTTGAAGGCAAGATCAATATCTGCATCT 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 612 CTATCAAGGCTTGACATCCGACATCTCTCATTAAGGCAAGTGTGAACGTCGCATCT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 548 GGTCTCTGTGCTATCTGTGGCATCTCTGCAATAGTCTTTGAGGACCAAGTCAAGG 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 672 GGGCGCTGCTTCTGTCTTTGGCATCCGACGATGATGGATCTGCAGATATATGAG 731
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QY 608 AAGA 611
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DB 732 AACA 735
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RESULT 50
AY401571 987 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens GPR7 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION Homo sapiens GPR7 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION AY401571
VERSION AY401571.1 GI:39757560
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snijsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trio
Science 302 (5652), 1960-1963 (2003)
14671302
PUBMED 2 (bases 1 to 987)
REFERENCE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
AUTHORS Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snijsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..987
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/gene="GPR7"
/locus_tag="HCOM935"

ORIGIN

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Best Local Similarity 51.8%; Pred. No. 3.7e-24;
Matches 452; Conservative 0; Mismatches 417; Indels 3; Gaps 2;

QY 154 GCGCATCTCCCGGCGCATCCGATCATCAACGCGGCTTACTCGTAGTGTGTC 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 88 GCGCGCTGCGCGGCGCGCTGGCGGTGATCAAGTGTCTACGCGGTATCTGGGCC 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 214 GTGGCTTTGGGCACTGCTGTGATGTTGTTGATTCATCCGATACAAAGATGAAG 273
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DB 148 GTGGTCTGGGGCACTCGCGTGTGATGATGATGATGATGATGATGATGATGATG 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 ACAGCAACCAATTTACATTTAACTGCTTTGAGATGCTTTAGTACTACAAAC 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 ACCGTACCAACCTGTTTATCTCACTGACCTGACCTGACCTGACCTGACCTG 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 334 ATGCGCTTCAAGATGAGTCTTACTTATATGATTAATCTGCGCTTTTGGAGATGCTGTGC 393
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DB 268 CTGGCCATCAACATCGCGCATCTTCTCTGCGGAGATGCGCTTCGGGGAGCTCATGTGC 327
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QY 394 AAGATGATTAATTTCAATTTACTTATACAAATGTTCAACGATCTTCACTTACCATG 453
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DB 328 AAGCTATCGTGTATCGACATGACATCAACCTTCTCAAGCTTCTTCAACGCTC 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 ATGAGCGTGACCGCTACATTTGCGGTGACACCCCGTGAAGCTTTGACCTTCGACA 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 ATGAGCGCGACCGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 514 CCTTTGAAGGCAAGATCATATATCTGCATCTGCTGCTGTGTGTATCTGTTGGCATC 573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 446 GCCGCACTTCAAGCGCGCGCGCGCGGTGAGCTGTGCGG--TGTGGGAGATGTACATC 504
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QY 574 TGTGCATATAGTCTTTGAGGACCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGTGC 633
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DB 505 GTCTGTGCTGCTTTCGAGATCTTGTGCGCGGTACAGACAGAGGCGCGGCACTGC 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 634 TTGCACTTCCCAATGATGACTACTCTGTGTGAGGACCTTCTCATGAAGATGTGCTTC 693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 565 GTGTAGATCTTTCCGAGCGCGGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 694 ATCTTGTGCTTGTGATCTCTGTCTGTATATATATATATATATATATATATATATAT 753
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DB 625 GTGTGTGGCTTGTGCACTCCCGTGTCCACCATGTGTCTCTTATACCATCTGTGTGC 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 754 CGTCTAAGAGCGTCCGCTCTTTTGTGCTCCGAGAGAAAGATGAGCACTGCGATAGG 813
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DB 685 CGGCTGATGCTATCGGCTGTGAGACGACGCAAGGCGCTGTGAGCGCGCAAGAGCGG 744
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QY 814 ATCAACGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
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Db 745 GTGACCTTCCTGGTGGTGGAATCCTGGCGGTGTGCTCTCTGTGAGACCCCTTACAC 804

Qy 874 ATATTCATTCCTGTGGAGGCTCTGGGAGACACTCTCCACAGACAGCTCTCTTCCAGC 933

Db 805 CTGACACCGTGTGGCGCTCACACGACCTCCCGACAGCCGGTGTCTCATCGTTATC 864

Qy 934 TATTACTTGTGATCGCCTTTAGGCTATTAACAACAGTAGCTGAATCCATTCTTACGCG 993

Db 865 TCTTACTTATATACCAAGCCTGAGCTACGCAACAGCTGCTCAACCCCTTCTCTACGCC 924

Qy 994 TTTCTGTATGAAAACTTCAAGCGGTGTTCCG 1025

Db 925 TTCTGTGACGCCAGCTTCCGACGAACTCCG 956

RESULT 51
BC033145/c 2724 bp mRNA linear HTC 04-MAR-2003

LOCUS BC033145 Homo sapiens, clone IMAGE:4040710, mRNA.

DEFINITION BC033145

ACCESSION BC033145.1 GI:23138699

VERSION BC033145.1 GI:23138699

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2724)

AUTHORS Strausberg, R.

JOURNAL Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Boeddel, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carlie Mathewson, Candice McLeay, Steven Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalnu, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teati, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
Series: IRAL.Plate: 43 Row: c Column: 19
This clone has the following problem: retained intron.
Location/Qualifiers
1. .2724
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/mol_type="mRNA"
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/clone="IMAGE:4040710"
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/clone_lib="NIH-MGC_18"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

ORIGIN

Query Match 15.5%; Score 178.8; DB 11; Length 2724;
Best Local Similarity 51.8%; Pred. No. 5.6e-24;
Matches 452; Conservative 0; Mismatches 417; Indels 3; Gaps 2;

154 GGGCAATCCCGCGCATCCCGGCATCATCAGCGGCTACTCCGTAGGTTCCG 213
|||||

Db 1123 GCGCCGTCGCCGGCCCGCTGGCGGGTGTACCAAGTTGTCAACGCGGTATCTGCGCC 1064

Qy 214 GTGGCTTGATGGGCAATCGTGTGATGTTTGTGATATCCGATACCAAGATGAAG 273

Db 1063 GTGGGTGTGGCGGGAATCCCGCGTGTGTATGTTGTCTCGGGCGCCCGCATGAAG 1004

Qy 274 ACAGAACCAATTTAATATTTAACTGCTTGGAGATGCTTTAGTTACTAACAC 333

Db 1003 ACCGTACCAACTGTTTATCTTCAACTGTGCATTCGCGAAGAGCTCTTCAAGCTGTG 944

Qy 334 ATGCCCTTACAGATGATGCGTCTATGTAATTCCTGCGCTTTTGGAGATGTCTGTC 393

Db 943 CTGCCCATCAACATGCGCGAATCTCTGCTGCGGAGTGAGCCCTTGGGGAGCTCATGTGC 884

Qy 394 AAGATGTAATTTCCATTGATTTACTTACCAATGTTTACCAAGATCTTACCTTGACATG 453

Db 883 AAGCTCATGTGTGCTATGACCACTTCAACACCTTCTCAAGCTTACTTCTCAACCGTC 824

Qy 454 ATGAGCGTGAACCGGTACATTGCGTGTGCCACCCCGTGAAGGCTTTGAGCTTCGACAC 513

Db 823 ATGAGCGCGACCGCTTACTGTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 766

Qy 514 CCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 573

Db 765 GCGGACCTTACAGCG 707

Qy 574 TCTGCAATATGTCCTTTGAGGACCAAAAGTCAGGGAAGAGTGTATTAGTGTCTC 633

Db 706 GTCTGTGCTGCCCTTGTGCGAGTTCGCCCGCGCTGACGACGACGAGCGCGCGCGCG 647

Qy 634 TTGCAATTCACAGATGATGATCTCTGCTGTGGGACCTTGTATGAAGTGTGCGCTTC 693

Db 646 GTGTAGTCTTTCGCGACCGCGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 587

Qy 694 ATCTTGTGCTGTGATCTGTCTGTCTCTCATCATCATCTGTGTGTGTGTGTGTGTGTGT 753

Db 586 GTGCTGGGCTTGTGCGATCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 527

Qy 754 GGTCTCAAGAGCGTGTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 813

Db 526 CGGCTGATGTCATGCGGT 467

Qy 814 ATCACAAGATGCTGT 873

Db 466 GTGACCTTCTGT 407

Qy 874 ATATTCATTCCTGTGGAGGCTCTGGGAGACACTCTCCACAGACAGCTCTCTTCCAGC 933

Db 406 CTGACACCGT 347

Qy 934 TATTACTTGTGATCGCCTTTAGGCTATTAACAACAGTAGCTGAATCCATTCTTACGCT 993

Db 346 TCTTACTTATATACCAAGCCTGATGACGCAACAGCTGCTCAACCCCTCTCTACGCGC 287

Qy 994 TTTCTGTATGAAAACTTCAAGCGGTGTTCCG 1025

Db 286 TTCTGTGACGCCAGCTTCCGACGAACTCCG 255

RESULT 52
AM489031/c 433 bp mRNA linear EST 24-FEB-2000

LOCUS AM489031 UI-M-BH3-ssd-d-09-0-UI.81 NIH_BMAP_M_S4 Mus musculus cDNA clone

DEFINITION UI-M-BH3-ssd-d-09-0-UI 3', mRNA sequence.

ACCESSION AM489031

VERSION AM489031.1 GI:7059301

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 433)

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT

Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mwest@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=No.

FEATURES

Location/Qualifiers
 1..433
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH3-asd-g-09-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH BMAP M_S4"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP M_S4 library is a subtracted library of a series,
 ultimately derived from a mixture of individually tagged
 normalized libraries from ten regions of the mouse brain
 (cerebellum, brain stems, olfactory bulbs, hypothalamus,
 cortex, amygdala, basal ganglia, pineal gland, striatum,
 hippocampus) after a series of subtractions to reduce the
 representation of cDNAs from which ESTs had already been
 generated. The following serially subtracted libraries
 were generated in this process: NIH BMAP M_S4,
 NIH BMAP M_S3.3, NIH BMAP M_S3.2, NIH BMAP M_S3.1,
 NIH BMAP M_S2, NIH BMAP M_S1. The subtracted library
 (NIH BMAP M_S4) was constructed as follows: PCR amplified
 cDNA inserts from NIH BMAP M_S3.3, NIH BMAP M_S3.2, and
 NIH BMAP M_S3.1 clones from which 3' ESTs had been derived
 was used as a driver in a hybridization with a pool of
 the NIH BMAP M_S3.3, NIH BMAP M_S3.2, and NIH BMAP M_S3.1
 libraries in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library)
 was purified by hydroxyapatite column chromatography
 converted to double-stranded circles and electroporated
 into DH10B bacteria (Life Technologies) to generate the
 NIH BMAP M_S4 library. This procedure has been previously
 described (Bonaldi, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG_TISSUE=cerebellum
 TAG_LIB=NIH BMAP M_S4
 TAG_SEQ=CGGNA"

ORIGIN

Query Match 15.5%; Score 178.4; DB 10; Length 433;
 Best Local Similarity 68.5%; Pred. No. 3.2e-24;
 Matches 261; Conservative 0; Mismatches 117; Indels 3; Gaps 1;
 QY 557 CTCGCGGAGGACCTTCATGAAGATCGCTCTTATCTTTGCTTCGATCCTGT 716
 Db 399 CTGGACTGGAACACTGACCAAGATCTGGTCTCTCTTCCTTCGCGGCGCAT 340
 QY 717 CCTCATCATCATCGTCTGTACACACCTGATGATCGTCTCAAGAGCGTCCGCTCT 776
 Db 339 CCTCATCATCATCGGTCGTCTATGCGCTCACTGCGCTCGCGCAGCGTCTGCT 280

QY 777 TTCTGCTCCGAGAGAAAGATCGCACTGCGTAGATACACAGACTGCTCTGTGGT 836
 Db 279 GTCCCGTTCCAAAGAGAACCGACGCTCGCGGATCAGCGAGATGGTGTGGT 220
 QY 837 GGTGACATCTTCGTCGTGCTGAGATCCGATTCACATATTCATCCGTGGAGGCTCT 896
 Db 219 GGTGGGCGCCTTCGTGTGTCTGTGGGCGCCCATCAATCTTGTCTGTGAGAGCT 160
 QY 897 GGGG---AGCACTCCACAGACAGACTGCTCTCTCCAGCTATTACTTGTGATCGCTT 953
 Db 159 GGTGACATCAATCGGCGCGACCCACATGTGTGTGGCGCACATGACCTGTGAGGCT 100
 QY 954 AGGCTATTCACACAGTAGACCTGAATCCCATTTCTTAGCGCTTTTGTATGAAACTTCAA 1013
 Db 99 GGGCTACCGCAACAGACGCGCTCAACCGGTTCTTAGCGCTTCTGACGAGAACTTCAA 40
 QY 1014 GCGGTGTTCCGGGAGACTTCTG 1034
 Db 39 GCGCTGCTTCGCCAGCTCTG 19

RESULT 53
 BUE13017 741 bp mRNA linear EST 20-FEB-2003
 LOCUS UI-M-FR0-cbd-m-06-0-UI.k1 NIH BMAP_FRO Mus musculus cDNA clone
 DEFINITION UI-M-FR0-cbd-m-06-0-UI.5, mRNA sequence.
 ACCESSION BUE13017
 VERSION BUE13017.1 GI:23272232
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: rgabbs@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

Seq primer: pyx-5.

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="UI-M-FR0-cbd-m-06-0-UI"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH BMAP_FRO"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGACAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National

ORIGIN
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

Query Match 15.5%; Score 178.4; DB 13; Length 741;
Best Local Similarity 64.3%; Pred. No. 4e-24;
Matches 283; Conservative 0; Mismatches 156; Indels 1; Gaps 1;

QY 660 CTGGGCGGACCTCTTCATGAAATCGGCTTT-CATCTTGGCTTCGGATCCCTGTC 718
DB 42 CTATTGGGGCCCTGATTTGGCCATCTGCACTCTCTTTTCTTTCATCATCCGGCTTC 101
QY 719 TCATCATCTCGCTCTGCTACCGCTGATCTGCTGCTCAAGAGCGCTCGGCTCTTT 778
DB 102 TCATCATCTCTCTCTCTGCTACCGCTGATCTGCTGCTGCTGCTGCTGCTGCTTT 161
QY 779 CTGGCTCCCGAGAGAAAGATCCCACTGCTGAGATCAACAGACTGCTCTGCTGCTG 838
DB 162 CAGGCTCCCGAGAGAAAGACCGGAACCTGCGACGATCAACAGGCTGCTGCTGCTG 221
QY 839 TGGCAGCTCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
DB 222 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 281
QY 899 GAGAGACCTCCCAACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958
DB 282 GTGCTCAGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 341
QY 959 ATACCAACAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
DB 342 ATGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 401
QY 1019 GTTTCGGGACCTCTGCTTCCATGAGATGAGATGAGAGCGGACGCTGCTGCTG 1078
DB 402 GCTTGAAGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
QY 1079 TCCGAATTCAGTTCAGAT 1098
DB 462 TCCGACGCTTCCCAAGAT 481

RESULT 54
B1753905 720 bp mRNA linear EST 25-SEP-2001
LOCUS 603022907P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193768 5',
DEFINITION mRNA sequence.
ACCESSION B1753905
VERSION B1753905.1 GI:15745483
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 720)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgapbs-r@mail.nih.gov
JOURNAL Tissue Procurement: Life Technologies, Inc.
COMMENT cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1484 row: m column: 01
High quality sequence stop: 716.
Location/Qualifiers

FEATURES
Source
1..720
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:5193768"
/lab_host="DH10B"
/clone_id="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 15.4%; Score 177.8; DB 12; Length 720;
Best Local Similarity 56.0%; Pred. No. 5.1e-24;
Matches 378; Conservative 0; Mismatches 292; Indels 5; Gaps 2;

QY 166 CCGGCGCATCCGGCTATCATCAAGGCGCTACTCCGATGCTGCTGCTGCTGCTGCTG 225
DB 49 CAGGCGAGCGCCATCTGATCTCTTCACTCACTCCGCTGCTGCTGCTGCTGCTGCTG 108
QY 226 GCGAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
DB 109 GGGAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
QY 286 ATTTAATATTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
DB 169 ATCTACATCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
QY 346 AGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 405
DB 229 GTACCTTCACCTTCTTGGCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 406 TCCATTTGATTTACATGATTTTCAACAGATCTTCACTTCACTTCACTTCACTTCA 465
DB 289 AGCGTGAAGCGGCTGATGATTTTCAACAGATCTTCACTTCACTTCACTTCACTT 348
QY 466 CGCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525
DB 349 CGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408
QY 526 AAGATCATCATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
DB 409 AAGGTAGTAACCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
QY 586 CTGAGGACCAACCAAGTACAGGAGACGCTGATGCTGATGATGATGATGATGATG 645
DB 469 TTCTCTGCAACCGCGGCAACGACGACGACGACGACGACGACGACGACGACGACG 525
QY 646 GATGATGACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
DB 526 GAGCCCGCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
QY 706 GTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
DB 586 CTG--CCCCGGGGGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643
QY 766 GTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825
DB 644 GTGGGCTCTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
QY 826 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 704 GTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718

RESULT 55
BX843850 828 bp mRNA linear EST 11-DEC-2003
LOCUS BX843850
DEFINITION BX843850 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:9981410117
ACCESSION ; IMAGE:4404805 5', mRNA sequence.
BX843850

VERSION BX843850.1 GI:39734073
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 828)
REFERENCE Hell, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
Schoth, A., Korn, B. and Landgrebe, J.
Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAG0998C1410117.
RZPDLIB: I.M.A.G.E. CDNA Clone Collection (amp- resistant) (RZPDLIB
No.988) http://www.rzpd.de/cgi-
bin/products/showlib.pl.cgi/response?libNo=998 RZPDLIB: Xenopus
laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
bin/products/showlib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heidenweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD.
contact RZPD (clone@rzpd.de) for further information. Seq primer:
SP6, 5' ATTTAGGTACACTAGG 3'.
FEATURES
source
1..828
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAG0998C1410117 ; IMAGE:4404805"
/tissue_type="embryo, stage 17/19"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Emb2"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 2.1 kb. Constructed by Life Technologies."

ORIGIN
Query Match 15.3%; Score 176; DB 13; Length 828;
Best Local Similarity 71.0%; Pred. No. 1,2e-23;
Matches 247; Conservative 0; Mismatches 100; Indels 1; Gaps 1;

253 ATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTTACCTGGCTTTGCA 312
DB ACCAGATACACCAAGATGAGACAGCAACCAATTTACATTTTACCTGGCTTTGCT 528
313 GATGCTTAACTTACACCAATGCTTTCAGAGTACGTTACTTGTATGTAATTCCTGG 372
DB GATGCTTAACTTACACCAATGCTTTCAGAGTACGTTACTTGTATGTAATTCCTGG 588
373 CCTTTGGGGAGATGCTGTCGCAAGATGTAATTTACATTTTACATTAACATGTTACC 432
DB CCTTTGGGGAGATGCTGTCGCAAGATGCTTACGATTAAGTCTTACATGTTTACC 648
433 AGCATCTTACCTTACCATGATGAGCGTGAACCGCTACATTCGCGTGCACCCCGTG 492
DB AGTATTTTACACATGATGAGCGTGAACCGCTACATTCGCGTGAATGTCACCTATA 708
493 AAGGCTTGGAGCTTCGACACCTTTGAAGG-AAAATCATCAATATTCGATCTGGCT 551
DB CGAGACACTGGAATTTGGAATCCCTTAAGGCTAAAGTTAATTAATGCTGATTTGAT 768
552 GCTGTCGATCTGTTGGCATCTGCAATAGTCCCTTGGAGGACACAA 599
DB CTTGCTTCTGCGATTTGGGTTCAATTAATGTTTAATGGAGTAACAA 816

RESULT 56

CNSLTIIBD
LOCUS 1307 bp mRNA linear HTC 18-JUN-2003
DEFINITION human full-length cDNA 5-PRIME end of clone CS0DK011YG11 of Hela
cells of Homo sapiens (human).
ACCESSION BX248780
VERSION BX248780.1 GI:28375508
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1307)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1307)
Genoscope.
Direct Submission
Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1..1307
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK011YG11"
/tissue_type="Hela Cells"
/note="end : 5-PRIME-Cot 25-normalized-vector pCMVSPORT_6"
332..661
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD66587.1"
/db_xref="GI:28375509"
/translation="MAVPCGAPTSWPLSTVACARAPRSCLQSPGNMAVAPAGAR
SRAPSGCALPGAGRLMAAGKRSGBGRRRRVREKAPALAPLPLSWDVPQMR
LISFLSLs"
CDS
ORIGIN
Query Match 14.9%; Score 171.6; DB 11; Length 1307;
Best Local Similarity 57.1%; Pred. No. 1e-22;
Matches 312; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

75 CAGCAGCGCGTGTTCCTCCGCTGGGCGGAGCCGACAGCAACGACCGCGGCTCGGA 134
DB CGCGCGCAGCAGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAA 748
135 GGAAGCGGAGCTGAGCGCGCGGACATCTCCCGCGCATCCCGGTCATCATCGAGGCT 194
DB TCGCTCCAGACGGAGCTTGAAGCGAGGCGCAGGCGCAGCGCATCTGATCTTTTCAT 808
749 TCGCTCCAGACGGAGCTTGAAGCGAGGCGCAGGCGCAGCGCATCTGATCTTTTCAT 808
195 CTACTCCGTAAGTGTGTCGTGCGGCTTGTGGGCACTCGCTGTCATGTTGATCAT 254
DB CTACTCCGTAAGTGTGTCGTGCGGCTTGTGGGCACTCGCTGTCATGTTGATCAT 254
809 CTACTCCGTAAGTGTGTCGTGCGGCTTGTGGGCACTCGCTGTCATGTTGATCAT 868
255 CGATACCAAAAGATGAAAGACGACGACCAACATTTTACATTTTAACTGCGCTTTGGCAGA 314
DB GCGGTATGCGCAAGATGAAAGACGCGCACCAACATTTTAACTGCGCGCATTTGCGA 928
869 GCGGTATGCGCAAGATGAAAGACGCGCACCAACATTTTAACTGCGCGCATTTGCGA 928
315 TGCTTTAGTTTCTCAACCATGCTTTCAGAGTACGCTACTTGTGATGTAATTCCTGGCC 374
DB TGAAGTGTATGCTCAGCGTGCCTTCTAGTACCTCCACGTTGTTGGCCACTGGCC 988
375 TTTTGGGAGATGCTGTCGCAAGATGTAATTTCCATGATTTACTTACCAACATGTTCCACG 434

QY 265 AGATGAAGACAGACCAACCAATTACATATTTAACTGGCTTTGGCAGATGCTTAGTT 324
 Db 205 CGCATTAAGACTCTACCAACCTGTTCAATCTCAACCTGCTATCCCGATAGACTCTTC 264
 QY 325 ACTACAAACATGCGCTTTGAGTAAGCTCTACTTGATGAATTCCTGACCTTTTGGGAT 384
 Db 265 ACCCTGCTGCTGCCCATCAACATCGCGACTTCCTGCTAGAGGCGCTGGCCTTCGGGAG 324
 QY 385 GTGCTGTGAAGATATATTTTTCATTTGATTAATAATATGTTACACGACATCTTAC 444
 Db 325 GTCATGTGAAGTCAATGTAGCCGTGACAGTAAACATTTCTTATGCTTCACTTC 384
 QY 445 TTGACCATGATGACGTGACCGCTACATTCGCTGTCACACCCGCTGAAGCTTTGAC 504
 Db 385 CTGCGCTATGAGCGCCGACCGATACCTGGTGTTCCTGACACAGAGTCCGCGCG 444
 QY 505 TTCCGACACCTTTGAAGCAAAAGATCAATCAATATCTGATCTGCTGTCTGATCT 564
 Db 445 GTGTCCGGCGACATTAACGTACAGCGCGTCTGTCAAGTCTGAGGCTGGCGCTGG 504
 QY 565 GTTGGATCTGCAATATCTCTTGAAGGACCAAGTACAGGAAGACCTGATGAT 624
 Db 505 AGCGTGTGTGCTGCTCTTTCGCTATTCGCTGACGAGAGAGAGGCTGCGCG 564
 QY 625 GAGTGTCTCTGACATTCAGATGATGACTACTCTGCTGAGGACCTCTTCAAGAATC 684
 Db 565 CAGTGTGTGTGTCTTCCGACGCCGAGGCTTCTGTG---GTGCGACCGCTCTC 621
 QY 685 TGGCTTCTATCTTGGCTTGTGATCTCTGCTCATCATCATCTGTCTGTACACCTG 744
 Db 622 TACACATGATATGAGGCTTTGCTCCATCCGCTGACACCATCTGCTCTATACACT 681
 QY 745 ATGATCTGTGCTCAAGAGCGTCCGCTCTTCTGCTCTCCGAGAGAAATGCGAC 804
 Db 682 CTGCTCTGCGACTGCTGCTATCCAGCTGATAGGACGACGCAAGCGCTGATGCTGC 741
 QY 805 CTGCTGATGATCAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
 Db 742 AAGAAAGCGGTGACCTTGTGTGAGGAGATCTGCTGTGTGCTGCTGCTGCTGCTGCT 801
 QY 865 CCCATTCATATTTATCTGCTGAGAGCTCTGAGGAGACCTCCACAGCAGCTGCT 924
 Db 802 CTTATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
 QY 925 CTCTCAGTATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 984
 Db 862 ATGCGATCTCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT 921
 QY 985 CTCTACGCTTCTTATGATGATAAATTCAAGCGGTGTTCCGGGACTT 1031
 Db 922 CTCTATGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968

 RESULT 59
 AY400986 1095 bp DNA linear GSS 15-DEC-2003
 LOCUS Homo sapiens SSTR5 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY400986
 VERSION AY400986.1 GI:39756975
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1095)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene titles

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1095)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source location/Qualifiers
 1..1095
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>1095
 /gene="SSTR5"
 /locus_tag="HCM0740"

 ORIGIN
 Query Match 14.6%; Score 169; DB 29; Length 1095;
 Best Local Similarity 52.1%; Pred. No. 3.1e-22;
 Matches 463; Conservative 0; Mismatches 405; Indels 21; Gaps 3;

 QY 140 CGCAGCTGAGGCCCGGCGACATCTCCCGGATCCCGGTCATCATCAGCGGCTTACT 199
 Db 83 CGCTGTGGGCGCGCGCGCTTCCGAGAGGCGCGGCGGTGTGTGCTGCTGCTGAC 142
 QY 200 CCGATGT 259
 Db 143 TGT 202
 QY 260 ACACAAAGATGAGACAGCAACCAATTATCATATTTAACTGCTTTGGCAGATCCT 319
 Db 203 TCGCAAGATGAGAACCGTCAACCAATCTCAATCTCAACCTGCGACGACCTCC 262
 QY 320 TAGTATCAACAACATCCCTTTCAGAGTACGCTCTGATGAAATCTCGGCTTTG 379
 Db 263 TGTATGT 322
 QY 380 GGGATGT 439
 Db 323 GCCCGTCTGT 382
 QY 440 TCACCTTGCATGATGAGGTGAGCCGCTACATGCTGCTGTGCAACCCGTAAGGCTT 499
 Db 383 TGTGCTGACAGTATGAGGTGAGCCGCTACCTGCGAGGTGTGCAACCCGTAAGGCTT 442
 QY 500 TGAAGTCCGCAACCTTGAAGGCAAGATCAATATCTGATGTGCTGTGCT 559
 Db 443 CCGCTGTGCGCGCGCGCGGTGTGCAAGCTGTGCAAGCGCGCGCGCTGTGCTGCTGCTG 498
 QY 560 CATCTGTGTGCTCTGCAATAGTCTTGTGAGGACCAAGTCAAGGAGAGAGTGTGATG 619
 Db 499 --TCTGTGATGATGTGCTGCGCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 556
 QY 620 TCATTGATGTCTCTTGCAGTTCACAGATGATGACTACTCTGCTGTGAGACTTCTATGA 679
 Db 557 GCAACGCAACCTGAGCCGAGACCCGTGGGCT-----GTGGGGGCGCGTCTTCA 604
 QY 680 AGATCTGCGCTTCAATCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
 Db 605 TCATTCAACAGCGCGGT 664
 QY 740 CCGTGTGATCTGCGCTCTCAAGAGGCTCGGCTCTCTTCTGTGCTCCGAGAGAAAGATC 799
 Db 665 TGT 721
 QY 800 GCAACCTGTGAGATCAACGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 859
 Db 722 GCTGTGAGCGGAAGTGAACGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 781

QY 860 GGATCCCATTCATATTCATCTGAGAGCTCTGGGAGACACCTCCACAGACAG 919
 DB 782 GGCTGCCCCCTTTCACACCGTCATCTCAACCTGGCCGTGGCCGCCACAGACCCG 841
 QY 930 CTGCTCTCTCAGACTATTAATCTTCTGCATGCGCTTACGCTATACCAACAGTAGCTGATTC 979
 DB 842 CCGCCGCGGGCCCTTACTTCTTGCTGTATCTCTTACGCAACAGCTGTGGCAAC 901
 QY 980 CCATCTCTACGCGCTTCTTGATGAAACTTCAGGCGGTCTTCCGGGA 1028
 DB 902 CCGCTCTACGCGCTTCTCTGACACTTCGCGCAGACTTCCAGAA 950

RESULT 60
 BI919235 627 bp mRNA linear EST 17-OCT-2001
 LOCUS 603181578F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245602 5',
 DEFINITION mRNA sequence.
 ACCESSION BI919235
 VERSION BI919235.1 GI:16200355
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 627)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: cgsapb@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Place: LBNL1619 row: 1 column: 19
 High quality sequence start: 4
 High quality sequence stop: 624.
 Location/Qualifiers
 1.627
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5245602"
 /lab_host="DH10B"
 /clone_11b="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 14.6%; Score 168.4; DB 12; Length 627;
 Best Local Similarity 71.0%; Pred. No. 3.2e-22;
 Matches 237; Conservative 0; Mismatches 96; Indels 1; Gaps 1;

QY 153 GCGGACATCTCCCGGACATCCGGTCTATCAACGCGGCTACTCCGTAGTGTGCT 212
 DB 295 GCGCTTCTCCCTCGGCTCAAGGTACCAATCGGGGCTCTACCTGGCCGTGTGT 354
 QY 213 CGTGGCGTTGTGGCACTCGCTGTCTATGTTCTGATCATCCGATACCAAGATGA 272
 DB 355 CGGAGGCGCTCTGGGGAATGCGCTTGTATGTACGTCATCTCAGGCAACCAATGA 414

QY 273 GACAGAACCAATTTACATTTTAACTGGCTTGGAGATGCTTGTACTACAC 332
 DB 415 GACAGCAACCAATTTTACATTTTAACTGGCTTGGAGATGCTTGTACTACAC 473
 QY 333 CATGCCCTTTCAGAGTACGCTTACTGTATGTAATTCCTGGCCCTTTGGGATGTGTG 392
 DB 474 GCTGCGCTTTCAGAGGCAAGACATCTCCTGGGCTTCTGGCCGTTGGAAATGGCTGTG 533
 QY 393 CAAGATGATTAATTTCCATTGATTACTACAAATGTTTACACAGACATCTTACCTTACCT 452
 DB 534 CAAGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
 QY 453 GATGAGCGTGAACGCTCATTTGCGGTGGCCAC 486
 DB 594 CATGATGTGATCGCTATGTAGCATCTGCAAC 627

RESULT 61
 R81583 183 bp mRNA linear EST 12-JUN-1995
 LOCUS YJ04b04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
 DEFINITION IMAGE:147727 5' similar to gb:U25119 MU-TYR OPIOID RECEPTOR
 (HUMAN);, mRNA sequence.
 ACCESSION R81583
 VERSION R81583.1 GI:858186
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 183)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
 Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

TITLE The Washu-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

Insert Size: 1518
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Insert length: 1518 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 1.
 Location/Qualifiers
 1.183
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:559413"
 /db_xref="taxon:9606"
 /clone="IMAGE:147727"
 /sex="female"
 /dev_stage="placenta obtained at birth (full term)"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_11b="Soares placenta Nb2HP"
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 modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACTGGAAGAATTCGCGCGCAGCAATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRTT3 vector. Library

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ORIGIN

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Best Local Similarity 53.2%; Pred. No. 1.7e-21;
Matches 410; Conservative 0; Mismatches 340; Indels 21; Gaps 2;

QY 256 CGATACACAAAGATGAAGACAGACCAACATTATTAACCTGGCTTTGGCAGAT 315
DB 2 CGCTATGCCAAGATGAAGACAGACCAACATCTACTACTCACTGGCCGCGCGCAT 61
QY 316 GCTTATGTTACTACCAACATGCCCTTTCAAGAGTACGGCTTACTGTAATTCCTGGCCT 375
DB 62 GAGCTCTTCATCTCAGCGCTGCCATTCTGTGGCCTCGCGCGCTGCCCTGGCAGACTGGCGG 121
QY 376 TTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACTGTTCCACGAC 435
DB 122 TTCCGGGGCGGTGCTGTGTGCGCGAGTCTTAGCGTGAGACGGCCTGAAACATGTTCACTACT 181
QY 436 ATCTTCACCTTGACCATGATGAGCGGTGACCGCTACATTCGGGTGCGCACCCCGTGAAG 495
DB 182 GTCTTCTGTCTACCGTGTCTGACGCTGACCGCTATGCTGTGTGTGACACCTCTGCGCG 241
QY 486 GCTTTGACCTCCGACACCTTTGAAAGCAAGATCATATATCTGCATCTGGCTGCTG 555
DB 242 GCCGCGACCTACCGCGCGCGCCAGCGGTGCGCAAGCTAATCACTGGAGATGTGGCTAGCA 301
QY 556 TGTGATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAAATGACGGAAGACGTC 615
DB 302 TCTTGTGCTGTACACCTGCCCATTCGACATCTTGTGCTGACACAGCGCAGCTCGTGGGGGC 361
QY 616 GATGTCAATGAGTGTCTCTTGCAGATTCACAGATGATGATCTCTGTGTGGACCTCTTC 675
DB 362 GAGGCGGTGTGCTGCAACCTGCACTGGCTCACCGGCTGTGTGTGGG-----TC 412
QY 676 ATGAAGATCTGCGCTCTTCATCTTGTGCTGTGTGATCTCGTCTCTCATCATCATCTGCTGC 735
DB 413 TTTGATCTATATCTTTTGTGTGGGCTTCTACTCCGCTTCTGGCCATCGGATATATGC 472
QY 736 TACACCTTGATATCTCTGCTCTCAAGAGCTCCGGCTCTTTTGGCTCCCGAAGAA 795
DB 473 TACCTGTATATGTGTGGCAAGATGCGCGCTGTGGCCCTGCGGCTGGCAACAAACG 532
QY 796 GATCGCAACCTGCTGATGATCAACAGACTGTGCTGTGGTGTGAGCTTTCCGTCGTC 855
DB 533 AGGCGCTGAGAAAGATGATCACTAGGCTGTGCTATATGTGTGACCGCTTTTGTGCTA 592
QY 856 TGTGTGACTCCCATTCACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAACG 915
DB 593 TGTGTGATGCTGCTGTATGTGTGACGCTTCTGAACCTGTTGTGACAGCTCCGATGTC 652
QY 916 AAGAGTGTCTCTCCAGCTATTAATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 975
DB 653 ACTGT-----CAACCATGTGTCTCTCATCTGAGCTATGCTCAACAGCTGTGTC 700
QY 976 AATCCCATCTCTACGCGCTTTCTGTGATGAACCTTCAACGCGGTGTTTCCG 1026
DB 701 AATCCCATCTCTATGTGCTTCTCTGTGCAACCTTCCGCGCTCTTTCCAG 751

RESULT 64
BX280512 502 bp mRNA linear EST 04-MAR-2003
LOCUS BX280512 NIH_MGC_114 Homo sapiens cDNA clone IMAGE998M0111484 ;
DEFINITION IMAGE:5193768, mRNA sequence.
ACCESSION BX280512
VERSION BX280512.1 GI:28613890
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 502)

AUTHORS

Ebert,U., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radloff,U., Schneider,D. and Korn,B.

TITLE

Human Unigeneset - RZPD3

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE998M0111484.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/cloncards/cgi-

bin/showLib.pl.cgi/respone?libNo=972 Contact: Ina Rolfs
bin/showLib.pl.cgi/respone?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101
Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: GGTGTAAACAGACGCGCAGT.

Location/Qualifiers

FEATURES

source

1..502

/organism="Homo sapiens"

/mol_type="mRNA"

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/lab_host="DH10B"

/clone_lib="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC library."

ORIGIN

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Best Local Similarity 59.0%; Pred. No. 2.1e-21;
Matches 281; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 140 CGCAGCTGAGCCCGGACATCTCCCGGCGCATCCGGTCAATCATCAGCGGCTTACT 199
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QY 200 CCGTATGTTCTGTGCGGCTTGTGTGGCACTCGGTGTGATGTTGTGTGATTCAGAT 259
DB 85 CCGTGTGTGCTGTGTGGGCTGTGTGGAACTTATGTGTATCTATCGTATCTTGGCT 144
QY 260 AACAAAGATGAAGACAGAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 319
DB 145 ATGCCAAGATGAAGACGCGCACCAATCTAATCTTAATCTGAGCATTTGAGTAGAC 204
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DB 265 GTGCGCTGTGTGCGGCTCGTGTCTACGCTGGAAGCGGCTCAACATGTTTCAACAGCATCT 324
QY 440 TCACTTGAACCATGATGAGCGGTGACCGCTTAATGTCCTGTGCGACCCCGTGAAGGCTT 499
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QY 500 TGAAGCTCCGACACCCCTTTGAAGCAAGATCATCAATATCTGCAATCTGGCTGTGCT 559

Db	385	CCCGCTACCGCGCGGCCACCCTGGGCCCAAGGTAAACTCTGGCGGTGTGGTCTATCCG	444
Qy	560	CATCTGTGGCATCTCTGTGAATATGCTCTTGGAGGACCAAAATCAGAGAAACGTC	615
Db	445	TGCTGTCATCTCGCCCATCGTGATGTCTTCTCTCGACCGCGGCCAACAGGACGCG	500
RESULT 65			
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LOCUS	AY400332	1257 bp	DNA linear GSS 15-DEC-2000
DEFINITION	AY400332		Human sapiens SSTR3 gene, VIRUTUAL TRANSCRIPT, partial sequence,
ACCESSION	AY400332		genomic survey sequence.
VERSION	AY400332.1	GI:39756321	
KEYWORDS	GSS		
SOURCE	Human sapiens (human)		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1257)		
	Clark,A.G., Gnanowsk,S., Nielson,R., Thomas,P., Kejaritwal,A.,		
	Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,		
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,		
	Adams,M.D. and Cargill,M.		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1257)		
AUTHORS	Clark,A.G., Gnanowsk,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.		
	Direct Submission		
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
TITLE	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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	Matches	436; Conservative	0; Mismatches 403; Indels 12; Gaps 2
Qy	178	GTCATCATCAGCGCGGTCTACTCCCTAGTGTTCGTCGAGGCTTGTGGGCAATCGCTG	237
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Qy	238	GTCATGTTCCGATCATCTCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATT	297
Db	193	GTCATCTATGTGTCTCGCGGACACCGGACGCCCTTTAGTCACCAAGTCTTACATCTTC	252
Qy	298	AACCTGGCTTTGGAGAGATGCTTATGTTACTCAACCATGACCCCTTTACAGATACGGTAC	357
Db	253	AACTGGCGCTGGCGGACGAGACTCTTACATGCTGTGGGCTGCTCTTCTGTGGCCGACAAAC	312
Qy	358	TTGATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTATTTCATTGATTAAC	417
Db	313	GCCCTGTCTTAATGACCTTCCTGGCTCCCTCATGTGCGCGCTGTTCATGCGATGGATGGC	372
Qy	418	TACAACATGTTTACACAGCATCTTACACCTTGACCAATGATGAGCGTGAACCGCTACATTGCC	477
Db	373	ATCAACAGTTTACACAGATATTTTGTGCTGTACTGTATGAGACGTGACCGCTTACCTGTGCC	432
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[illegible]

source

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/notes="Vector: pDNR-Dual; Site_1: loxp-Sall; Site_2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      14.0%; Score 162; DB 14; Length 798;
Best Local Similarity 54.1%; Pred. No. 6.1e-21;
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DB 766 ATCTGAACCTGGCAGCTGACGACGGGCTCTTCAAGCTGTACGCTCTCAACATGCGGA 707
QY 354 CTACTTGATGATTCCTGGCTTTTGGGATGTGCTGTCAGATAGTAAATTTCAATTA 413
DB 706 GCACCTGCTGCACTACTGCGCTTTGGGAGAGCTGCTCTGCAAGCTGCTGCGGCTGCA 647
QY 414 TTACTACAACATGTTTCAACAGCATTTTCACTTGAACATGATGAGCGGTGACCTACAT 473
DB 646 CCATACAAACATCTTCTCCAGCATCTACTTCCAGCCGATGAGGTGAGCCGATACCT 587
QY 474 TGCCGTGACCAACCCCGTGAAGC-----TTTGACTTCGGCAACACCTTGAAGCAAA 527
DB 586 GGTGTGTGTGGCCACCGTGAAGGTCCGCAATGCGCTTGGCCGACCTTACCGGGGCGGA 527
QY 528 GATCATCAATATCTGCATCTGCTGTGCTGATCTGTGTGGCATCTCTGCAATAGTCT 587
DB 526 GGTGCCAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 467
QY 588 TGGAGGCAACCAAGTCAAGGAAAGAGTGCATGTGATGATGCTCCTTGCAGTTCACGA 647
DB 466 CGCTGGCGGTCA--CAGCAACGAGGTGAGTCCCAAGCTGTGGGCTGAGCTTCCCGG 410
QY 648 TGATGACTACTCTGTGTGGAACCTCTTCAATGAAGATTCGCGTTCATTTTGGCTTGT 707
DB 409 GCCCAGAGAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 353
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DB 232 CTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 173
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DB 172 GGCCTGACACGAGACTGCGCCAGACCCCACTGTGTCATCAATGTCTTACATCATC 113
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DB 112 CAGCCTCAGCTTACGCAACTGCTGCTGCAACCCCTTCTCTTACGCTTTCTGATGACA 53
QY 1008 CTTCAAGCGGTGTTCG 1025
DB 52 CTTCCGGAAGAACTTCCG 35

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LOCUS
DEFINITION
Mus musculus SSTR5 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION
AY400988
VERSION
AY400988.1 GI:39756977
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1089)
Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
TITLE
2 (bases 1 to 1089)
Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
COMMENT
FEATURES
source
location/Qualifiers
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Best Local Similarity 50.4%; Pred. No. 9e-21;
Matches 458; Conservative 0; Mismatches 436; Indels 15; Gaps 2;

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QY 120 CAGCGCGGCTTGAAGAGCGGACGTGAGCCCGGCAATCTCCCGGCAATCCCGGT 179
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QY 180 CATCATCAACGCGGTCTACTCGGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 239
DB 114 ATTAAGTCTGTGTCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 173
QY 240 CATGTTCGTGATCATCCATACCAAGATGAAGACAGCAACCAATTTAATTTA 299
DB 174 CATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 233
QY 300 CTTGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCTTTGAGAGTGTCTACTT 359
DB 234 CTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 293
QY 360 GATGAATTCCTGCGCTTTTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 419

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QY	660	CTGTGTGGAGACTCTTTCATGAAAGATCTGGGCTTCATCTTGGCTTCGATACCTGTGCT	719
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QY	840	GGCAGTCTTCGTGCTGTGCTGAGTCCCATTCACATATTCCTGTGTGAGAGGCTCTGGG	899
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Db	819	CACGTCATCCCGAGGAGCCACCTCTGCGGCTCTCACTTCTTGTGTGTCTGTCTT	878
QY	960	TACCAACAGTAGCTGAATCCCATCTCTACGCCCTTCTGTATGAAACTTCAAGCGGG	1011
Db	879	TGCCAATAGCTGTGCCAACCCCTGCTCTATGAGCTTTCTCTGTGATTACTTCCGCAAG	938
QY	1020	TTTTCCGGGA 1028	
Db	939	TTTTCCGGGA 947	
RESULT 68			
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LOCUS	BB631900	714 bp	mRNA linear EST 26-OCT-2001
DEFINITION	BB631900	musculus cDNA clone A230051A20 5', mRNA sequence.	
ACCESSION	BB631900		
VERSION	BB631900.1	GI:16468581	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (baes 1 to 714)		
AUTHORS	Arakawa, T., Carinci, P., Fukuda, S., Furuno, M., Hanaigaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, T., Komuro, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, Y., Tanaka, T., Toyata, T., Muramatsu, M. and Hayashizaki, Y.		
TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute		

The Institute of Physiscal and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
url: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagai, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuru, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Komdo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

Source

location/Qualifiers
1..714
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/clone_1fb="RIKEN full-length enriched, adult male hypothalamus"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 5' GAGGAGAGAGAGATCCAAAGCTCTTTTCTTTTCTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and trehalose enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGGAGAGAGATCTCCAGTTAATTAATTAATTCCTCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda

ORIGIN

Query Match	13.9%	Score 160	DB 10	Length 714
Best Local Similarity	65.8%	Prod No. 1.4e-20		
Matches 229	Conservative 0	Mismatches 119	Indels 0	Gaps 0
QY	154	GGCGACATCTCCCGGCAATCCGGATCATCATCGAGCGAGTCTACTCCGTAAGTTTCGTC	213	
Db	296	GCCTTCCTCGCCCTTGGACTCAAGTCATCCATCGTGGGGCTCTACTTGGCTGTGGCATC	357	
QY	214	GTGGGCTTGTGGGCAATCGCTGTCATTTGATATCATCGATACCAAMGATGAAG	273	
Db	358	GGGGGGGCTCTGGGGGAATCGCTGTCATTTATATGATCATCTTCAAGGACACCAAGTTGAG	417	

Query Match	13.8%	Score 159.4	DB: 10	Length 550
Best Local Similarity	71.0%	Pred. No. 1.7e-20		
Matches 211	Conservative 0	Mismatches 86	Indels 0	Gaps 0

Oy	153	CGCGACATCTCCCGCCATCCCGGTATCATACGCGGAGTCTTACTCCGAGTGTCTGT	212
Ob	253	CGCCTTCTGCCCCCTCGGGCTCAAGTCAACATCGTGGGCGCTTCACTTGGCAGTGTGTGT	312

Query Match	Similarity	Score	DB	Length
Best Local	47.5%	159.4	29	987
Matches	414	0	Mismatches	455
			Indels	3
			Gaps	2
OY	154	GGCGACATCTCCCGGCGCATCCGGTACATCAAGCGGATCTTACCCGATGTTGCTC	213	
DB	88	GGCGCGCTGCGGGCGCGCGCTGGCGGTGACCAATTTGTTACGCGGTATCTCGGCC	147	
OY	214	GTGGGCTTGTGGGCACTCGCTGTCTATGTTGATCATCCGATACAAAGATGAAG	273	
DB	148	GTGGGCTTGTGGGGAACCTCGCGGTGTAACGTTGTCGCGGCGCGCGCATGAAG	207	
OY	274	ACAGCAACCAACATTTACATATTTAACTCGCTTTGGCAGATGCTTTAGTTACTACACC	333	
DB	208	ACCGTACCAACCTGTTTCATCTTCAACTGGCGCATCGCGAGANNCTTTCACNCTGATG	267	

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QY 334 ATGCCCTTCAAGTACGGCTACTTGATGAATTCCTGGCTTTGGGATGNGCTGCG 393
    |||||
Db 268 CTGCCCATCAACATGCCCACTTCTGCTGGCACTGGCCCTTCGGGGAGCTCATGTGC 327
QY 394 AAGATGATATTTTCATTTGATTAATAAACAATGTTGACAGACATCTTCACTTGACCATG 453
    |||||
Db 328 AAGCTCATGTGGCTATGACAGTACAAACACTTCTCCAGCCTCACTTCTCAACCGTC 387
QY 454 ATGAGGTGAGACCGCTACATGCGGTGTGCACCCGTTGAGGCTTTGACCTTCCGACAG 513
    |||||
Db 388 ATGAGGCGGACCGCTACCTGG--TGTGTCTGGCTCACTGGGAGTGCAGCGGCTGGCGG 445
QY 514 CCTTGAAGGCAAAAGATCATCAATATCTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 573
    |||||
Db 446 GCGGACCTACACAGCGCGCGCGCGGTAGAGCTGGCCG-TGTGGGGAGTCTCACATTC 504
QY 574 TCTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAGAGAGCTGATGTCAATTGAGTGTCC 633
    |||||
Db 505 GTGTGTGCTGCTTGTGCACTTCTGCGCGGCTAGAGAGAGAGAGCGCGGCGCAGTGC 564
QY 634 TTGCAATTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
    |||||
Db 565 GTGCTAGTCTTTCGCGAGCGCCGAGGCTTCTGTGTGGCGCGAGCANNNTCTACACGCTTC 624
QY 694 ATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
    |||||
Db 625 GTCTGTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 754 GCTCTCAAGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
    |||||
Db 685 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 814 ATCACCAAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
    |||||
Db 745 GTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
QY 874 ATATTTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
    |||||
Db 805 NNAGACACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 864
QY 934 TATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
    |||||
Db 865 TCCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 924
QY 994 TTTCTTGATGAATACTTCAAGCGGTGTTCCG 1025
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Db 925 TTCTGTGAGCGCAGCTTCCGAGAACTCCG 956

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RESULT 71
BU18522 768 bp mRNA linear EST 28-NOV-2002
LOCUS 603855068p1 CSECHN62 Gallus gallus cDNA clone CHEST857h18 5', mRNA
DEFINITION
sequence.
ACCESSION BU18522
VERSION BU18522.1 GI:25826523
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 768)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
2235534
MEDLINE 12445392
PUBMED

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REFERENCE
AUTHORS
CONTACT: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology

```

(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 768
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST857h18"
/dev_stage="36"
/lab_host="DH10B"
/clone_id="CSECHN62"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 13.8%; Score 159.2; DB 13; Length 768;
Best Local Similarity 65.4%; Pred. No. 2.1e-20;
Matches 233; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 202 GTAGTGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
    |||||
Db 1 GTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 262 ACAAGATGAAGACAGACCAACATTTACATTTAACTGGCTTGGAGATGCTTTA 321
    |||||
Db 61 GCCAAGATGAAGAGGCGCACMACATCTTAACTTGGCATTTGGCGAGAGACTG 120
QY 322 GTTACTCAACCAATGCCCTTTCAGAGTACGGTCACTTGAATTCCTGAGCTTTGGG 381
    |||||
Db 121 CTATGCTTACGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 382 GATGTGCTGTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 441
    |||||
Db 181 TCTCTGCTGTGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 442 ACCTTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 501
    |||||
Db 241 TGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 502 GACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGATCTGCTGCTGCTGCTGCTG 557
    |||||
Db 301 AGTATCCGCGCGGCCACCGTGGCTAAGATGTCACTCGGTGTGTGTGTGTGTGTGTGTGT 356

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RESULT 72
CD559491/c 795 bp mRNA linear EST 19-NOV-2003
LOCUS
DEFINITION
IMAGE:6971827 5', mRNA sequence.
ACCESSION CD559491
VERSION CD559491.2 GI:38453539
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 795)

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585559.
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: IRBK2 row: d column: 06
High quality sequence start: 5
High quality sequence stop: 728.
Location/Qualifiers

FEATURES
SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971827"
/tissue_type="mixed"
/lab_host="DH5A (TI phage-resistant)"
/clone_lib="NIH_MGC_195"
/notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match      13.8%; Score 158.8; DB 14; Length 795;
Best Local Similarity 54.8%; Pred. No. 2.5e-20;
Matches 382; Conservative 0; Mismatches 303; Indels 12; Gaps 3;

QY 335 TGCCTTTGAGAGTACGCTCTACTGATGATCTCTGAGCTTTTGGGAGTGTCTGTGCA 394
DB 725 TCCCGATCAACATCCGAGAGACCTGCTCAGACTAGCGCCCTTCGGGAGTGTCTGTGCA 666
QY 335 AGATAGTAAATTTCCATTGATTTACTAATAATGTTCACCGAGCATCTTACCTTGACCATGA 454
DB 665 AACTGCTGTGGCCGCTGACACTACAAATCTTCTCCAGCACTTACTTCCTAAGCCGTGA 606
QY 455 TGAGGTGAGACCGCTACATTGCGGTGTCACCCCGCTGAAGC-----TTTGAACCTTC 508
DB 605 TGAAGGTGAGACCGATACCTGTGTGTCTGTGCGCCACCGTGAAGTCCGCCACATGCTGTGAC 546
QY 509 GCACACCTTTGAAGGCAAAATATCATATCTGATCTGCTGTCTGTCTGTCTGTCTGTG 568
DB 545 GCACCTTACCGGGGGGAGAGTGTGCGACCTGTGTCTGTGCTGTGCGCTCACGCTCTCG 486
QY 569 GCATCTGTGCATTAATGCTCTGTGAGAGCAACAAAGTCAAGGAACGTCATGATTTGAGT 628
DB 485 TTCTGCTCTTCTTCTTCTGCTGTGAGTGA---CAGCAACAGAGCTGACGATCCCAAGCT 429
QY 629 GCTCTTGTGAGTCCAGATGATGACTACTCTCTGTGTGGAGACCTTTCATGAGATCTGTG 688
```

```
DB 428 GTGGGTGAGCTTCCCGTGAGCCCGAGACAGTCTGTGT---TCAAGCCAGCCGTGTCTACA 372
QY 689 TCTTATCTTTTGGCTTCTGATGATCCCTGTCTCTATATCATGCTGTCTACACCTTATGA 748
DB 371 CGTTGTCTGTGAGCTTGTGTGTGCGCCGTGTGACCAATGTGTGTCTCTACACAGACTCC 312
QY 749 TCTGTGCTTCAAGAGCGTCCGAGCTCTTCTGTGCTCCGAGAGAAAGATCCGAACCTCG 808
DB 311 TCGCGAGGCTGCGGGCGCGTCCGCTCCGCTCTGAGCCAAAGCTCTAGGCAAGCCAGCG 252
QY 809 GTAGATCAACAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 868
DB 251 GGAAGGTGACCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 192
QY 869 TTCACATATTTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 928
DB 191 TCCACCTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 132
QY 929 CCAGCTATTACTTCTGTGATCGGCTTATGAGCTTATACCAAGTAGCCTGAATCCATTCTCT 988
DB 131 GTATGCTCTAAGCTATCATCAGCCTGATGAGCCCAACTGTGTGTGTGTGTGTGTGTGT 72
QY 989 ACGCTTTCTGTATGAAAACCTTCAAGCGGTGTTCG 1025
DB 71 ACGCTTTCTGTATGAAAACCTTCCGAGAAGACTTCG 35
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RESULT 73
AY410422          910 bp      DNA      linear      GSS 16-DEC-2003
LOCUS            Pan troglodytes SSTR4 gene, VIRUTUAL TRANSCRIPT, partial sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AY410422
VERSION        AY410422.1 GI:39766390
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Pan troglodytes
```

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

TITLE
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanendaaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
Fieriera,S., Wang,G., Zheng,X.H., White,T.J., Slnesky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission

COMMENT
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source
1..910
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>910
/gene="SSTR4"
/locus_tag="HCW3885"

ORIGIN

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Query Match      13.7%; Score 158.4; DB 29; Length 910;
Best Local Similarity 53.7%; Pred. No. 3.2e-20;
Matches 396; Conservative 0; Mismatches 321; Indels 21; Gaps 3;

QY 289 TACATATTAACTGCTTGTGCGAGATGCTTATGATTAACAACATGCCCTTTCAGAT 348
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Db      1 TACCTCTCANNCTGCGCCGATGCGGATGAGCTCTTATGCTGAGCGCTGCTTCTGCGCC 60
Qy      349 AGGCTTACTTATGATGATTCCTGCGCTTTGGGATGCTGTCGAAGATGATTTATTC 408
Db      61 TCGTCGGCGCGCCCTGCGCACTGCGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy      409 ATTGATTACTACAAAGTTCACACGATCTTACCTTACCTTACCTTACCTTACCTTACCTT 468
Db      121 GTTCAGCGCTCAACAGTTCACACGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy      469 TACATTCGCGTGTGCGCCGCGGATGAGCTTTGAGCTTCCGACACCTTGAAGGCAAG 528
Db      181 TAGTGGCGGCTGAGTGAACCTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy      529 ATCATTAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
Db      241 TTCTATCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy      589 GGAGGACCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 648
Db      301 GAGAGACACTAGACCGATCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 357
Qy      649 GATGACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Db      358 ---CAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
Qy      709 ATCCCTGTCTCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db      412 CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
Qy      769 CGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
Db      472 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531
Qy      829 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
Db      532 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
Qy      889 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
Db      580 GTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
Qy      949 GCTTATGCTATACCAAGTTCACACGATCTTACCTTACCTTACCTTACCTTACCTTAC 1008
Db      640 ATCTCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
Qy      1009 TTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
Db      700 TTCCGCGCATCTCTCCAG 717

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RESULT 74
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LOCUS        Mus musculus SSTR3 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION   genomic survey sequence.
ACCESSION    AY400334
VERSION      AY400334.1 GI:39756323
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 1287)
AUTHORS      Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
              Adams,M.D. and Cargill,M.
              Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
              Science 302 (5652), 1960-1963 (2003)
JOURNAL      PUBMED
14671302

```

```

REFERENCE    2 (bases 1 to 1287)
AUTHORS      Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
              Adams,M.D. and Cargill,M.
              Direct Submission
              Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
              This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
COMMENT      Location/Qualifiers
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ORIGIN
Query Match      13.5%; Score 156.2; DB 29; Length 1287;
Best Local Similarity 50.8%; Pred. No. 9.8e-20;
Matches 439; Conservative 0; Mismatches 408; Indels 18; Gaps 2;
Qy      179 TCATCATCAGCGCGCTCTACTCCGATGCTTCGTCGCTGCTGCTGCTGCTGCTGCTGCTG 238
Db      137 TCTTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196
Qy      239 TCATGCTGATCATCCGATACCAAGATGAGAGACAGCAACCAATTATATTTA 298
Db      197 TGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
Qy      299 ACTGCGCTTGGCAGATGCTTATGTAATACATCAACATGCTGCTGCTGCTGCTGCTGCT 358
Db      257 ACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
Qy      359 TGATGATTCCTGCGCTTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
Db      317 CCTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
Qy      419 ACAAGATGTCACGACATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 478
Db      377 TCAACAGTTCACGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
Qy      479 TGTGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
Db      437 TGTGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
Qy      539 TGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
Db      497 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
Qy      595 ACCAAGTCAAGGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
Db      557 CCGGAGCATAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
Qy      655 TACTCTGCTG-----GACCTCTTCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 700
Db      617 CTTTATCATCTTACACGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
Qy      701 CTTTATCATCTTACACGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
Db      677 GCTACTGCTCATCTTGTGTAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
Qy      761 AGAGCGTCCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
Db      737 GTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
Qy      821 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
Db      797 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 856
Qy      881 TCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940

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Db	857	ACATGCTCAATGTGTGTGTCGCCGCTGCGGAGAGACCCGCTTTCTTGCGGCTTACTTCC	916
Qy	941	TCGTCATCGCCTTAGCTATACCAACAGTAGCCTGAATCCCATTTCTTACGCTTTCTTG	1000
Db	917	TGTCGTGTCGCGCTGCTGCCCTTACGCGAACACTGTGGCAAAACCCATCTCTTACGCTTCTCT	976
Qy	1001	ATGAACCTTCAAGCGGTGTTCCG	1025
Db	977	CCTACCGCTTCAAGCAGGCGTTTCG	1001
RESULT 75			
LOCUS	CF147827		
DEFINITION	AGENCOURT 14740147 NIH MGC 145 Homo sapiens cDNA clone		
ACCESSION	IMAGE:6971894 5', mRNA sequence.		
VERSION	CF147827		
KEYWORDS	CF147827.1 GI:33244095		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 701)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: csapbbs-remail.nih.gov Tissue Procurement: GPCR Consortium cDNA Library Preparation: GPCR Consortium DNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: IRB102 row: b column: 01 High quality sequence scop: 430. Location/Qualifiers		
FEATURES			
source	1..701		
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	/clone="IMAGE:6971894"		
	/tissue_type="mixed"		
	/lab_host="DH10B"		
	/clone_id="NIH MGC 145"		
	/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ScorV-Xm1/Xho1-3', 5'-ScorV-Xm1/Not1-3', ScorV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnl.gov/Image/retarrayed_plates/IRB1.presv.dat a Note: this is a NIH_MGC library."		
ORIGIN			
Query Match	13.5%	Score 156;	DB 14; Length 701;
Best Local Similarity	57.6%	Pred. No. 8.4e-20;	
Matches	279;	Conservative	0; Mismatches 205; Indels 0; Gaps 0;
Qy	75	CAGCAGCCCTGTGTTCCCGCTGGGCGGAGCCCGCAGCAAGCAGCGACGCGCGCTCGGA	134
Db	81	CGCGGCGAGCAGAGGGCCCCGGGGCGGCGCTGCGAGCGCATGAGAGCGACGAGGCGGAAA	140
Qy	135	GAGCGCGAGCTGAGAGCCCGGCGACATATCCCGGCGCATCCCGGTATCATCAGCGCGGT	194
Db	141	TGCGTCCAGAACGGGACCTTGAGCGAGGGCGAGGGCAGCGCCCATTCGATCTCTTCAT	200

OY		195	CTACTCCGTAAGTGTTCGTGGCGCTTGCGGCAACTCGGTGCATGTTCCGATCAT	254
Db		201	CTACTCCGTAAGTGTTCGTGGCGCTTGCGGCAACTCGGTGCATGTTCCGATCAT	260
OY		255	CCGATTACAAGAAGTGAAGACAGCACCAACATTATCATATTTAACTGGCTTGGCAGA	314
Db		261	GCGATTAGCCAAAGTAGAAGACGGCACCAACATCTAATCTTAATCTGGCATTTGCTGA	320
OY		315	TGCTTTAGTACTACAAACCATGCCCTTTCAGAGTACGATCTTACTTGATGTAATTCCTGACC	374
Db		321	TGAGCTCTCATAGTCTAGCGTGCCCTTCTTAAGTCACTCCACGTTGTTGGCCACTTGGCC	380
OY		375	TTTTGGGGAATGTCGTGTGCAGATGTAATTTTCATTGATTAATACACATGTTCCACAG	434
Db		381	CTTGGGTGCGCTGCTGCGCGCTTCGTGTCAAGCGTGAAGCGCGGTCAACATGTTCAACAC	440
OY		435	CATTCTTACCTTGAACCATGATGAGCGTGAACCGGTATATTCGCTGTCGCCACCCCGTGA	494
Db		441	CATTCTTGTCTGTGATCTGTGCTCAGCGGTGAACCGGTATATTCGCTGTCGCCACCTCA	500
OY		495	GAGCTTTGAGACTTCGCGACACCCCTTGAAGAGCAAGATCATCAATATCTGCATCTTGCTCT	554
Db		501	GCGGCGCCCGTACCGCGGCTCTTCGTGACATAGCATACACTGGCGGTATGTCCT	560
OY		555	GTCG	558
Db		561	ATAG	564
RESULT 76				
B0057593			688 bp	MRNA linear EST 26-AUG-2002
LOCUS			UI-M-FRO-ca3-c-15-0-UI.r1 NIH BMAP_FRO Mus musculus cDNA clone	
DEFINITION			IMAGE:6413126 5', mRNA sequence.	
ACCESSION			B0057593	
VERSION			B0057593.1	GI:22497882
KEYWORDS			EST.	
SOURCE			Mus musculus (house mouse)	
ORGANISM			Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS			1 (bases 1 to 688)	
TITLE			NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL			National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT			Unpublished (1999)	
			Contact: Robert Straubeberg, Ph.D.	
			Email: sgabois-femail.nih.gov	
			Tissue Procurement: Dr. Jim Lin, University of Iowa	
			cDNA library preparation: Dr. M. Bento Soares, University of Iowa	
			CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	
			DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
			Clone Distribution: MGC clone distribution information can be	
			found through the I.M.A.G.E. Consortium/LINL at:	
			http://image.lnll.gov	
			This clone was contributed by the Brain Molecular Anatomy Project	
			(BMAP)	
FEATURES			Seq primer: pyx-5.	
SOURCE			Location/Qualifiers	
			1..688	
			/organism="Mus musculus"	
			/mol_type="mRNA"	
			/strain="C57BL/6"	
			/db_xref="taxon:10090"	
			/clone="IMAGE:6413126"	
			/tissue_type="whole brain"	
			/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"	
			/lab_host="DH10B (r1 phage resistant)"	
			/clone_1b="NIH BMAP FRO"	
			/note="Organ: Brain; Vector: pyx-Aec; Site_1: EcoR I;	
			Site_2: Not I; The library was constructed according	
			Bonaldo, Lennon and Soares, Genome Research, 6:791-806,	
			1996. Denatured RNA was size fractionated on a 1% agarose	

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 13.5%; Score 155.4; DB 13; Length 688;
Best Local Similarity 64.7%; Pred. No. 1, ie-19;
Matches 231; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 252 CATCCGATACACAAAGATGAAGACCAACCAATTACATTTTACCTGGCTTGGC 311
DB 331 CAGCAGGACACCAAGATGAAGACTCTACCAACATTTACATTTATCTGGCACTGGC 390
QY 312 AGATGCTTAGTACATCAACCAATGCCCTTGAAGTACGCTTACTTGAATCTCTG 371
DB 391 TGAATACCTGGTCTTCTCTGACACTGCTTCCAGGACAGACATCTTCTGGCTTCTG 450
QY 372 GCGTTTGGGAGATGCTGCTGCAAGATAGTAATTTTCATTGATTTACTACACATGTTAC 431
DB 451 GCCATTGGGATGACCTGTGCAAGACGGTCACTGATGATGATGATGATGATGATGATG 510
QY 432 CAGCATCTTACCTTGAACCATGATGAGCGTGAACCGCTACATTCGCTGGCCACCCGT 491
DB 511 CAGCATCTTACCTTGAACCATGATGAGCGTGAACCGCTACATTCGCTGGCCACCCGT 570
QY 492 GAAGGCTTGAACCTTCCGACACCCCTGAAGGCAAGATCATCATATCTGATCTGGT 551
DB 571 CCGTCCCTTGAATGTTTGGACATTCAGTAAAGCCAGGCCGTTAATGAGCCATATGAGCC 630
QY 552 GCTGTCGATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAACCAAGTACAGGA 608
DB 631 CCGTCCCTTGAATGTTTGGACATTCAGTAAAGCCAGGCCGTTAATGAGCCATATGAGCC 687

RESULT 77 916 bp mRNA linear EST 15-MAY-2003
BX433241/c
LOCUS BX433241 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0BF038YK09 3-PRIME, mRNA sequence.
ACCESSION BX433241
VERSION BX433241.1 GI:30773198
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 916)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8778.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BA1015ZB06_CS01389_2&cluster=8778.f.
Contact: Feng Liang Email: fliang@life.techn.com URL:
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CS0BA1015ZB06_CS01389_2.
Location/Qualifiers
1..916
/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0BF038YK09"
/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/clone.lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 13.3%; Score 153.4; DB 13; Length 916;
Best Local Similarity 49.3%; Pred. No. 3e-19;
Matches 413; Conservative 0; Mismatches 417; Indels 7; Gaps 3;

QY 217 GAGCTTGGGCACTCGCTGATGTTGCTGATCATCCGATACACAAAGATGAAGACA 276
DB 915 GNGTGTGNNNNNNNNNNNNCTGTGCATATGATCATCTNNCTATNCAATNNNCA 856
QY 277 GCACCAACATTTACATATTTAACCTGGCTTGGCAAGTCTTTAGTTACTAACCAATG 336
DB 855 TNN 796
QY 337 CCGTTTCAAGATAGG-GTCTACTGATGAATTCCTGGCCTTTGGGATGCTGTGCA 395
DB 795 GCTTCTTGNCTATGACAGTGGGCTCTGTGTCACCTGCCCCCTTGGCAAGCATTTNCG 736
QY 396 GATAGTATTTTCATTTATTTACTTACCAATGTTTACCAAGATCTTCACTTGAACATGAT 455
DB 735 GGTGTATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 676
QY 456 GAGGTGACCGCTACATTTGCGGTGTCACCCCGTGAAGCTTGGACTTCCGACACC 515
DB 675 GAGATGACGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
QY 516 CTGGAAGCAAGATCATCATATATCTGATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575
DB 615 CCGACCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 559
QY 576 TGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGATGATGATGATGATGATGATGATG 635
DB 558 GCCCATCATGATATATATCTGGGCTCCGAGACCAACAGTGGGAGAAAGACGTGCACAT 499
QY 636 GCAATTCGCAATGATATCTCTGCTGGGACCTTTTATGAAGATCTGCTTTCAT 695
DB 498 CAATGCGCAGGTGAATCTGGGCTTGTGTACACAGGATTCAT--CATCTACACTTTCAT 442
QY 696 CTTTGCCTGATGATCCCTGCTGCTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755
DB 441 TCTGGGCTTCTGTATCCCTTCAACATCATCTGCTTGTCTTACTGTTACTTATCATCA 382
QY 756 TCTCAAGAGGCTCGGCTCTTCTTCTGCTCCGAGAGAAAGATGCAACCTGGGTAGAT 815
DB 381 GATGAATCTCTGGAATCGAGTGGGCTCTCTTGAAGAGAAAGATGAGAAAGAT 322
QY 816 CACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875
DB 321 CACCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 262
QY 876 ATTCAATCTGATGAGGCTTGGGAGACCTCCACAGACAGCTGCTTCCAGCTA 935
DB 261 ATTCAAGTCTTCTCGTCTCCATGAGCACTACACCCACCCAGCCCTTAAGAGCATGT 202
QY 936 TTAATCTGATGCTTGAAGCTTATACCAAGTACAGTACCTGATTCATCTTACGCTTT 995
DB 201 TGAATTTGTGTGTCTCTCACTATGCTTACAGCTGTGCCAACCTTATCTATATGCTT 142
QY 996 TCTTGAAGAACTTGAAGGCTTTCGGGAGCTTCTGTTTCCACTGAAGATGAG 1052
DB 141 CTGTCTGACACTTCAAGAGGCTTCCAGAAATGCTCTGCTGCTGCTGCTGCTGCTGCTG 85

RESULT 78
LOCUS AZ966515 702 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0237H04F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0237H04 F, genomic survey sequence.
ACCESSION AZ966515
VERSION AZ966515.1 GI:13837742
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 702)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0237 row: H column: 04
Seq primer: CGTGTAAACGACGCGCCAGT
Class: Plasmid ends
High quality sequence stop: 702.
Location/Qualifiers
1..702
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0237H04"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 13.3% Score 153.2; DB 28; Length 702;
Best Local Similarity 74.8%; Pred. No. 2.9e-19;
Matches 205; Conservative 0; Mismatches 66; Indels 1; Gaps 1;
242 TGTTCGTATCATCCGATACACAAAGATGAAGACGACCAACATTATATTTAAC 301
429 TGCTCTCTCTCCATGACGATACCAATGAGACCGCCACCAACATCTCAATCTCAATC 488

QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACGATGCCCTTTGAGATGAGTACTTGA 361
DB 489 TGGCTTTGGCTGATCGCTGGCCACGACGCTGCTTCCAGAGCGCAAGTACTTGA 548
QY 362 TGAATTCCTGGCTTTGGGAGATGCTGTGTGCAAGATAGTAATTTCCATTTGATTA 421
DB 549 TGGAAACGCGCGCTTTGGCGAGCTGCTGTGCAAAAGCTGTCTTCATTAAGTACTA 608
QY 422 ACATGTTACACGACATCTTACCTTGACCATGATG-AGCGTGAGCGCTACATTTGCCG 480
DB 609 ACATGTTACATGACATCTTACCTTGACCATGATGATGAGCGTACATTTTGTCTGC 668
QY 481 TGGCAGCCCGTGAAGCTTTGAGACTTCCGACAC 514
DB 669 TGCATCTCTGTACAGCCCTGACCTTCCGACAC 702

RESULT 79
LOCUS B1224313 741 bp mRNA linear EST 11-JUL-2001
DEFINITION 602940621P1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5103821 5', mRNA sequence.
ACCESSION B1224313
VERSION B1224313.1 GI:14677752
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/MLN at: http://image.llnl.gov
Plate: L1M11250 row: 1 column: 06
High quality sequence stop: 599.
Location/Qualifiers
1..741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5103821"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Query Match 13.3% Score 153; DB 12; Length 741;
Best Local Similarity 61.8%; Pred. No. 3.3e-19;
Matches 243; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
166 CCGGCATCCGATCATCAACGCGGCTACTCTCGATGTTGTCGTGGCTTGGTG 225
DB 136 CAGGCAAGCGCATCTGATCTTTTCATCTACCTCGGTGTGCTGTGGGGCTGTGT 195
QY 226 GCGAATCGCTGTGATTTGTGATCATCGGATACAAAGATGAAGACGACCAAC 285
DB 196 GGAAGCTTAATGATCATCTAGATGATCTGTGGCTATGCAAGATGAAGACGACCAAC 255
QY 286 ATTAATATTTAACTGCTGGCTTTGGCAGATGCTTTAGTTACTACAAACGATGCCCTTTGAG 345

Db 256 ATCTACATCTTAATCTGGACATTGCTGATGAGCTGCTCATGCTGACGCTCCCTCTTA 315
Qy 346 AGTACGCTTACTTGTATGAAATTCCTGCTTTGGGAGATGCTGTGCAAGATAGTAAT 405
Db 316 GTCACCTCCACGCTGTTGGCCCACTGCGCTTGGGCGCTGCTGCGCTCGGCTC 375
Qy 406 TCCATGATTAATACAAAGTGTACACAGATCTTCAACCTGACCAATGATGAGCGGAC 465
Db 376 AGGTGAGAGCGGCTCAACATGTTTACACAGATATCTGCTGCTGCTGCTGAGCGGAC 435
Qy 466 CGTACATTTCCGCTGTCGCAACCCGCTGAAGGCTTTGAGCTTCGACACCTTGAAGGCA 525
Db 436 CGCTACGTGGCGGTGCTGATCCATCAAGGGGCGCGCTACCGCTGCTCAACCGTGAC 495
Qy 526 AAGATCATTAATCTGCAATCTGCTGCTGCTGCTG 558
Db 496 AAGGTAGTAAACCTGGCGGTGCTGCTGCTGCTG 528

RESULT 80
BB656301 663 bp mRNA linear EST 26-OCT-2001
DEFINITION BB656301 RIKEN full-length enriched, 12 days embryo spinal ganglion
MUS musculus CDNA clone D130013H04 5', mRNA sequence.
BB656301
BB656301.1 GI:16490129
EST
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 663)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshinobu Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wegli, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, Y.,
Masuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for

FEATURES
source
e mouse tissues
location/Qualifiers
1..663
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D130013H04"
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="VDH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal ganglion"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGCGCGCAACTCGAGTGTGTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTTAAATTAATATATCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from lambda P1C 1."

ORIGIN

Query Match 13.2%; Score 152.8; DB 10; Length 663;
Best Local Similarity 59.0%; Pred. No. 3.4e-19;
Matches 262; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

Qy 108 CGACGAGACGCGCAGCCGCTGCGAGAGCGCAGCTGAGCCCGCAGACATCTCC 167
Db 192 CGCCAGCTGGGCTCCGAGCAGAGAGAGAGATGCGATGGGTCGACGACAGAGAC 251
Qy 168 GGCATCCCGCTATCATACAGCGGCTCTACTCCGTAGTGTGCTGCTGGCTGG 227
Db 252 AGCGGATGCTCATCTTCCAGTGCATCTAGCGCTGCTGCTGCTGGCTGG 311
Qy 228 CAATCGCTGCTCATCTGCTGATCATCCGATACAAAGATGAGAGACAGCAACAT 287
Db 312 AAAGCCCTGCTATCTTCTGATCTTACGCTTACCAAGATGAGACACACCAAT 371
Qy 288 TTACATATTAACCTGCTTGGCAGATGCTTATGATTAACAACATGCTTTCAGAG 347
Db 372 CTACCTACTCAACTGCGCGCTGCGCATGAGCTTTCATGCTCAGCGTGCATTCGG 431
Qy 348 TAGCTTACTTATGAAATTCCTGCTTTTGGGATGCTGCTGCAAGATTAATTC 407
Db 432 CTGCGCGCTGCTGCGCAGCTGCGCTGCGGCGGCTGCTGCTGCGCAATGCTT 491
Qy 408 CATGATTAATCAACAGTGTTCACAGCATCTTCACTTGAACATATGAGCGTGA 467
Db 492 CGTGAAGCGCTCAACATGTTTCACTGATGCTTCTGCTCAACGCTGACGCG 551
Qy 468 CTACATTCGCTGTCAGCCCGCTGAAGGCTTTGACCTTCGCAACCTTGAAGCA 527
Db 552 CTATGTCGCTGTTGTGACCTCTGCGCGCGCACCTACCGCGGAGCGCTGACCA 611
Qy 528 GATCATCAATATCTGATCTGGCT 551
Db 612 GCTAATCACTGAGAGTGGCT 635

RESULT 81
CNS04RP2/c
LOCUS
DEFINITION CNS04RP2 927 bp DNA linear GSS 01-SEP-2000
Tetradodon nigroviridis genome survey sequence pUC-ori end of clone
003122 of library H from Tetradodon nigroviridis, genomic survey
sequence.

ACCESSION AL304175
VERSION AL304175.1 GI:8190656
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS 1 Roest Crolius, H., Jallion, O., Daaliva, C., Bouneau, L., Fisher, C., Bernot, A., Fitzmes, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645

REFERENCE
AUTHORS 2 Roest Crolius, H., Jallion, O., Daaliva, C., Ozouf-Costaz, C., Fitzmes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 927)
AUTHORS Genoscope.
TITLE Direct Submision
JOURNAL Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
 1..927
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="003122"
 /clone_1ib="H"
 /note="Genoscope sequence ID : C0BH03DPL1XE1-end : PUC-Or1"

ORIGIN
 Query Match 13.2%; Score 152.2; DB 29; Length 927;
 Best Local Similarity 70.0%; Pred. No. 5.1e-19;
 Matches 219; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

219 CTTGGTGGCAACTGCGTGCATGTCGTGATCATCCGATACACAAAGATGAAGACGC 278
 |||||
 313 CTTCTTTTGTATGATCTTTTCAAAACCTCTTTTAGTACACCAAAATGAAGCGCG 254
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 279 AACCAACATTTACATATTTAACTGCGCTTTGGCAAGATGCTTTAGTTACTACACCATGCG 338
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 253 CACAAACATCTACATCTTCAACCTGCGCCGCGACCGCTTGTCACGACGCGTTCC 194
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 339 CTTTGAAGTACGGTCTACTGTGATGAATTCCTGGCCTTTTGGGAGATGTCGTGCAAGT 398
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 193 CTTCCAGAGCGTCAACTACCTGATGGGACGCGGCC-TTCGGCGAGCGTGTGTGCAAGT 135
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 399 AGTAATTTTCATGATTTACTACAAACATGTTCAACGATCTTACCTTGACCATGATGAG 458
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 124 CGTCAATGTCATGACTACTACAAAGTGTCACTTCATCTTCAAGCTCACCAACATGAG 75
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 459 CGTGAACGCTACATTTGCGGTGTCACCCCGTGAAGGCTTTGAGCTTCCGACACCTT 518
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 74 CTTGACCCGCTACCTGCGCGTGTGCGCATCCGGTCAAAAGCGTGGACCTTGAGAGCGCCGCA 15
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 519 GAAAGCAAAAGATC 531

Db 14 CAAGCCACTTTC 2
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RESULT 82
CNS03JCN/C
LOCUS CNS03JCN 881 bp DNA linear GSS 01-SBP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 03JC21 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL246704
VERSION AL246704.1 GI:7967716
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS 1 Roest Crolius, H., Jallion, O., Daaliva, C., Bouneau, L., Fisher, C., Bernot, A., Fitzmes, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645

REFERENCE
AUTHORS 2 Roest Crolius, H., Jallion, O., Daaliva, C., Ozouf-Costaz, C., Fitzmes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 881)
AUTHORS Genoscope.
TITLE Direct Submision
JOURNAL Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
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 1..881
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="03JC21"
 /clone_1ib="G"
 /note="Genoscope sequence ID : C0B803J1AB11LP1-end : T7"

ORIGIN
 Query Match 13.1%; Score 151.6; DB 29; Length 881;
 Best Local Similarity 70.6%; Pred. No. 6.5e-19;
 Matches 216; Conservative 0; Mismatches 89; Indels 1; Gaps 1;

219 CTTGGTGGCAACTGCGTGCATGTCGTGATCATCCGATACACAAAGATGAAGACGC 278
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 305 CTTCTTTTGTATGATCTTTTCAAAACCTCTTTTAGTACACCAAAATGAAGCGCG 246
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 279 AACCAACATTTACATATTTAACTGCGCTTTGGCAAGATGCTTTAGTTACTACACCATGCG 338
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 245 CACAAACATCTACATCTTCAACCTGCGCCGCGACCGCTTGTCACGACGCGTTCC 186
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 339 CTTTGAAGTACGGTCTACTGTGATGAATTCCTGGCCTTTTGGGAGATGTCGTGCAAGT 398
 |||||
 185 CTTCCAGAGCGTCAACTACCTGATGGGACGCGGCC-TTCGGCGAGCGTGTGTGCAAGT 127

OY		399	ACTAATTTTCATTGATTACCAACAATGTTCACACACATCTTCACTTGACCATGATGAG	455
Db		126	CCTCAGTCATCGATCGATACTACAAKATGTTTCACTTGCATCTTCAAGCTCACCAACCATGAG	67
OY		459	CGTGACCCGCTACATTTGCCGTGTGGCCACCCCCTGAAGGCTTTGACCTTCGACACCCCTT	518
Db		66	CGTGACCCGCTACATTTGCCGTGTGGCCATCCGGTCMAAGCGCTGACCTTAGAGCGCCGCA	7
OY		519	GAAAGC	524
Db		6	CACAGC	1
RESULT 83				
LOCUS		CB557233	662 bp	mRNA linear EST 02-APR-2000
DEFINITION		AMGNNUC:Uxgpl-00001-all-A uxrpl (14349) Rattus norvegicus cDNA		
ACCESSION		CB557233		
VERSION		CB557233.1	GI:29496633	
KEYWORDS		EST.		
SOURCE		Rattus norvegicus (Norway rat)		
ORGANISM		Rattus norvegicus		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae;		
TITLE		Rattus.		
JOURNAL		1 (bases 1 to 662)		
COMMENT		Amgen EST Program. Amgen Rat EST Program Unpublished (2003) Contact: Dan Fitzpatrick Amgen, Inc One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel.: 805 447-4881 Plate: 00001 row: a column: 11.		
FEATURES				
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		1..662		
		/organism="Rattus norvegicus"		
		/mol_type="mRNA"		
		/db_xref="taxon:10116"		
		/clone="uxrpl-00001-all"		
		/clone_lib="uxrpl (14349)"		
		/note="Vector: pSPORT1; Rat GPCR library rearrayed internal psport vector"		
ORIGIN				
Query Match		13.1%; Score 151; DB 14; Length 662;		
Best Local Similarity		69.5%; Pred. No. 7, 6e-19;		
Matches		205; Conservative 0; Mismatches 90; Indels 0; Gaps 0;		
OY		153	CGCGACATCTCCCCGGCCATCCCGGTGATATACAGCGGGCTTACTCCGATAGTGTGT	212
Db		368	CGCTTCCTCGCCCTTGAGCTCAAGAGTACACATCGTGGGGCTTACTTGGCTGTGTGAT	427
OY		213	CGTGGGCTTGGTGGCAACTCGCTGTCATGTTCTGTATCATCCGATACACAAAGATGAA	272
Db		428	CGGGGGGCTCTCGGGGAATGCTCTGTCATGATATCATCTCGAGGACACCAAGATGAA	487
OY		273	GACAGCAACAACATTACATATTTAACCTGGCTTTGGCAAGTCTTAGTTACTTACAAC	332
Db		488	GACAGCTACCAACATTACATATTTAACTGGCACTGGCTGATACCCGTGCTTGCTAAC	547
OY		333	CATGCGCTTTAGAAGTACGATCTACTGATGAATTCGCGCTTTTGGGAGTGGCTGTG	392
Db		548	ACTGCGCTTCAAGGGCAAGACATCTTACTGGGCTTCTGGCCATTTGGGAATGACCTTG	607
OY		393	CAAGATGAATTTTCATTGATTACTACAAACATGTTTCAACAGCATCTTCAACCTTG	447
Db		608	CAAAGCTGTACTTGGTATTCGACTACTTACAAACATGTTTACGAGACTTTTACCTG	662
RESULT 84				
CD5359492/c				

LOCUS	CD559492	792 bp	mRNA	linear	EST 19-NOV-2003
DEFINITION	AGENCOURT_144966666 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971826 5', mRNA sequence.				
ACCESSION	CD559492				
VERSION	CD559492.2	GI:38453541			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 792)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585560. Contact: Daniela S. Gethard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-remail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: Bhat Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: IRBK2 row: d column: 05 High quality sequence start: 12 High quality sequence stop: 76. Location/Qualifiers				
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	/clone="IMAGE:6971826"				
	/rissue_type="mixed"				
	/lab_host="DH5A (T1 phage-resistant)"				
	/clone_id="NIH_MGC_195"				
	/note="Vector: pDNR-Dual; Site 1: loxP-salI; Site 2: loxP-HindIII; clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBK_prev.dat a Note: this is a NIH_MGC library."				
ORIGIN					
Query Match	13.0%;	Score 150.2;	DB 14;	Length 792;	
Best Local Similarity	55.0%;	Pred. No. 1.2e-18;			
Matches 382;	Conservative 0;	Mismatches 299;	Indels 13;	Gaps 4;	
QY	338	CCITTCAGAGTAAAGCTCTACTTGTATGAATTCCTCGGCTTTTGGGAGATGCTGTGCAGA	397		
DB	720	CCNGTCACATCGCGGAGACCTCTCTGCAAGTACGGCTTTCGGAGAGCTCTGCAAGC	662		
QY	398	TAGTAATTTTCATTGATTACTACACATGTTCACAGCATCTTCACTTACCATGATGA	457		
DB	661	TGCTGCTGGCGCGTTCGACCACTTAACAATCTTCTTCAGCACTTAATCTTCTAGCGGTATGA	602		
QY	458	GGGTGACCGCTACATTTGCCGTGTGCGAACCCTGTGAGGCTTTTGGACTTCCGCA	511		
DB	601	GGCTGACCGCTACATTTGCCGTGTGCTGTGCGAACCCTGTGAGGCTTTTGGACTTCCGCA	542		

Oy		5112	CACCCCTTAAGGCAAAAGATCATTCATATCTGCATCTGGCTGTGTCGTCATCTGTGGACA	571
Oy		5113	CACCCCTTAAGGCAAAAGATCATTCATATCTGCATCTGGCTGTGTCGTCATCTGTGGACA	571
Dd		5411	CCYACCAGGGGGCGGAAGGTCGCCGACCTGTGTGTCTGGCTGGAGGCTCACGGTCTCCTGTC	482
Oy		5712	TCTTGCAATAGTCCCTTGGAGGCAACAAAGTCAGGAAAAGACGTGCANTGCAATTGAGTCT	631
Dd		4811	TGCCCTTCTTCTCTTTCCTGGCGCTCA---CAGCAACGAGCTGACGGATCCCAAGCTGTG	425
Oy		6312	CCTTGCACTTCCCAGAATATGACTCTCTGTGGGAACTCTTCAATGAAATCTGCCCT	691
Dd		4241	GAGTAGGCTTCCCCGTGGGCCCGAGGAGGCTGTGGT---TCAAAGGCAAGCCGTGTCTAACAGT	368
Oy		6912	TCATCTTTGACCTTGTGTGATACCCCTGTCTCATCATCATGCTGTGCTACACCCGTAGATCC	751
Dd		3671	TGCTCTCGGGCTTCCTGCTGCTGCCCGCTGTGACACATGTGTGTGCTTACACAGACTCTGCG	308
Oy		7512	TGCGTCTCAAGAGCGTCCGGCTCTCTTCTGTGCTCCCGAAGAAAGATCGCAACTGCGTA	811
Dd		3071	GCAGGCTCCGGGCGCTGCGGGCTCCGCTCTGGAGCCAAAGGCTTAAAGGCAAGGCGAGCGGA	248
Oy		8112	GGATACACGAAGTGGTCCGTGGAGGTGGAGTGGAGCTTGTGTGCTGTGCTGCACTCCCATTC	871
Dd		2471	AGGTACCCGCTCTGTGCTCTCTGCTGCTGCGCTGGCCGTGTGCTCTCTGTGCTGGAGCCCTTCC	188
Oy		8712	ACATATTCATCCTGTGTGAGGCTCTGGGAGACACTCCACAGCACAGCACTGCTCTTCCA	931
Dd		1871	ACCTGCGCTCTGTCTGTGCGCCCTGACACAGAGACCTGCCACAGCCCACTGGATCATCACTA	128
Oy		9312	GCTATTACTTGTGCATCGCCTTAAAGGCTATACCAACAGTAGTCCCTGAATCCATTCTTACG	991
Dd		1271	TGTCCCTAAGTATCACAGCCTCAGCTACGCCCAACTCGTGCCTGAACCCCTTCCCTTACG	68
Oy		9912	CCTTCTTGATGAAGAACTTCAAGCGGTGTTCCG	1025
Dd		671	CTTCTTGAATGACAACTTCCGGAAGAACTTCCG	34
RESULT 85				
BX390825				
LOCUS		1114 bp	mRNA	linear EST 13-MAY-2003
DEFINITION		BX390825 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens		
ACCESSION		CDNA clone CS0DKO1IYG11 5-PRIME, mRNA sequence.		
VERSION		BX390825		
KEYWORDS		BX390825.1 GI:30623183		
SOURCE		EST.		
ORGANISM		Homo sapiens (human)		
REFERENCE		Homo sapiens		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL		Li, W.B., Gruber, C., Jessee, J. and Polayars, D.		
COMMENT		Full-length cDNA libraries and normalization unpublished (2001)		
		Contact: Genoscope - Centre National de Sequencage		
		Genoscope - Centre National de Sequencage		
		BP 191 91006 Evry cedex - France		
		Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr		
		Library was constructed by Life Technologies, a division of		
		Invitrogen. This sequence belongs to Sequence cluster 7532.f For		
		more information about this cluster, see		
		http://www.genoscope.cns.fr/		
		cgl-bin/ccluster.cgi?seq=CS0BAQ049ZF03 CS04630_1&custer=7532.f.		
		contact: Feng liang Email : fliang@lifetech.com URL :		
		http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
		Paradey Avenue Genoscope sequence ID : CS0BAQ049ZF03_CS04630_1.		
FEATURES				
Source		Location/Qualifiers		
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/cell_line="HELA"
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 /note="1st strand cDNA was primed with a NotI-oligo (dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 13.0%; Score 150; DB 13; Length 1114;
 Best Local Similarity 59.7%; Pred. No. 1.5e-18;
 Matches 252; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY TCCGTAAGTGTGTCGTGGGCTTGCGGGGCAACCGCGGTCATGTCGATCATCGCA 258
 DB 1 TCCGTGGTGTCCCTGGTGGGGCTGTGGGAACCTTAAGTCATCTACGTATCCTGGC 60
 QY 259 TACACAAAGATGAAGACAGCAACCAACATTTATTAACCTGGCTTGGCAGATGCT 318
 DB 61 TATGCCAAGATGAAGACGGCCACCAACATCTACATCTTAATCTGGCATTTGCGATGAG 120
 QY 319 TTAGTTACTACACCAATGCCCCCTTTCAGAGTACGGTCTACTTGATGAATTCCCTGGCCCTTTT 378
 DB 121 CTGCTCATGTCTACACGTCGCCCCCTTCTTAAGTACCTCCACGTTGTGCCCATCTGCCCTTTC 180
 QY 379 GGGGATGTCGTGTCACCAAGATAGTAATTTCCATTTGATTAACAAACATGTTCCACAGATC 438
 DB 181 GGTGCGCTGTCTGTCGCGCTCTGTGCTCAGCTGAGCGCGGTCAACATGTTCCACAGATC 240
 QY 439 TTCACTTGAACCATGATGAGCGGTGAGACCGGTACATTCCTGGTGCACCCCGTAAAGCT 498
 DB 241 TACTGTCTGACTGTGCTCAGCGTGTGACCGCTACTGCGCGGTGTCATCCCATTAAGGCG 300
 QY 499 TTGACCTTCCGACACCCCTTGAAGGCAAAATCATCAATCTGCACTGGCTGCTGTGC 558
 DB 301 GCCGCGTACCGCGCGCCCAACCGGTGCAAGTATGAACCTGGGCGTGTGGGTCTATCG 360
 QY 559 TCATCTGTGGCATCTCTGCAATAGTCTCTTGGAGGCGCAAAATCAGGAAAGACTGAT 618
 DB 361 CTGCTGTGATCTCTGCGCCATCTGAGACTTCTTCTGCAACCGGCGCAACGACGACGACG 420
 QY 619 GT 620
 DB 421 GT 422

RESULT 86
 LOCUS BB632308
 DEFINITION BB632308 RIKEN full-length enriched, adult male hypothalamus Mus
 musculus CDNA clone A230027D20 5', mRNA sequence.
 ACCESSION BB632308
 VERSION BB632308.1 GI:16468911
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 643)
 AUTHORS Arakawa,T., Carininci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,T.,
 Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Saseki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222

[illegible]

Db	203	TCGCCAGATGATAAACCCTCACCAACATCTACATTTCTCAACCTTGCAGATGGCCAGCTCC	262
Qy	320	TAGTTACTACACCATGCCCCCTTTGACAGTACGGTCTACTTGATGAATTTCTGGCCCTTTTG	379
Db	263	TGTACATGCTGGGGCTGCTTTCTCTGGGCAAGCAAGAACGCCGGCTCTTCTGGCCCTTGG	322
Qy	380	GGGATGTGCTGTGCAAGATAGTAA'TTTTCATGTATTA'CTACACATGTTTCAACGACATCT	439
Db	323	GCCCCGTCCTGTGCGCGCTGGTCA'TGACGCTGACCGCGTTCACACAGTTCACCGATGTCT	382
Qy	440	TCACCTTGACCATGATAGGAGGTGACCGCTACATTTGCGGTGTGCAACCCGCTGAAGCTT	499
Db	383	TTGCTCTGACAGTATAGAGTGGACCGCTACCTGGGAGGTGTGACACCGCTGAGCTTCG	442
Qy	500	TGACATTTCCGCACACCCCTTGAAAGCAAAAGATCATCAATATCTGCATCTGGCTGTCTGT	559
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Db	499	--TCTCTGTGCATGTCCCTGCGCGCTCTCGGTGTTTCCGCGACGTACAGAGAGGACGTACT	556
Qy	620	TCATTGAGTGTCTCTTGCAATGCCAATATGATCTACTCTGTGTGGAGCCTCTTCAATGA	679
Db	557	GCAACGCCAGCTGGCGCGAGACCCCTGAGGC-----TGTGGAGCGCCCTCTTCA	604
Qy	680	AGATCTGCGTCTTTCATCTTTGCTCTTGTGATACCTCTGCTCATCATCATGCTGTCTACAA	739
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Qy	740	CCCTGATGATCTCGTGTCTCAAGAGCGTCCGGCTCTTTCTGCTCCCGAAGAAATGC	799
Db	665	TGCTCATTTGTGTGAAGGTGAGGCGCGCGGCGCGCGCTGTGGGCT--GCGTGGCGCGCG	721
Qy	800	GCAACCTGCGTAGATACACGAGCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	859
Db	722	GCTCGGAGCGGAAGTACCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	781
Qy	860	GGACTCCCATTCATCATATTCATCTGTGTGAGGCTCTGGGAGACCTCCACACGACAG	919
Db	782	GGCTGCGCTTCTTACCGGTCAACATGTCTCAACCTGGCGGTGTGCGCTGCCACGAGAGCGC	841
Qy	920	CTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAG	968
Db	842	CCTCGCGCGCGCTCTACTTCTTNNNNNCATCTCTCTACGCCACAG	890

RESULT 89

BU708032

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BU708032 835 bp mRNA linear EST 15-JUL-2003

UI-M-FRO-cao-j-10-0-UI-r1 NIH BMP_FRO Mus musculus cDNA clone

IMAGE:6415209 5', mRNA sequence.

BU708032

BU708032.1 GI:23640094

EST.

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (basee 1 to 835)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>

REFERENCE 1 (bases 1 to 785)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LLM11503 row: 1 column: 14
 High quality sequence stop: 728.
 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:5201053"
 /lab_host="DH10B"
 /clone_1ib="NIH MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains; age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library."

ORIGIN

Query Match 12.3%; Score 142; DB 12; Length 785;
 Best Local Similarity 69.5%; Pred. No. 4.5e-17;
 Matches 235; Conservative 0; Mismatches 100; Indels 3; Gaps 3;

153 CGCGACATCTCCCGGCGCATCCGCTATCATCAGCGGCTCTACCTCGTAGTTCGT 212
 Db CGCCTTCCTCGGCGGCTCAAGGTACATCGGGGCTCTACCTGCGGTGTGTGT 363
 QY 213 CGTGGCTTGGTGGGCACTCGCTGTCTATCTTCGTGATCCGATACACAAAGTGA 272
 Db 364 CGAGGCGCTCGGGGAATGCTGTCTATCGTATCTTCAGGACACCAAAATGAA 423
 QY 273 GACAGCAACCAATTTATATATTTAATCTGCTTGGAGATGCTTATTTACTACAC 332
 Db 424 GACAGCCACCAATTTATATCTTTAATCTGCGCCCTGCGC-GACACTCTGTCTGTGAC 482
 QY 333 CATGCCCTTTCAAGATACGCTCTAATTGATGAATTCCTGAGCTTTGGGGATGTGCTG 392
 Db 483 GCTGCCCTTCCAGGACGAGACATCTCTCGGGGCTTGGCGTTGGGAATGCGCTGG 542
 QY 333 CAAGATAGAAATTTCCATTTGA-TTACTATAAAGATGTC-CCAGATCTTTCACCTGAC 450
 Db 543 CAAGACAGTATTCCTTGAATGATCTTAACAATGTTCCACGACCTTTCACCTTAAT 602
 QY 451 ATGATGAGCGGTGACCGCTACATTTGCGGTGACCAACC 488
 Db 603 GCCATGAGTGTGGATGCTATGATGACATCTGCGACCC 640

RESULT 92
 LOCUS BM951523 714 bp mRNA linear EST 14-MAR-2002
 DEFINITION UI-M-BG-bup-g-01-0-UI.r1 NIH_BMAP_EG0 Mus musculus cDNA clone
 IMAGE:5685144 5', mRNA sequence.
 ACCESSION BM951523
 VERSION BM951523.1 GI:19435113
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 714)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source

Seq primer: pYX-5.
 Location/Qualifiers

1..714
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5685144"
 /tissue_type="whole brain"
 /dev_stage="embryo 18.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1ib="NIH BMAP EG0"
 /note="Organ: brain; Vector: pYX-Anc; Site 1: EcoR I; Site 2: Not I. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Anc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 12.2%; Score 141; DB 12; Length 714;
 Best Local Similarity 64.0%; Pred. No. 6.7e-17;
 Matches 213; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 766 GTCCGGCTCTCTTCTGCTCCCGAGAGAAAGTCCAACTTCGTAAGATCACAGACTG 825
 Db 2 GTCCGGCTCTCTTCAAGCTCCCGAGAGAAAGCCGAACTTCGACGATCACAGGCTG 61
 QY 826 GTCCGGCTCTCTTCTGCTCCCGAGAGAAAGTCCAACTTCGTAAGATCACAGACTG 885
 Db 62 GTACTGATGATGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 121
 QY 886 GTGAGAGCTCTGGGAGACCTCCACAGCAGCTGCTCTCCAGCATTAATCTTCTG 945
 Db 122 GTTCAAGAGCTGGGT 181
 QY 946 ATGCTTAAAGCTATACCAACAGTACGTAATCCATTTCTTACGCTTTTATGAA 1005
 Db 182 ACAGCCCTGGGCTATGTAACAGTGTCTCAATCCATTTCTTATGATGATG 241
 QY 1006 AACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGGAAGATGAGAGGGGCG 1065
 Db 242 AACTTCAAGCGGTGTTGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301
 QY 1066 AGCACTAGCAGAGTCCGAAATACAGTTCAAGAT 1098
 Db 302 GTTCTGATCGTGTGCGCAGCATTTGCCAAGAT 334

RESULT 93
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 LOCUS AGENCOURT 6494036 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729211
 DEFINITION 5', mRNA Sequence.
 ACCESSION BM546464
 VERSION BM546464.1 GI:18779448
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1383)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL12726 row: c column: 04
 High quality sequence start: 48
 High quality sequence stop: 526.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5729211"
 /issue_type="hippocampus"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_124"
 /note="Torgan: brain; Vector: pCMV-SPORT6; Site_1: EcorV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

ORIGIN

FEATURES
 source

Query Match 12.2%; Score 141; DB 12; Length 1383;
 Best Local Similarity 70.2%; Pred. No. 8,7e-17;
 Matches 203; Conservative 0; Mismatches 85; Indels 1; Gaps 1;
 QY 153 CCGGCAATCTCCCGGCATCCGTCATCATCAGCGCGGTCTAATCCGTAAGTGTTCGT 212
 DB 373 CGCCTTCTGCCCCCTCGGCTCAAGTCAACATCGTGGGGCTCTACCGCCGTGTGTGT 432
 QY 213 CGTGGCTTGGTGGCACTCGCTGATGTTGTGATCCGATACCAAGATGAA 272
 DB 433 CGAGGGCTCTCGGGAAGCTGCTGTATGATGATCCTCAAGGCAACCAAAATGAA 492
 QY 273 GACAGCAACCAATTTACATTTTAACTGCTTTGGCAGATGCTTTAGTTACTACAC 332
 DB 493 GACAGCAACCAATTTACATTTTAACTGCTTTGGCAGATGCTTTAGTTACTACAC 552
 QY 333 CATGCCCTTTTGAAGTACGCTTACTGATGATTAATTCCTGGCCCTTTTGGGAGTGTCTGTG 392
 DB 553 GCTGCCCTTTTCAAGGCAAGCAATCTCTCGGGCTTCTGGCCGTTTGGGAATGGCGTGTG 612
 QY 393 CAAGTAAATTTTCCATGATTTACTAGACA-TCCTTACAGAGATCTT 440
 DB 613 CAAGCCGTCATTCGATTTGACTACTACAAATGTTCCAGACCTT 661

RESULT 94
 CNS03GSG
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 025E10 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL243385
 VERSION AL243385.1 GI:7964397
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.
 REFERENCE 1
 AUTHORS Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 TITLE Estimate of human gene number provided by genome-wide analysis
 JOURNAL using Tetraodon nigroviridis DNA sequence
 MEDLINE Nat. Genet. 25 (2), 235-238 (2000)
 PUBMED 20296633
 REFERENCE 2
 10835645
 AUTHORS Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coetzee,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837
 PUBMED 10899143
 REFERENCE 3 (bases 1 to 937)
 10899143
 AUTHORS GenomeScope.
 TITLE Direct Submission
 JOURNAL Genoscope.
 MEDLINE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrel@genoscope.cns.fr)
 PUBMED

COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.
 Location/Qualifiers
 1..937
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="025E10"
 /clone_1lb="ng"
 /note="Genoscope sequence ID : COB025BC05LPL-end : T7"

ORIGIN

Query Match 12.1%; Score 140.2; DB 29; Length 937;
 Best Local Similarity 57.0%; Pred. No. 1.1e-16;
 Matches 256; Conservative 0; Mismatches 193; Indels 0; Gaps 0;
 QY 111 CAGCAAGCGAGCGCGGCTCGAGGAGCGGAGCTGAGCCCGGCACATCTCCCGGC 170
 DB 151 CACCTACAAAGGACGAGCAAGAACTTTCACCTCCGACCCGAGATCCACCCCGGCT 210
 QY 171 CATCCCGTATCATACCGCGGCTTACTCCGTAAGTGTCTGTGGGCTTGTGGGCA 230
 DB 211 GACCGGAGTTTATCCCTCTGTATTCAGGGAAGGTGTGTGTGGCTCGTGGGCA 270
 QY 231 CTCGCTGTATGTTGTGTATTCATCCGATACAAAGATGAGAGCAACCAATTTA 290
 DB 271 CAGGTGTATCATATGATTTGTCCACACCAAGAAAGAGTCCGTACCAACTCTA 330
 QY 291 CATATTTAATCTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTCAAGATAC 350
 DB 331 CATCTCAACCTGGCATGCGGACGAGCTTTCATGTGGGCTGCTGCTTCTGTGCGGT 390

QY 351 GGCTACTGATGATTCCTGGCCCTTTGGGGATGCTGTGCAAGATGTAATTTCAT 410
 DB 391 GAGAAAGCGTCTGCTCTCTGAGCCCTTCGAGCTGCTCATGATGCCGTGTGATGACGT 450
 QY 411 TGATTAACCAACATGTTACACGACATCTTCACTTACCATGATGAGCGGACGCTA 470
 DB 451 GAGCGCATCAACAGTTCACGAGCATCTTGTGCTGACAGATGTGTCGTGACCGCTA 510
 QY 471 CATTCGCTGTGTCACCCCTGTGAAGCTTTGACTTCGACACACCTTTGAAGCAAGAT 530
 DB 511 CTTGCTGTGTGACACCCCATCCGCTCTTGTGTGTGCGCGCGAGGTTGCGAAGGC 570
 QY 531 CATCAATATCTGCATCTGCTGTGCT 559
 DB 571 CATCAGACCAACGCTGTGCGGGGCTCT 599
 RESULT 95
 CD559647 791 bp mRNA linear EST 26-NOV-2003
 LOCUS AGENCOURT_14496669 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971826 5', mRNA sequence.
 ACCESSION CD559647
 VERSION CD559647.2 GI:38559005
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 791)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585715.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK2 row: d column: 05
 High quality sequence start: 4
 High quality sequence stop: 766.
 Location/Qualifiers
 1..791
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971826"
 /csize_type="mixed"
 /lab_host="DH5A (71 phase-resistant)"
 /clone_1ib="NIH MGC 195"
 /note="Vector: PDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BP Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the PDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please

visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 12.1%; Score 139.8; DB 14; Length 791;
 Best Local Similarity 54.8%; Pred. No. 1.2e-16;
 Matches 345; Conservative 0; Mismatches 272; Indels 12; Gaps 3;
 QY 166 CCGGCATCCCGGTATCATACGCGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTG 225
 DB 147 CCGTTCCTTATGCTCTCTACCCGCGGTGACTCCGGATGTGCTGTGGGGCTGACT 206
 QY 226 GCGCACTGCTGTGATGTGTGATTCATCCGATACAAABAATGAAGACCAACCAAC 285
 DB 207 GCGCAACGCGCGGTATCTGTATATCTTAAGAGGCGCCCAAGATGAAGCGGTGAAC 266
 QY 286 ATTACATATTTAACTGCTTGGCAGATGCTTAGTTACTACAAACATGCCCTTTGAC 345
 DB 267 GTGTTCAATCCGAACTGCGCGGTCCGCGACGCGGCTTTCAACGCTGTGACTGCCGTCAC 326
 QY 346 AGTACGCTCTACTTATGATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATGTAATT 405
 DB 327 ATCGCGGAGACCTGCTCAGTACTGGCCCTTCGCGGAGTGTCTGTGCAAGCTGTGCTG 386
 QY 406 TCCATTGATTTACTAACAATGTCACAGCATCTTACCTTGACATGATGAGCGGTGAC 465
 DB 387 GCGGTGACCACTAACAATCTTTCACGACATCTTCTAGCCGTATGAGCGGTGAC 446
 QY 466 CGCTCATTTGCGGTGTCACCCCGTGAAGC-----TTTGAATTCGACACCCCTTG 519
 DB 447 CGATACCTGTGTGTCTGTGACCGGTGAGTCCGCGCATGCTTGGCGCATACCGG 506
 QY 520 AAGGCAAGATCATATATCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
 DB 507 GGGGGAAGGTGTGACGCTGT 566
 QY 580 ATATGCTTGTGAGGACCAAACTCAGGAAGACGTGATGATGATGATGATGATGATGATGAT 639
 DB 567 TTCTCTTTCGCTGT 623
 QY 640 TTCCGAGATGATGATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
 DB 624 TTCCGCTGT 680
 QY 700 GCTTGT 759
 DB 681 GCTTGT 740
 QY 760 AAGAGCTCCGCGCTCTTCTGTGCTCCG 788
 DB 741 CCGGCGGTGCGGCTCCGCTGTGAGCCAG 769
 RESULT 96
 BE252309 642 bp mRNA linear EST 13-JUL-2000
 LOCUS 601114162P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354783 5',
 DEFINITION mRNA sequence.
 ACCESSION BE252309
 VERSION BE252309.1 GI:9122447
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 642)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LHCN157 row: 1 column: 16
 High quality sequence stop: 630.

FEATURES

source
 1..642
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3354783"
 /cvsuise_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_16"
 /note="Organ: eye; Vector: pOT7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.1%; Score 139.4; DB 10; Length 642;
 Best Local Similarity 53.8%; Pred. No. 1.3e-16;

Matches 334; Conservative 0; Mismatches 281; Indels 6; Gaps 2;

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QY 155 GGCACATCTCCCGGCATCCGGTCATGACGCGGCTTACCTCCGTAAGTGTGCTG 214
DB 20 CCTACTATGACCTGACCAAGCAAGAGAGTCTCTCATATTAATTTTGTGCTGATCA 79
QY 215 TGGGCTGTGGGCACTGCTGCTGATGTTGTGATCATCCGATACCAAGATGAAGA 274
DB 80 TTGGGTGTGTG3CAACACATTTGATTAATGATCCTCCGCTATGCAAGATGAAGA 139
QY 275 CAGCAACCAACATTTATATTAACCTGCTTGGAGAGATGTTAGTACTAACAACA 334
DB 140 CCATACCAACATTTATATCTCAACTGCGCATGAGATAGCTCTTCATGCTGGGTC 199
QY 335 TGCCTTTTCAAGTACGCTCTAATTGATGAAATTCCTGGCTTTGGGAGATGCTGCA 394
DB 200 TGCCTTTTCTGCTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
QY 335 AGATGATATTTCCATGATTTACTACACATGTTCAACAGACTTTTCACTTGCACATGA 454
DB 260 GGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319
QY 455 TGAAGGTGAGACCGTACATTTGCTGTGTCACCCCGTGAAGGCTTTGACCTTCCGACAC 514
DB 320 TGAAGATGAGACCGATATCTGCTGTGTCACCCCATCAAGTCCGCAAGTGAAGAGAC 379
QY 515 CTTGAAGGCAAGATCATATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
DB 380 CCGGACCGGCAAGATGATCAACATGCTGTGTGGGAGTCTCTCT---GCTGTGATCT 436
QY 575 CTGCAATAGTCTTGAAGGACCAAGTCAAGGAGAGAGTGTGATCTTGAAGTGTCTCT 634
DB 437 TGCATATATATATATCTGAGGCTCCGAGGCAACATGAGGAGAGGAGGAGGAGCA 496
QY 635 TGAAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694
DB 497 TCAATGAGGCAAGTGAATCTGGGGCTTGTGATCAAGGTTTCTAT---CATCTACCTTTCA 553
QY 695 TCTTTGCTTGTGATCTCTGCTCTCATATCATGCTGTGCTAACCCTGATGATCTGCTG 754
DB 554 TTTGGGGTCTCTGTATACCCCTCAACATCATCTGCTTGTCTACCTGTTATATATCA 613
QY 755 GTCTCAAGAGGCTCGGCTCC 775
DB 614 AGGTGAAGTCTCTGGAATCC 634

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RESULT 97
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 LOCUS 603855026r1 CSEQCHN62 Gallus gallus CDNA clone CHEST85748 5', mRNA
 DEFINITION sequence.

ACCESSION BU317021.1 GI:25825022
 VERSION BU317021.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Archobania; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Phasianidae; Gallus.
 1 (bases 1 to 793)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Trickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 2233534
 PUBMED 12445392

COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..793
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, H1sex"
 /db_xref="taxon:9031"
 /clone="CHEST85748"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_id="CSEQCHN62"
 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI. This normalized library was
 constructed from 1 million independent clones. CDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 12.1%; Score 139.4; DB 13; Length 793;
 Best Local Similarity 71.8%; Pred. No. 1.4e-16;

Matches 196; Conservative 0; Mismatches 76; Indels 1; Gaps 1;

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QY 159 CATCTCCCGCCCATCCGGTCTATCATCAAGCGGCTCTACTCCGTAGTGTTCGCTGGG 218
DB 89 CCGCGCGCTGAGATCAAGATACCAATTTGGTGGCTGCTACTCATATGTGTGATGTTGGG 148
QY 219 CTTGGTGGGCACTCGTGTGATGTTGCTGATCATCCATACCAAGATGAAGACAGC 278
DB 149 GCTGTGGGCACTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 208
QY 279 AACCAATTTATATTAACCTGCTTGGAGATGCTTATAGTACTACCAACATGTC 338
DB 209 AACCAATTTATATCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTACC 268
QY 339 CTTTCAGATGACGCTACTGATGATGATTCCTGCTTTTGGGAGATGCTGTGCAAGAT 398

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Db 269 CTTCAGGGGTACAGACACGTTCTGGGCTTGGCC-TTTGGCAATGTCTCGCAAGAT 327
 QY 399 AGTAATTTCCATTGATTACTACACACATTTTCAC 431
 Db 328 CGCTATCTCTATAGACTACTACAAACATGTTTAC 360

RESULT 98
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 LOCUS AGENCOURT 14740155 NIH_MGC_145 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971895 5', mRNA sequence.
 CFI47826
 VERSION CFI47826.1 GI:33244094
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC http://mgi.nci.nih.gov/
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga9b8-r@mail.nih.gov
 Tissue Procurement: GPCR Consortium
 cDNA Library Preparation: GPCR Consortium
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRB102 row: b column: 02
 High quality sequence stop: 728.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="mixed"
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 /clone_11b="NIH_MGC_145"
 /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
 varies by clone; ORFs were PCR-amplified and cloned into
 pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
 clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
 5'-EcoRV-XbaI/XhoI-3', EcoRV (TA cloned, non-directional).
 For information about which gene each clone represents,
 please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.1%; Score 139.2; DB 14; Length 729;
 Best Local Similarity 54.1%; Pred. No. 1.5e-16;
 Matches 329; Conservative 0; Mismatches 273; Indels 6; Gaps 2;

QY 155 CGCAATCTCCCGGCGGCGGTCATATACGGCGGTCTACTCGTAGTGTGCTCG 214
 Db 116 CGTACTATGACCTGACACAGCAATGACGCTCTCATCTTATTTTGGGTCTGCATCA 175
 QY 215 TGGGCTGTGGGCAACGCTGTCATGTCATCGATACACAAAGATGAAGA 274
 Db 176 TTGGGTGTGTGGCAACACACTTGTATTTATGTCTCTCGCTATGCCAAGATGAAGA 235
 QY 275 CAGCAACCAACATTTACATATTTAACTGCTTGGCAGATGCTTATGTTACTACACCA 334
 Db 226 CCATCACCACCAATTTACATCTCTCAACCTTGGCATGATAGGCTTTCATGCTGGGTC 295

QY 335 TGGCCCTTCAGAGTAAGGCTCTACTTGAATTTCCGCTTTGGGGATGTGCTGTGA 394
 Db 296 TGCCTTTCTGGCTATGACAGGTGCTCTGTGTCACATGGCCCTTTGGCAAGCCATTGGC 355
 QY 395 AGATAGTAATTTCCATTGATTACTACACATGTTGACAGCATCTTACCTGACCATA 454
 Db 356 GGGTGTGATGACCTGTGATGATGACATCAATCACTTTCACAGCATCTTCTGACGTCA 415
 QY 455 TGAGCTGAGACCGCTACATTTGCTGTGTCACCCCGTGAAGCTTTGACCTTCCGAC 514
 Db 416 TGAGCATCACCGAATACCTGCTGTGTGTCCACCCATCAAGTCGGCAAGTGAAGAGAC 475
 QY 515 CCTTAAGGCAAGATCATATCTGATCTGCTGTGTCATCTGTTGATCT 574
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 VERSION CD559646.2 GI:38559003
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 791)
 NIH-MGC http://mgi.nci.nih.gov/
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga9b8-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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FEATURES

source

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 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.0%; Score 138.6; DB 14; Length 791;
 Best Local Similarity 54.7%; Pred. No. 2e-16;
 Matches 342; Conservative 0; Mismatches 269; Indels 12; Gaps 3;

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 DB 155 CCGTTCCTATATGTGTCTGCTGCGCGCGGTATCTCGGGATCTGTGCTGTGGGCTGACT 214
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RESULT 100
 CD559648
 LOCUS CD559648 792 bp mRNA linear EST 26-NOV-2003

DEFINITION AGENCOURT.14496622 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971825 5', mRNA sequence.
 ACCESSION CD559648
 VERSION CD559648.2 GI:38559007
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 792)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585716.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: IRBK2 row: d column: 04
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FEATURES

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 /tissue_type="mixed"
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 /clone_lib="NIH_MGC_195"
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 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
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 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
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 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.0%; Score 138.2; DB 14; Length 792;
 Best Local Similarity 54.7%; Pred. No. 2e-16;
 Matches 344; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

QY 166 CCGGCCATCCCGCTATCATACAGGCGGTCTCTCCGTAGTGTGCTGCGGCTTGCTG 225
 DB 146 CCGTTCCTATATGTGTCTGCTGCGCGCGGTATCTCGGGATCTGTGCTGTGGGCTGACT 205
 QY 226 GGCACATGCTGTCATGTTCTGATCATCCGATACAAAGATGAGACAGCAACCAAC 285
 DB 206 GGCACACGCGCGCTATCTTGTATCTTAAGGGGCGCCAAAGATGAAGAGGTGACCAAC 265
 QY 286 ATTACATATTTAACTGCTTGTGCGAATGCTTTAGTTACTCAACCAATGCGCTTTGAG 345
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Db      566 TTCTCTTTGCTGGCGCTTA---CAGCAAGAGCTGCAAGTCCCAAGCTGTGGCTGAGC 622
OY      640 TTCCAGATGATGACTACTCTGCTGGGAGCCTTTCATGAGATGCGCTTCACTTT 699
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